

PROGRAM OF THE
**88TH ANNUAL MEETING OF THE
AMERICAN ASSOCIATION OF PHYSICAL
ANTHROPOLOGISTS**
MARCH 27 – 30, 2019

To be held at the

Hilton Cleveland Downtown

100 Lakeside Ave East • Cleveland, OH44114

AAPA Scientific Program Committee

Steven R. Leigh, Chair

Amanda Agnew	Rebecca Gilmour	Kent Johnson	Sean Prall
Kari Allen	C. Eduardo Guerra Amorim	Erin Kane	Melissa Schaefer
Ben Auerbach	Lauren Halenar-Price	Claire Kirchhoff	Elizabeth St Clair
Jonathan Bethard	Ashley Hammond	Myra Laird	Claire Terhune
Nicole Burt	Donna Harrison	Kristi Lewton	Sam Urlacher
James Calcagno	Geoff Hayes	Christina Nicholas	Qian Wang
Zachary Cofran	Amber Heard-Booth	Heather Norton	Timothy Webster
Paul Constantino	Brian Hemphill	Robert O'Malley	Katherine Weisensee
Lynn Copes	Nathan Holton	Alejandra Ortiz	Julie Wieczkowski
Jennifer Cramer	Rob Hoppa	Nicholas Passalacqua	Frank Williams
Andrew Deane	Jennifer Hotzman	Christine Pink	John Willman
Maureen Devlin	Rebecca Jabbour	Stephanie Poindexter	
Christina Fojas	Jessica Joganic	Emma Pomeroy	

AAPA Meetings Director

Lori Strong, Burk & Associates, Inc.

Cleveland Advance Team

Leslie C. Aiello	Edward H. Hagen	W. Scott McGraw
Anne L. Grauer	Christopher Kuzawa	Denise Su
M. Geoffrey Hayes	Steven R. Leigh	

Program Assistant

Kathleen McGuire

Local Arrangements Committee

Denise Su
Yohannes Haile-Selassie

2018-2019 AAPA Executive Committee

Leslie C. Aiello
President

Anne L. Grauer
President-elect

Steven R. Leigh
Vice President and Program Chair

Rachel Caspari
Treasurer

Gabriela Cabana
Secretary

Peter T. Ellison
Editor, *American Journal of Physical Anthropology*

Lyle W. Konigsberg
Editor, *Yearbook of Physical Anthropology*

Nathaniel Dominy
Career Development

Christina Torres-Rouff
Student Affairs

Lisa Sattenspiel
Membership

Robin Nelson
History and Honors

MESSAGE FROM THE VP & PROGRAM CHAIR

Welcome!

It is my great pleasure to welcome you to the 2019 meeting of the American Association of Physical Anthropologists. This year's meeting is our 88th, and will be held in Cleveland, Ohio. The main conference hotel, the Hilton Downtown Cleveland, is attached to our main venue, the Huntington Convention Center. We are excited to be visiting Cleveland for the first time since 1946, and particularly delighted to be partnering closely with the renown **Cleveland Museum of Natural History (CMNH)**, given the tremendous role and impacts the museum has had for our discipline. We are grateful to our colleagues from CMNH and local arrangements committee, Denise Su and Yohannes Haile-Selassie.

Scientific Program

Our program includes almost 1100 peer-reviewed scientific papers, which will be presented in either podium or poster sessions beginning Thursday morning. The 62 scientific sessions include 7 invited podium symposia, 14 invited poster symposia, 18 contributed podium sessions, and 23 contributed poster sessions. In addition, there are 15 innovative and exciting workshop sessions that run in parallel to the scientific program. Once again, our program is truly international, with scientists from all over the world including Africa, Asia, Australia, Europe, Latin America, and the Middle East. We are pleased to be joined in Cleveland by our partner organizations, the **Paleopathology Association (PPA)**, the **Human Biology Association (HBA)**, the **American Association for Anthropological Genetics (AAAG)**, and the **Dental Anthropology Association (DAA)**. The **American Anthropological Association (AAA)** is also joining us in sponsoring a session this year.

Programming officially begins on Wednesday, March 27, 2019, with the **Committee on Diversity Undergraduate Research Symposium** (open to everyone from 6:00-8:00 pm) and the **Opening Reception** (8:00-11:00 pm). The Convention Center is truly an exceptional space, and will promote a very productive set of meetings.

We've grown in size, complexity, and scope of our meetings. Like last year, podium presentations need to be uploaded onto a central secure server in the Speaker Ready Room no later than a half day before the

presentation. This server will then "push" presentations to the appropriate meeting room and will be available for the session.

Schedule and Poster Session Timing. This year's daily sessions schedule will follow a similar timetable to previous years. This includes morning (8:00 am) and afternoon (2:30 pm) podium sessions, with invited poster symposia starting at the same times. This year, the Convention Center affords us adequate space for all-day poster sessions. Poster set-up will begin at 8:00 am, and end at 9:00 am, with sessions opening at 10:00 am. Even-numbered posters will have presenters in attendance at 1:30-2:30 pm, while presenters will be present at odd-numbered posters from 6:00-7:00pm on Thursday and Saturday (5:30-6:30pm on Friday to allow Business Meeting attendance). Posters should be removed from 7:00-7:30pm on Thursday and Saturday (6:30-7:00 pm on Friday). The start (2:30 pm) of podium presentations and invited poster symposia allows dedicated time for viewing of posters as well as an assortment of lunchtime events and workshops. Given the complexity of our meetings, we are fortunate to again have an **AAPA Meetings App**, developed by Ed Hagen, to help us track times and locations! The app is available for both Android and Apple.

Joint sessions. Our joint AAPA-PPA session, **The Evolution of Syphilis: A New Approach**, organized by Brenda Baker, will be held on Saturday afternoon. The joint AAPA-AAAG-HBA and American Anthropological Association (AAA) session this year is also our Wiley Symposium, and will be held on Saturday morning. The session is **Interpreting and Communicating Genetic Variation in 2019: A Conversation on Race**, organized by Jennifer Raff. The **Presidential Panel** will be held immediately following this symposium, and will offer a chance to extend the discussion of topics raised in the symposium.

Workshops

This year we have planned a number of workshops that occur in conjunction with our annual meeting. Because of space limitations, some of the workshops and events may require pre-registration (information is available on our meeting website; pre-registration closes March 15).

MESSAGE FROM THE VP & PROGRAM CHAIR

These events include a full slate of workshops, with six scheduled for Wednesday, three on Thursday, four on Friday, and then two on Saturday. The workshops cover a range of important topics. The CMNH is also sponsoring a Wednesday workshop at the museum engaging with the Hamann-Todd Collection. Our workshops should afford special professional opportunities to a broad range of our membership, and we encourage you to choose, and if necessary, register for workshops that are of interest.

Special Events

On Thursday, we are excited to hold our annual **Auction**, which starts as a silent auction (10:00 am-7:00 pm) and ends with the always entertaining live auction (7:00-8:30 pm). Once again, it will be emceed by auctioneer Jon Bethard. Each year, the auction raises thousands of dollars to support Pollitzer Student Travel Awards. Please participate through donations (contact co-organizers Myra Laird [U Chicago] and Shara Bailey [NYU], or Jon Bethard [USF], if interested) and by bidding on our array of tantalizing auction items. As the meetings approach, we will update you on other special events.

Friday, following the conclusion of the scientific sessions, we will hold the annual **Business Meeting and Awards Presentation** (6:30-8:30 pm). The critically important vote concerning our name change will be conducted at the meeting, so we strongly encourage attendance by all voting members. In addition, the meeting will include acknowledgement of this year's IDEAS Scholars, Early Career Grants, and Pollitzer and COD Undergraduate Research travel awards, as well as presentations of the Charles R. Darwin Lifetime Achievement Award (awarded to Professor Matt Cartmill) and the Gabriel W. Lasker Service Award (awarded to Professor Susan Antón). Please join us in celebrating this year's outstanding winners.

This year's **Presidential Panel** (Saturday, 1-2:30pm) focuses on scientific and public discourse involving genetics and race: a topical issue that biological anthropologists are uniquely positioned to evaluate, discuss, and contribute. It follows the AAPA-AAAG-AAA-HBA sponsored symposium, **Interpreting and Communicating Genetic Variation in 2019: A**

Conversation on Race. The Presidential Panel is an open session that will offer guided discussion and the opportunity to exchange ideas on the important issues raised in the symposium. Everyone is encouraged to attend and participate.

Saturday brings our meetings to a close, with the **Student Awards Ceremony and Closing Reception** from 6:00-9:00 pm. Please join us to learn who won the 2019 Student Presentation Awards!

Finally, as we approach the meetings, we will be publicizing additional information regarding special events. These will be listed in the final meetings program.

Acknowledgements and Appreciation

My sincere thanks to everyone who helped assemble the 2019 program. Thanks are due to our extraordinary business partners, Lori Strong and her team (from Burk & Associates), as well as Ed Hagen (our webmaster, app developer, and member of the Cleveland Advance Team). We are immensely grateful to the 50 remarkable and dedicated members of our Program Committee, who conducted and completed reviews thoughtfully, thoroughly, and expeditiously. We also thank the Cleveland Advance Team. The team includes our colleagues and representatives from Burk who came together in Cleveland in January to arrange the scientific program and to finalize hotel details. The program assistant, Kathleen McGuire, has been a tremendous help, as have the Officers and other members of the Executive Committee. Special thanks to Leslie Aiello for stepping in on numerous occasions to help with details and evaluate workshop proposals. Finally, we extend our most sincere thanks to the Local Arrangements Committee, Dr. Denise Su and Yohannes Haile-Selassie. These meetings would not have been possible without all these exemplary individuals, so please join me in thanking them when you see them in Cleveland!

Steve Leigh
AAPA Vice President and Program Chair

ABSTRACTS

Mating behavior and paternity in wild woolly monkeys (*Lagothrix lagotricha poeppigii*): is mating success a good predictor of reproductive success?

LAURA ABONDANO¹, KELSEY M. ELLIS^{1,2} and ANTHONY DI FIORE¹

¹Anthropology, University of Texas at Austin, ²Anthropology, Miami University

Among primates, males' reproductive success is often correlated with the number of copulations recorded during behavioral observations. However, observed copulations are not always an accurate predictor of offspring production. We investigated the relationship between observed copulation data and genetic paternity over four birth seasons (2013-2017) in three groups of wild woolly monkeys (*Lagothrix lagotricha poeppigii*) in Amazonian Ecuador. Woolly monkeys live in multimale-multifemale social groups and are characterized as having a promiscuous mating system, where animals of both sexes routinely mate with multiple partners. Though groups typically contain only a single "large" adult male, distinguished by his exaggerated secondary sexual characteristics, females are observed to mate with males of all ages and sizes. We genotyped a total of 21 infants, their dams, and 25 potential sires from both focal and neighboring groups using a panel of 12 polymorphic STR loci and then assessed paternity using maximum likelihood methods. More than half of all offspring (52%) were sired by the resident "large" adult male in each group, which is more than expected based on their proportional representation in each group ($p < 0.05$). However, for the 154 copulations recorded over the same time period, "large" males were not seen copulating more often than expected. Our results suggest that mating success in woolly monkeys is not a good predictor of male reproductive success, which could be due to female choice for "large" males during their peak fertile period and/or reflect an important role for sperm competition in the mating system.

Funded by NSF (BCS 1540403, 1638822, 1732326), the L.S.B. Leakey Foundation, the Wenner-Gren Foundation, the National Geographic Society, and the University of Texas at Austin.

The Deciduous Dilemma – New perspectives from Neolithic Northern Vietnam for studying health and stress in infants

ALISHA B. ADAMS¹, SIAN E. HALCROW¹ and MARC F. OXENHAM²

¹Biological Anthropology Research Group, Department of Anatomy, University of Otago, ²ANU College of Arts and Social Sciences, Australian National University

The study of childhood stress through linear enamel hypoplasia of permanent dentition is commonplace in bioarchaeology. However, the use of deciduous dentition to assess linear

enamel hypoplasia is difficult due to morphological differences that may mask these indicators, thereby inhibiting our ability to study *in-utero* and infant stress. Stress in early development has not been studied in detail, especially within prehistoric contexts, despite it being a sensitive indicator of overall population health. This paper examines the use of topographic profiling of enamel, a microscopic method of measuring changes in enamel depth, to identify linear enamel hypoplasia on modern human deciduous dentition, using a sample of mandibular ($n=10$) and maxillary ($n=10$) incisors and canines from Neolithic Northern Vietnam, the site of Man Bac. The micropolynomial method of quantifying enamel depth changes was used to determine if significant changes indicative of hypoplastic defects could be measured in tooth enamel. The preliminary results of this study show that linear enamel hypoplasias are present within deciduous enamel and they occur throughout tooth development including the *in-utero* period, and interestingly, these stress episodes appear to extend for several weeks at a time. The results of this study are interpreted within the context of changing subsistence strategies within Neolithic Northern Vietnam, and illustrates the use that deciduous dentition has for understanding maternal-infant stress in the past.

University of Otago Doctoral Scholarship.

The impact of sensory mode on anti-predator responses of Rylands' bald-faced saki monkeys (*Pithecia rylandsi*) in Peru

DARA B. ADAMS¹ and DAWN M. KITCHEN^{1,2}

¹Anthropology, The Ohio State University, Columbus, ²Anthropology, The Ohio State University, Mansfield

Although acoustic playbacks are considered a reliable method of simulating predator presence, the mode of presentation may significantly impact prey behavioral responses based on which sensory modality dominates. Here, we conducted predator simulation experiments on wild Rylands' bald-faced saki monkeys (*Pithecia rylandsi*) at La Estación Biológica Los Amigos in southeastern Peru to test whether sakis vary responses to presentations in different sensory modes. We exposed sakis to acoustic playbacks ($n = 26$) and visual models ($n = 12$) of harpy eagle (*Harpia harpyja*) and jaguar (*Panthera onca*) stimuli. Presentation style (audio vs. visual) affected the strength and type of behaviors elicited. Regardless of predator type, sakis responded significantly quicker ($F_{1,31} = 6.294$; $p = 0.018$) to visual models (mean + SE: 4.9 ± 0.7 s) than to playbacks (23.00 ± 4.5 s). While subjects immediately moved toward models in all visual experiments (12 of 12 trials, 100%), they rarely approached the speaker in playbacks (6 of 26 trials, 23%). Similarly, individuals emitted significantly more calls ($F_{1,36} = 30.854$,

$p < 0.001$) following exposure to visual models (81.4 ± 28.3 calls) than playbacks (7.0 ± 2.5 calls) and resumed normal activity (e.g., foraging or feeding) significantly sooner ($F_{1,33} = 18.674$, $p < 0.001$) after exposure to playbacks (293.3 ± 61.8 s) than visual models (1710.1 ± 342.4 s). These vastly different responses to visual and acoustic simulations call into question the reliability of using acoustic-only stimuli to assess anti-predator behavior in some primate species.

This research was supported by National Science Foundation (BCS-1341174), Animal Behavior Society, The Society for Integrative and Comparative Biology, Tinker Foundation, and The Ohio State University (Columbus and Mansfield)

Race science and its misuse of research in biological anthropology

DONOVAN M. ADAMS and MARIN A. PILLOUD
Anthropology, University of Nevada, Reno

Despite valid scientific research dismissing race science, this field of inquiry is seeing a current resurgence. Various organizations, known to be associated with white nationalist/supremacist groups, fund and sponsor "academic" journals noted for their publication of content related to race science. Within these journals, anthropological research is often mischaracterized or misinterpreted to validate racist agendas. To understand the depths of this misuse, a content analysis was conducted on three such journals: *Mankind Quarterly* (1992-2018); *The Journal of Social, Political, and Economic Studies* (1994-2018); and *The Occidental Quarterly* (2000-2018). Data were collected on the origin of research, the types of data utilized in the article, attitudes towards racial differences and hierarchy, terminology use, average impact, and attitude towards the scientific community ($n=137$).

Results show a pervasive presence of research and academic discussion regarding racial differences, racial hierarchy, and eugenics. Authors express a conspiratorial view of the majority of the scientific community, with the opinion that they are fighting for the truth against politically correct academia. Despite their mistrust of science, authors routinely incorporate scientific research to validate their claims. Approximately 26.0% of research in *Mankind Quarterly* was bioanthropological in nature, drawing from topics on genetics, skeletal and dental morphology, anthropometrics, and paleopathology to underscore racial differences. As biological anthropologists, it is important that we are well informed of race science and its misuse of our work to justify racist ideologies, so that as a discipline we are positioned to combat the misappropriation of science and further marginalization of oppressed groups.

ABSTRACTS

Patterns of variation in trabecular bone volume fraction in the calcaneus and C2 vertebrae of *H. sapiens*

BRIAN J. ADDISON¹ and DANIEL E. LIEBERMAN²

¹Human Evolutionary Biology, Harvard University,
²Human Evolutionary Biology, Harvard University

Trabecular bone volume fraction (BVF) is influenced by variations in locomotor patterns, and recent declines in BVF in *H. sapiens* are often attributed to sedentary lifestyles in modern populations. However, this inference is limited by studies of bony regions with highly complex loading patterns and regions that experience large mechanical stimuli from locomotor forces. This study therefore tests the hypothesis that presumed variations in mechanical loading between populations can predict recent declines in BVF observed in *H. sapiens*. We examined BVF using high-resolution microCT scanning in four *H. sapiens* populations: the Pleistocene, semi-sedentary Natufians; Holocene hunter-gatherers from Point Hope, Alaska; Holocene nomadic pastoralists from medieval Europe; and modern, sedentary Americans. We studied BVF in the calcaneus, where locomotor forces are less-variable and better-understood, and in C2 vertebrae where mechanical stimuli from locomotion is likely reduced. We used ANOVA to compare BVF between groups, the Tukey-HSD method to correct for multiple comparisons and statistical significance was set to $p < 0.05$. Natufians had 36%, 46% and 46% greater calcaneal tuberosity BVF than the Alaskan ($p = 0.02$), European ($p = 0.005$) and modern American ($p = 0.002$) groups. Natufian C2 BVF was 53% and 25% greater than in the Alaskan ($p = 0.0001$) and European ($p = 0.048$) populations (modern American C2 vertebrae were not examined). In total, these results suggest that BVF declined systemically in *H. sapiens* after the Pleistocene and that mechanical loading alone cannot explain the observed decline.

This project was funded by the Leakey Foundation (#06180443-01) and the Wenner Gren Foundation (#06321163-01).

Skeletal-wide variation in phylogenetic signal across *Order Primates*

GINA M. AGOSTINI^{1,2} and JASON M. KAMILAR^{3,4}

¹Department of Anthropology, University at Buffalo,
²Division of Biological Infrastructure, National Science Foundation, ³Department of Anthropology, University of Massachusetts Amherst,
⁴Organismic and Evolutionary Biology, University of Massachusetts Amherst

Fragmentary skeletal material is critical for reconstructing phylogeny, particularly for primates as they possess extreme morphological diversity. Extinct species are often phenotypically mosaic, making it difficult to discern species affiliation. However, few studies have assessed

how reliably trait variation reflects underlying phylogeny (phylogenetic signal), particularly for postcrania. This is especially true at broad (Order) taxonomic levels reflecting very ancient relationships.

Here we calculated phylogenetic signal (Blomberg's *K*) for 158 continuous, mass-standardized traits reflecting all major primate lineages (30-155 taxa per trait). We subsequently investigated whether there was significant variation in *K* across skeletal regions, including the dentition, skull, vertebrae, girdles, and limb segments. We also assessed the confounding effects of dimorphism and covariation by calculating sex-specific and multivariate *K* values for a subset of data.

K ranged widely but was generally low-to-moderate, suggesting most trait variation did not strongly reflect phylogeny. However, there were significant differences in *K* across skeletal regions (p -value < 0.001). *K* values were highest for vertebrae and *os coxae* ($p < 0.05$), higher for limbs than crania ($p < 0.006$), higher for proximal than distal limb segments ($p < 0.004$), and higher for forelimbs than hind limbs ($p < 0.001$). There was no difference in the strength or pattern of *K* between sexes, and multivariate *K* was not higher than that calculated trait-by-trait.

These results suggest that a combination of vertebral, pelvic, and proximal limb traits may produce the most reliable phylogenies at broad taxonomic levels, such as those reflecting the transition from proto-primates to primates.

Hierarchical Patterns of Constraint and Functional Trait Complexes in the Primate Shoulder and Hip Regions

ELIZABETH R. AGOSTO and BENJAMIN M. AUERBACH

Anthropology, The University of Tennessee - Knoxville

Studies of primate shoulder evolution often focus on traits of the scapula alone. However, the scapula shares both functional and developmental relationships with the basicranium, vertebral column, humerus, and clavicle. As a limb girdle, it also has analogous characteristics to the pelvis. Genetic covariances underlie these relationships, and these covariances among traits result in non-independent evolution of morphologies. Thus, accounting for the constraints imposed by these covariances is essential for accurate models of trait responses to selection.

To investigate this, we obtained cranial and postcranial linear dimensions from a sample of 66 adult *Macaca mulatta*. We examine if the functional and developmental relationships between the scapula and clavicle with the basicranium are reflected in genetic covariances among their morphological traits, that in turn would influence the ability of these elements to respond to

selection. Pelvic dimensions are included as well, given developmental and functional parallels between the limb girdles. We calculated evolvability in R following equations in Hansen and Houle (2008. *J Evol Biol* 21:1201-1219) to assess our questions. Lower evolvability indicates greater constraint among traits. All dimensions were standardized by measurement means.

Results show a privileged relationship between the scapula and basicranium, where the evolvability indices, especially conditional evolvability, are significantly lower than the evolvabilities of the scapula and pelvis, the basicranium and pelvis, and all three regions together. We conclude that the scapula and basicranium constrain each other in response to directional selection, forming a functional trait complex, and has important implications for models of shoulder evolution.

This research is supported by a National Science Foundation Doctoral Dissertation Improvement Grant (NSF BCS-1825995).

Effective seed dispersal of an economically important plant resource by western chimpanzees at Fongoli, Senegal

WILLIAM D. AGUADO¹, HALDRE S. ROGERS², STACY LINDSHIELD³ and JILL D. PRUETZ⁴

¹Anthropology, Rutgers, the State University of New Jersey, ²Ecology, Evolution and Organismal Biology, Iowa State University, ³Anthropology, Purdue University, ⁴Anthropology, Texas State University

Seed-dispersing primates maintain natural plant populations throughout the tropics and this presumably includes plants that are valuable resources for humans. However, few studies have documented effective dispersal—dispersal that results in the production of new individual plants—for such resources. We examined whether western chimpanzees (*Pan troglodytes verus*) at Fongoli, Senegal effectively disperse the seeds of an economically important fruit resource, *Saba senegalensis*. We hypothesized that these apes promote the early stages of *Saba* regeneration through the beneficial effects of gut passage and dispersal to high-quality sites. We conducted germination experiments comparing the germination capacity of gut-passed seeds to seeds removed from fruits and recorded the success rates of germination and seedling establishment of chimpanzee-dispersed seeds *in situ*. Germination trials showed that gut-passed seeds germinated faster and had an increased likelihood of germination. Chimpanzee-dispersed seeds deposited *in situ* germinated and established and were distributed non-randomly throughout their home range. Seeds were dispersed to high-quality gallery forest habitats more often than expected, and to low-quality grassland habitats less often than expected. This suggests that these critically endangered apes are effective *Saba* seed dispersers that aid in the early stages of *Saba* recruitment, and likely play an important

ABSTRACTS

role in maintaining its populations. This insight that chimpanzees can promote the well-being of people by sustaining a valued resource should help justify their protection. Exploring the benefits accrued to humans via seed dispersing primates elsewhere may be a fruitful technique to promoting primate conservation globally.

Funding was provided by Iowa State University and the Center for Global and Regional Environmental Research, University of Iowa.

Evolutionary changes in neurocranial structure do not correlate with cortical reorganization in humans

JOSÉ LUIS ALATORRE WARREN¹, MARCIA PONCE DE LEÓN¹, WILLIAM D. HOPKINS^{2,3} and CHRISTOPH P.E. ZOLLIKOFER¹

¹Department of Anthropology, University of Zurich, ²Neuroscience Institute, Georgia State University, ³Division of Developmental and Cognitive Neuroscience, Yerkes National Primate Research Center

The human brain is approximately three times as large as that of our closest living relatives, the great apes, and exhibits autapomorphic sulcal patterns in several regions. Fossil neurocrania are regularly examined—both qualitatively and quantitatively—to document when and how these differences emerged during hominin evolution. Using MRI and same-individual CT/MRI data of 41 humans and 24 chimpanzees, we quantify the topographical relationships between brain sulci and internal and external neurocranial features, associated patterns of covariation and integration/modularity between brain and neurocranial features. Our results show a posterior shift of the pre- and postcentral gyri in human relative to chimpanzee brains, reflecting the well-documented reorganization of the opercular region. Likewise, human neurocrania differ from those of chimpanzees in having relatively larger parietal bones and a more anterior position of the cerebellar fossa. Modularity/integration analysis suggests that changes in neurocranial and brain morphologies occurred largely independently during human evolution.

Funded by Swiss NSF grant #31003A_135470 to CPEZ.

The role of spatial memory as it relates to nutritional balancing in Bornean orangutans (*Pongo pygmaeus wurmbii*)

SHAUJIN E. ALAVI¹ and ERIN R. VOGEL^{2,3}

¹Anthropology, University of California, Davis, ²Anthropology, Rutgers, the State University of New Jersey, ³The Center for Human Evolutionary Studies, Rutgers, the State University of New Jersey

Recent studies have demonstrated that macronutrient balancing plays an important role in primate foraging decisions. Macronutrients however, are bound to foods in environments with complex

spatial structures. An important question about the underlying mechanism behind foraging is how primates decide which resource to travel to next. We use simulation models to study the roles of perception and memory in orangutan nutritional balancing at the Tuanan Research Station in Central Kalimantan, Indonesia. First, a supervised machine learning algorithm was used to map the available nutrients at Tuanan. We then simulated individuals balancing macronutrients while foraging on the nutrient landscape. Simulations following a perception model and a memory model were compared to empirically observed orangutan nutritional intakes and spatial trajectories. The machine learning algorithm identified trees with 70–83% accuracy, providing a reasonably accurate model domain. The perception model overestimated non-protein intake relative to observed values, with a mean squared error of 4.53. The memory model however, matched the observed ratio of macronutrients precisely with a mean squared error of 0.16. Furthermore, orangutan movement exhibited uncorrelated movement between nearby resources, and correlated linear movement to far away resources (GAMM, $p = 0.004$). These results suggest that memory may be an important mechanism enabling orangutans to maintain their target ratio of macronutrients. Orangutans likely employ a flexible foraging strategy, switching between modes of behavior whereby they utilize nearby detectable resources and known far away resources, with their target resource updated as a function of their current nutritional status.

United States Agency for International Development; The Center for Human Evolutionary Studies; International Primatological Society, National Science Foundation (NSF-805182), Rutgers Department of Anthropology

New macaque remains from the Middle Pleistocene of Gruta da Aroeira, Portugal

DAVID M. ALBA¹, JOAN DAURA², MONTSERRAT SANZ², ELENA SANTOS^{3,4}, ALMUDENA S. YAGÜE², ERIC DELSON^{1,5,6,7,8} and JOÃO ZILHÃO^{10,11,9}

¹Institut Català de Paleontologia Miquel Crusafont, Universitat Autònoma de Barcelona, ²Grup de Recerca del Quaternari (GRQ)-SERP, Departament d'Història i Arqueologia, Universitat de Barcelona, ³Departamento de Paleontología, Facultad de Ciencias Geológicas, Universidad Complutense de Madrid, ⁴Centro Universidad Complutense de Madrid, Instituto de Salud Carlos III de Investigación sobre la Evolución y Comportamiento Humanos, ⁵Department of Anthropology, Lehman College of the City University of New York, ⁶Department of Vertebrate Paleontology, American Museum of Natural History, ⁷PhD Program in Anthropology, The Graduate Center of the City University of New York, ⁸New York Consortium in Evolutionary Primatology, New York, ⁹Departament d'Història i Arqueologia, Universitat de Barcelona, ¹⁰Institució Catalana de Recerca i Estudis Avançats, (ICREA), ¹¹UNIARQ-Centro de Arqueologia da

Universidade de Lisboa, Faculdade de Letras, Universidade de Lisboa

The Middle Pleistocene site of Gruta da Aroeira (formerly Galeria Pesada), in the Almonda karst system (Torres Novas, central Portugal), has yielded a rich Acheulean lithic assemblage coupled with a human cranium and associated faunal remains. Although the presence of macaques at Gruta da Aroeira was mentioned years ago, the material remains undescribed. Here we report a juvenile macaque mandible (ARO17-J8-Xa-934) that was recovered in 2017 from Unit 2 hard breccia, which is correlated to Marine Isotope Stage 11 and radiometrically dated to 436–390 ka. After mechanically preparing the specimen, a μ CT scan was performed to extract digital 3D models of the unerupted permanent teeth. The specimen preserves the symphysis and most of the left ramus and both corpora, including the erupted right dP_3-M_1 and left dP_4-M_1 , as well as the permanent incisors, canines, premolars and M_2 inside their crypts. The size and shape of the lower canine and third premolar indicate that the specimen belongs to a female individual that, based on dental eruption, would have died when 2–2.5 years old. The lower incisors appear devoid of lingual enamel and the molars display a bilophodont occlusal pattern with a generalized papionin morphology, congruent with the dentally-conservative genus *Macaca*. Dental size and proportions fit well with both extant *Macaca sylvanus* and its various extinct subspecies from the European Pleistocene. Pending a better characterization of these subspecies, the Gruta da Aroeira specimen is attributed to *M. sylvanus* cf. *pliocena* on biochronological and paleogeographic grounds.

Funded by the Generalitat de Catalunya (CERCA Program) and Ministerio de Economía y Competitividad: HAR2017-86509, CGL2015-65387-C3-2-P, CGL2016-76431-P, and CGL2017-82654-P (MINECO-AEI/FEDER EU); RYC-2015-17667 to J.D.; and IJCI-2017-33908 to M.S.

Osteological development of the foot during the Medieval to Post-Medieval transition

MALORIE E. ALBEE

Department of Anthropology, The Ohio State University

Research on the morphology of the human foot has focused almost exclusively on hominins and the origins of bipedalism. However, our biocultural environment has continued to place selective pressures on our skeletons. The rise of industrialization during the Medieval to Post-Medieval transition in England was an important shift in the human biocultural environment, and this study explored changes in the pedal bones associated with this environmental shift; specifically, frequencies of osteoarthritis, robusticity, and frequency and severity of enthesal changes.

ABSTRACTS

Moreover, the study explores whether these gross morphological changes contributed to differences in total length of the talus and calcaneus. The sample analyzed consists of metric and nonmetric data of 1466 individuals from 14 London sites (Medieval $n=8$, Post-Medieval $n=6$), available in the Oracle Wellcome Osteological Research Database (WORD). Tali and calcanei total lengths were compared between periods using t-tests as well as ANCOVAS to take into account the influence of several covariates (age, sex, stature, hypoplasia, non-specific infections, blood disorders, vitamin D deficiency, and osteoarthritis). Results show that tali and calcanei are significantly longer in the Medieval period ($p<0.001$). This relationship between period and pedal metrics remains statistically significant even when accounting for the effect of the covariates, suggesting that these differences cannot be attributed to differences in health between the periods. Instead, it is likely that cultural factors, such as changes in footwear and activity patterns between periods, may have contributed to differences in development of the tali and calcanei with the adoption of an industrialized life-style.

Men's secretory immunoglobulin-A, testosterone, and cortisol are significantly associated within a single day and across two sequential days

GRAHAM ALBERT¹, NICHOLAS LANDRY², TRIANA L. ORTIZ², JUSTIN M. CARRÉ², STEVEN A. ARNOCKY² and CAROLYN R. HODGES-SIMEON¹

¹Anthropology, Boston University, ²Psychology, Nipissing University

Previous studies show a positive relationship between testosterone (T) and secretory immunoglobulin-A (slgA) when saliva is sampled at a single time point, suggesting that men with relatively higher T levels have higher concentrations of one biomarker of mucosal immunity. The purpose of this investigation was to explore intra-individual associations between secretory slgA, cortisol (CORT), and T within a single day (i.e. morning vs. evening) and across 2 sequential days. As part of a larger study on health and human mating, 119 young men provided saliva samples at three time points, upon waking and before sleep on the first day and upon waking the following day. Samples were assayed in duplicate for slgA, T and CORT, and averaged for all analyses. To analyze within- and between-day relationships, we computed difference variables between the log transformed concentrations for all bio-markers for all sample provision times and compared them using Pearson correlations. Changes in T were significantly positively correlated with changes in slgA. Fluctuation of slgA and CORT from evening to the following morning were significantly negatively correlated. To analyze the interactive affect that T and CORT may have on slgA, we multiplied T and CORT

concentrations (T*CORT), and again computed difference variables. Changes in T*CORT were also significantly positively correlated with slgA variation. This provides the first evidence that salivary T and slgA concentrations are associated within a single day and across sequential days. These results have the potential to add to our understanding of the standard and stress-linked immunocompetence handicap hypotheses.

Glucocorticoid levels predict lifespan in wild female baboons

SUSAN C. ALBERTS^{1,2,3}, FERNANDO A. CAMPOS⁴, JEANNE ALTMANN⁵, LAURENCE GESQUIERE² and ELIZABETH A. ARCHIE^{5,6}

¹Evolutionary Anthropology, Duke University,

²Biology, Duke University, ³Institute of Primate Research, National Museums of Kenya,

⁴Anthropology, University of Texas San Antonio,

⁵Ecology and Evolutionary Biology, Princeton University, ⁶Biological Sciences, University of

Notre Dame

Glucocorticoid levels (GCs) are regularly measured in humans and other primates as a biological marker of stress. In a recent review, however, Beehner and Bergman (*Hormones & Behavior* 2017) reached the remarkable conclusion that not a single study has drawn a clear connection between environmental stressors, the GC-mediated stress response, and fitness-related outcomes. As a result, it remains unclear whether chronic stress (as indexed by GCs) influences lifespan in wild primates. To address this challenge, we used longitudinal data on wild female baboons to investigate the relationship between GC levels and survival—the single greatest determinant of fitness variation among female baboons. Using repeated measures of GCs from 197 adult females ($n=1784$ female-years), we show that elevated GCs predict survival in a time-varying Cox proportional hazards model ($p=0.029$). This relationship is even stronger ($p=0.005$) when controlling for the effects of age, dominance rank, social integration, group size, reproductive state, and seasonality on GC values, and it is not explained by collinearity between GCs and social integration, another known predictor of lifespan in this population. Importantly, our results are not trivially explained by a spike in GCs at the very end of females' lives. Instead, females who have chronically elevated GC levels have shorter lifespans. Together, our results both support the value of GCs as a window into primate health, fitness, and aging and suggest that they may mechanistically contribute to the established link between sociality and lifespan.

This research was funded by the National Institutes of Health, the National Science Foundation, the Leakey Foundation, and the Max Planck Institute for Demographic Research.

Got fish? Diet and dental health of the Late Intermediate (ca. 1000-1450 CE) peoples in the Atacama Desert, northern Chile

MARTA P. ALFONSO-DURRUTY¹, EUGENIA M. GAYÓ², VIVIEN G. STANDEN³, VICTORIA CASTRO^{4,5}, CLAUDIO LATORRE⁶, CALOGERO SANTORO⁷ and DANIELA VALENZUELA³

¹SASW, Kansas State University, ²Centro de Ciencia del Clima y la Resiliencia, Universidad de Concepción, ³Departamento de Antropología, Universidad de Tarapacá, ⁴Departamento de Antropología, Universidad Alberto Hurtado, ⁵Departamento de Antropología, Universidad de Chile, ⁶Instituto de Ecología y Biodiversidad, Pontificia Universidad Católica de Chile, ⁷Instituto de Alta Investigación, Universidad de Tarapacá

This study assesses the dietary diversity of Late Intermediate Period (LIP; 1000-1450 CE) groups in the Atacama Desert, Chile. Within the region's prehistory, the LIP corresponds to the regional developments that emerged after Tiwanaku's decline. While LIP coastal and inland groups were stylistically unified, their subsistence patterns differed. But, stable isotope (SI) analyses show they shared a diet composed mainly of marine resources. Seventy-seven individuals from a coastal (Cam-8) and two inland (Llu-54 and Az-8) archaeological sites were analyzed. Ten individuals from each site ($n = 30$) were selected for SI analyses ($d^{13}C_{coll}$ and $d^{15}N$). Two bayesian isotopic mixing models were used to estimate the relative contribution of different food sources (SIAR). Dental pathologies ($n=1845$ teeth) analyzed included: AMTL, alveolar reabsorption, caries, abscesses, fractures, and chipping. SI results show variations in the dietary contribution of C4 crops (Cam-8= $<9\%$; Llu-54= 14.2-17.4%; Az-8=14.3-20.5%), marine resources (Cam-8 & Llu-54= $>60\%$), and mammalian herbivores and domestic-wild plants (Az-8= $\sim 47\%$; Llu-54 and Cam-8= $<37\%$) by site. Trophic niche analyses showed Cam-8's to be homogenous and specialized in marine resources, while Llu-54 and Az-8 had broader trophic niches. Analyses of permanent teeth show that Llu-54 had the highest rates of AMTL (13.2%), caries (26.4%), and abscesses (10%), whereas Cam-8 had the highest degree of dental wear (Mode=4), chipping (22.3%) and fractures (3.3%). Results for the deciduous dentition follow similar trends. Both IS and dental pathology analyses showed dietary diversity between groups. These differences reflect variation in the types and relevance of food sources, as well as their preparation.

FONDECYT 1151046

ABSTRACTS

Age Indicators Reveal Population Information: A New Computational Framework for Estimating Ancestry from Pubic Symphyseal Shape

BRIDGET FB. ALGEE-HEWITT^{1,2} and JIEUN KIM²

¹Center for Comparative Studies in Race and Ethnicity, Stanford University, ²Scientific Computing, Florida State University

When estimating skeletal age from the pubic symphysis, prior knowledge of ancestry is advisable, as population-specific standards arguably produce more accurate approximations of chronological age. The correct determination of ancestry is a difficult task as the accuracy of its estimation is reliant upon the preservation and typicality of the diagnostic characteristics, choice of methods, availability of appropriate comparative samples, and the recovery context of the remains relative to practitioner experience. To reduce potential error associated with the misspecification of ancestry in adult age estimation, we propose a fully-computational framework to derive probabilistic estimates of continental ancestry from the pubic symphysis using the same data already shown to produce robust estimates of age-at-death. We apply three published shape algorithms to laser-scan generated coordinates for a mixed-sex sample of White, Black, and Hispanic adult skeletons to generate measures of pubic symphyseal surface morphology. We subject these measures to unsupervised model-based clustering for trihybrid ancestry estimation, discriminant function analysis for classification, and standard multivariate statistics to quantify the shape variation attributable to ancestry. Our analyses generate estimates in agreement with prior admixture studies, find that ancestry accounts for ~42% of variation in shape, and produce reasonable rates of classification, 63-91%. While we conclude that shape differences in the pubic symphysis are informative of both age and ancestry and it is possible to create a pipeline for their analysis, further work is needed to understand how environmental or life-history factors common to individuals sampled from the same labeled group may affect pubic symphyseal morphology.

NIJ award 2015-DN-BX-K010

Daily Lives of Samburu Pastoralist Children: Work, herding, and food consumption

DIANDRA ALLEN¹, CHARLES E. HILTON² and BILINDA STRAIGHT³

¹Anthropology, University at Albany - SUNY, ²Anthropology, University of North Carolina at Chapel Hill, ³Anthropology, Western Michigan University

In pastoralist societies of northern Kenya, children, aged 3-14 years, are tasked with economic responsibilities associated with livestock herding, domestic obligations, and allocare of younger

siblings. Mixed age groups of children lead livestock some distance away from the settlement, often away from direct supervision of adults and from the benefit of ready-food access during the day. Our study analyzes Samburu children's physical activities in conjunction with daily food consumption in a community where traditional diet has been replaced with low quality processed food such as maize meal. A focal follow approach was applied, sampling 5 boys and 4 girls each for over a 36-hour period. Physical activity levels (PALs) were examined through the use of non-invasive accelerometers and time allocation observations. Food consumption was monitored through direct observation and measurements by volume for each food type with additional 24-hour food recalls. Physical activity pattern differed between boys and girls, apparently driven by an early household application of the sexual division of labor. Time allocation indicated that girls are tasked more frequently with household economic work compared to boys. Additionally, food consumption patterns also differed by gender. Girls were more likely to be involved in food processing and preparation thereby allowing for greater access to predominately processed food throughout the day. However, boys engaged in small-scale hunting of birds and other animals, thus, supplementing their diets with protein and fat. The implications of our study are discussed within the context of energy balance during childhood in an energy-poor environment.

This research was funded by A Research Experience for Undergraduate Supplement to National Science Foundation Award #1728743, "A Bio-Cultural Investigation of Intergenerational Epigenetic Mechanisms" (Bilinda Straight, PI).

In Service to the Sultan: Biological affinity analysis of Vlach Ottoman vassals from southern Croatia

KATHRYN GROW ALLEN¹, MARIO ŠLAUS², ANITA ADAMIĆ HADŽIĆ² and NOREEN VON CRAMON-TAUBADEL³

¹Department of Anthropology/Sociology, Eastern Oregon University, ²Anthropological Center, Croatian Academy of Sciences and Arts, ³Buffalo Human Evolutionary Morphology Lab, Department of Anthropology, University at Buffalo

Since the 10th century, the term 'Vlach' was used as an ethnic determinant in Southeast Europe, communities under this title living and governing separately from non-Vlach populations. The true origins and identity of Vlach communities is a debated historical question. Biologically, both Slavic and pre-Slavic heritages have been credited. Alternatively, at certain times in history written records labelled communities as 'Vlach' based on a nomadic, pastoral lifestyle. With both cultural and biological definitions, this ethnicity is not well understood. During the Ottoman period in particular, Vlach could be a catch-all

administrative term for pastoral clans in service to the state, biological identities not considered as smaller pastoral communities were absorbed into this title.

This research analyzed a Vlach community of Ottoman vassals, examining whether cultural isolation and ethnic division were matched by biological distance. Metric and non-metric cranial variation highlighted the biological affinity of a southern Croatian Vlach population. A sample of 32 Vlach crania were compared to a nearby non-Vlach sample, as well as more distant Eurasian samples. Analyzing 32 cranial measurements and 24 non-metric variables with D²-matrices, Principal Coordinates Analysis, and Mean Measure of Divergence tests, results highlight a Vlach population with biological affinity most similar to the very proximate, nearby community. This begs consideration of the division maintained historically between these Vlach and non-Vlach populations, labelled as an ethnic divide. Analyses such as these remind us that ethnic divisions do not necessarily indicate biological divisions.

This material is based upon work supported by the National Science Foundation under grant no.1642007

Life histories, aging, and testosterone levels among Datoga, Hadza, and Qom men

LOUIS C. ALVARADO¹, CLAUDIA R. VALEGGIA², PETER T. ELLISON³, CAITLIN L. LEWARCH³ and MARTIN N. MULLER⁴

¹Anthropology, University at Albany-SUNY, ²Anthropology, Yale University, ³Human Evolutionary Biology, Harvard University, ⁴Anthropology, University of New Mexico

Relative to industrial populations, men from subsistence groups exhibit lower testosterone levels and more modest declines with age. Limited energy availability has been hypothesized to downregulate testosterone production, particularly among young adults when testosterone levels are highest, resulting in attenuated age-decline. However, energetic constraint is not unique to the evolutionary ecology of humans and yet significant age-related testosterone decline is observed in numerous species of wild primates. Conversely, human life history is distinguished by extensive bi-parental care and male provisioning. Because men show decreased testosterone with parenting effort, we argue that within more naturalistic and evolutionarily relevant ecologies, natural fertility and earlier reproduction suppresses testosterone in emerging adulthood such that a lower relative baseline dictates less age-decline across the remaining lifespan. We examine men's testosterone levels as contrasting functions of energetic status and paternal involvement across three traditional populations with substantial variability in men's nutritional condition and parental investment. Anthropometric

ABSTRACTS

and demographic data along with saliva samples were collected from 83 Datoga, 31 Hadza, and 48 Qom men, ages 17-72 years. Population variation in salivary testosterone was greatest at younger ages and patterned so paternal involvement associated with lower morning and evening testosterone, along with diminished age-decline in both measures. Men's energetic status as indicated by their body mass index was not associated with testosterone values or age-related decline. Within socioecological contexts of small-scale society, we find that blunted age-decline in men's testosterone levels is primarily due to population variation in parental investment rather than energetic constraint.

Examining patterns in gut microbial eukaryotes and bacteria across the primate phylogeny

KATHERINE R. AMATO¹, ALLISON MANN^{2,3,4}, FLORENT MAZEL^{2,3}, EVAN MORIEN^{2,3,4}, VINCENT BILLY^{2,3,4} and LAURA PARFREY^{2,3,4}

¹Anthropology, Northwestern University, ²Botany, University of British Columbia, ³Biodiversity Research Centre, University of British Columbia, ⁴Zoology, University of British Columbia

Given the influence of the gut microbiome on host health via effects on metabolism, immune function, and behavior, there is widespread interest in determining the factors that affect host-gut microbe interactions. Examining patterns of microbial variation across multiple host species can provide insight into these factors. However, existing comparative studies largely overlook the true complexity of the gut system, focusing on bacteria and excluding archaea, microbial eukaryotes, and viruses. In an effort to broaden our understanding of the primate gut microbiome, here we use 18S rRNA gene amplicon sequencing to describe the gut microbial eukaryote profiles of 12 species of wild primates. We detect many of the same taxa that are known to inhabit the human gut, including nematodes, *Entamoeba*, *Blastocystis*, and *Giardia*, and find that both host dietary niche and phylogenetic group influence taxonomic diversity. Additionally, the prevalence of some microbial eukaryote taxa varies by host phylogenetic group. For example, while several species of nematodes are prevalent throughout the primate phylogeny, *Entamoeba* is only detected in Old World monkeys and apes. Comparisons with previously generated bacterial data for the same fecal samples will allow us to describe co-occurrence patterns between bacteria and microbial eukaryotes. Given that a subset of bacteria co-diversify with hosts, it is possible that interactions between co-diversifying bacterial taxa and widely prevalent eukaryotic taxa are stronger compared to

interactions among other microbial taxa. These dynamics are likely to have implications for host physiology across both proximate and evolutionary timescales.

Water availability, primate ranging behavior, and implications for parasite transmission: an experimental and observational study of wild red-fronted lemurs (*Eulemur rufifrons*) in a dry deciduous forest

CAROLINE R. AMOROSO¹, PETER M. KAPPELER^{2,3}, CLAUDIA FICHTEL² and CHARLES L. NUNN^{1,4}

¹Evolutionary Anthropology, Duke University, ²Behavioral Ecology and Sociobiology, German Primate Center, ³Sociobiology/Anthropology, University of Göttingen, ⁴Global Health Institute, Duke University

For primate species in dry habitats, water may be among the most important factors driving ranging patterns. In this study, we investigated whether and how water distribution impacts ranging behavior in a wild lemur population. We monitored the habitat use of a habituated population of red-fronted lemurs (*Eulemur rufifrons*) in a dry deciduous forest in western Madagascar using GPS collars. We conducted experiments that introduced water resources and compared ranging patterns during the experiments to those before and afterward. We found that lemur groups shifted their intensity of habitat use relative to changes in natural and experimental water availability. Specifically, lemurs were more likely to spend time in areas near experimental water sources during the experiment than in the same areas before water was present (exponential model better supported than null model; $\Delta AIC > 2$ for four groups). Lemurs were less likely to spend time near previous habitual water sources while experimental water sources were available (GLM; $p < 0.01$, $t = -3.24$, $df = 146$). We observed shifts in ranging intensity in response to natural changes to water availability when waterholes dried up over time (GLM; $p < 0.01$, $t = -2.81$, $df = 103$). Based on these findings, we conclude that lemurs are flexible in their ranging patterns in response to water availability, and we consider implications of aggregations of lemur groups around waterholes for parasite transmission. These results highlight the importance of water distribution for determining primate habitat use, especially given the potential for climate change and human land use to alter water availability for wild primates.

This research was funded by NSF BCS-1613482 (DDRIG), the Margot Marsh Biodiversity Foundation, and Primate Conservation, Inc.

Porotic cranial lesions in living forager-horticulturalists: theoretical pathways and preliminary evidence

AMY S. ANDERSON¹, AARON D. BLACKWELL^{1,18}, BENJAMIN C. TRUMBLE³, RANDALL C.

THOMPSON², L.S. WANN⁴, ADEL H. ALLAM⁵, BRUNO FROHLICH⁶, M. LINDA. SUTHERLAND⁷, JAMES D. SUTHERLAND⁷, JONATHAN STIEGLITZ⁸, DANIEL EID. RODRIGUEZ⁹, ANDREI IRIMIA^{10,5}, MENG LAW¹⁰, GIUSEPPE BARISANO¹⁰, HELENA CHUI¹⁰, DAVID E. MICHALIK⁷, CHRIS ROWAN¹¹, GUIDO LOMBARDI¹², RAM BEDI¹³, ANGELA R. GARCIA³, DANIEL CUMMINGS¹⁷, JAMES K. MIN^{1,14}, JAGAT NARULA¹⁵, CALEB E. FINCH¹⁰, GREGORY S. THOMAS⁷, HILLARD KAPLAN¹⁶ and MICHAEL GURVEN¹

¹Anthropology, University of California Santa Barbara, ²Saint Luke's Mid America Heart Institute, University of Missouri, ³School of Human Evolution and Center for Evolution and Medicine, Arizona State University, ⁴Cardiology, Ascension Healthcare, ⁵Medicine, Al Zahar University, ⁶Anthropology, Dartmouth College, ⁷Medicine, Memorial Care Hospital, ⁸Anthropology, Institute for Advanced Study in Toulouse, ⁹Medicine, Universidad de San Simón, ¹⁰Medicine, University of Southern California, ¹¹Cardiology, Renown Institute for Heart and Vascular Health, ¹²Laboratorio de Paleopatología, Catedra Pedro Weiss, Universidad Peruana Cayetano Heredia, ¹³Bioengineering, University of Washington, Seattle, ¹⁴Radiology, Weill Cornell Medical College, ¹⁵Icahn School of Medicine, Mount Sinai, ¹⁶Economic Science Institute, Chapman University, ¹⁷Anthropology, University of New Mexico, ¹⁸Anthropology, Washington State University, Pullman

Porotic hyperostosis (PH) and cribra orbitalia (CO) are cranial lesions often identified in archaeological assemblages but rarely in clinical cases. This disparity is surprising, since the factors that bioarchaeologists link to these skeletal lesions include microbial and macroparasitic infection, food insecurity, and inadequate dietary diversity, which all remain common globally. We aim to shed light on the biocultural causes and pathophysiology of PH/CO by examining their expression in a living population with chronic parasitism and anemia.

The Tsimane, contemporary tropical subsistence horticulturalists, have been studied by the Tsimane Health and Life History project (THLHP) since 2002. We utilize THLHP data to examine associations between anemia and cranial lesions. In a preliminary sample of 50 cranial CT scans of Tsimane adults aged 45+ (52% male) we find evidence of PH in 4% and CO in 10%. Analyses of dietary data suggest that dietary iron deficiency is unlikely, and vitamin D deficiency is minimal in the tropics, yet we find that 20% of Tsimane adults and 38% of children are anemic. Parasitism is endemic and systemic inflammation is high: 45% are infected with hookworm, white blood cell counts are ~1.5 times higher than US values. Thus, blood loss anemia and anemia of inflammation may have simultaneous opposing forces on erythropoiesis, leading to hidden heterogeneity in skeletal phenotypes. In future work, we will test

ABSTRACTS

theoretical pathways between environment and protic cranial lesions by expanding our sample of CT scans to 775 individuals and linking these scans to 15 years of longitudinal health data.

This research made possible by NIH/NIA grants R01AG024119-01, R01AG024119-02, and R56AG024119

Bioarchaeological Signatures of Health and Inequality at the Middle Bronze Age Rural Site Kaman-Kalehöyük

CHERYL P. ANDERSON¹, LEVENT ATICI² and SACHIHIRO OMURA³

¹Anthropology, Boise State University,

²Anthropology, University of Nevada, Las Vegas,

³Archaeology, Japanese Institute of Anatolian Archaeology

This research study focuses on the bioarchaeology of Kaman-Kalehöyük and seeks to provide baseline data, investigating the effects of socio-economic inequalities on rural communities during the Middle Bronze Age (MBA) (ca. 2000-1750 years Before Current Era) in central Anatolia (present-day Turkey). In particular, this project addresses the impact of the political landscape during the MBA on population health at the small rural settlement Kaman-Kalehöyük using multiple lines of evidence. This is accomplished through comprehensive documentation and analyses of human skeletal remains. More specifically, health indicators of biological stress and activity patterns are discussed in order to assess whether a biological signature of health is present at this MBA rural community.

The results show a minimum of 64 individuals and include all age categories and both sexes. Some aspects of the health profile, such as the demographic profile, fertility rates and prevalence of dental caries, are consistent with an agricultural lifestyle. The demographic patterns appear to be relatively normal for an agrarian rural community and fertility is high (0.3774). Based on the evidence for overall nutritional quality and general stress, we argue that occupants of the MBA Kaman-Kalehöyük show health profiles similar to low socio-economic individuals at the MBA urban site of Kültepe-Kanesh.

The taxonomic status of the large-bodied colobine specimen KNM-WT 16827

MONYA ANDERSON

Department of Anthropology, University of Oregon

KNM-WT 16827 is an associated partial skeleton of a large-bodied colobine monkey from the Lomekwi Member of the Nachukui Formation, West Turkana dated to approximately 2.6 Ma. This specimen includes associated cranial, maxillary, and mandibular fragments along with several postcranial elements with well-preserved articular surfaces from the forelimb, hindlimb, and ankle. It was initially classified as *Paracolobus*

mutiwa based on craniodental similarities with specimens from Koobi Fora and Omo and is the only specimen with associated postcrania attributed to this taxon. The inclusion of *P. mutiwa* within *Paracolobus* has since been questioned due to craniodental and postcranial morphologies distinct from the *P. chemeroni* specimen KNM-BC 3.

Postcranially KNM-WT 16827 is distinct not only from *P. chemeroni*, but also compared to contemporaneous fossil colobines such as *Rhinocolobus turkanensis* and *Cercopithecoides williamsi*. The scapula and humerus are shorter and more robust than *P. chemeroni*, and although it is not as extremely terrestrial as *C. williamsi*, appears more terrestrial than the arboreally adapted *R. turkanensis*. The hindlimb is smaller with more robust muscle attachments compared to *P. chemeroni* with morphologies more consistent with terrestrial locomotion at the hip. The calcaneus and astragalus, although distinctly colobine, also differ morphologically from *P. chemeroni* and the other large-bodied colobines suggesting differences in locomotor adaptations of the ankle joint. KNM-WT 16827's unique postcranial morphology calls into question its inclusion within *Paracolobus* and in combination with its unusual cranial morphology may warrant generic distinction.

This research was supported by the University of Oregon and the National Science Foundation (Proposal No. 1650923).

Application of Synchrotron micro-Computed Tomography and Confocal Laser Scanning Microscopy to evaluate sex-related differences in the human osteocyte lacunar-canalicular network across the lifespan

JANNA M. ANDRONOWSKI¹, REED A. DAVIS¹, GINA TUBO¹ and DAVID ML. COOPER²

¹Biology, University of Akron, ²Anatomy, Physiology, and Pharmacology, University of Saskatchewan

Osteocytes are believed to play a central role in the sustained health of bone, thus a decline in their numbers is detrimental and alterations in the lacunar-canalicular network (LCN) may be linked to accelerated bone remodeling and subsequent bone loss. Due to the preferential bias of particular bone diseases in females, such as osteoporosis, the exploration of age-associated sex differences in the LCN is warranted. This study addresses two hypotheses: (1) there will be a decline in lacunar volume in the female middle-age group, indicating that the onset of changes may be associated with menopause, and (2) the LCNs of young women will have a greater surface area. Cortical bone samples were sourced from the femora of modern American males ($n=20$) and females ($n=20$) between the ages of 20 and 100. Synchrotron micro-Computed Tomography (SR μ CT) and Confocal Laser

Scanning Microscopy (CLSM) techniques were used to image samples from males and females across the lifespan. Parameters include osteocyte lacunar density, LCN area, and canalicular area. SR μ CT results indicate that lacunar density is reduced in older individuals of both sexes (60+). CLSM data reveals that LCN area is 26.8% greater in younger females (<40) and declined in older females (50+) by ~44.5%. Canalicular area was further reduced in aged females. Lower LCN areas in older females may contribute to impaired communication between osteocytes due to fewer canalicular connections and impair their mechanotransduction functions. Overall, this work has implications for selecting possible targets for intervention during menopause linked to the bone remodeling process.

Supported by the Canadian Institutes of Health Research, Training Grant in Health Research Using Synchrotron Techniques

The Role of Broca's Area in Stone Toolmaking Action Perception

ZARA ANWARZAI¹, SHELBY S. J. PUTT², LANA RUCK^{1,2}, CHUNG-LIN YANG³ and P. THOMAS SCHOENEMANN^{1,2}

¹Department of Anthropology and Cognitive Sciences Program, Indiana University, ²Stone Age Institute, Stone Age Institute, ³Department of Brain & Cognitive Sciences, University of Rochester

The possible co-evolution of stone tool manufacturing and language has long been a subject of speculation, partly driven by the recognition that key aspects of language are left-lateralized in the brain, and that most people are also left-lateralized for manual motor behavior by being right-handed. Neurocognitive studies of stone tool manufacturing, however, have not reported clear evidence of activation in Broca's area in the left hemisphere, though they have reported activation in the right hemisphere in BA44/45 for Acheulian stone tool technology. Using fMRI, we scanned an expert stone toolmaker watching a naturalistic video of himself making different kinds of stone tools, while also imagining himself performing these actions. Our analysis shows a strong correlation of activation for BA44/45 in both hemispheres. Positive and negative peaks of activation in BA44/45 that were independent of changes in overall activation occurred mostly during periods of observation, when the subject was assessing the current intermediate state of the tool, suggesting that BA44/45 in both hemispheres aid in action planning. In addition, exposures to new behaviors during the ~23 minutes of video yielded the highest positive peaks in BA44/45; this activation decreased over time, suggesting that BA44/45 may aid in monitoring new steps in toolmaking sequences and have less to do with processing familiar behaviors. The outcome of this analysis offers a greater understanding of Broca's area in coordination

ABSTRACTS

with its right analogue, providing further support for how stone toolmaking studies can offer insight into the evolutionary expansion of Broca's area.

This research was supported in part by grant 52935 from the Templeton Foundation titled: "What Drives Human Cognitive Evolution?"

Evolutionary genomic patterns of recent natural selection on body size sexual dimorphism in *Homo sapiens*

AUDREY M. ARNER¹, KATHLEEN E. GROGAN¹, CHRISTINA M. BERGEY¹, HUGO REYES-CENTENO², MARK GRABOWSKI^{2,3} and GEORGE PERRY^{1,2}

¹Departments of Anthropology and Biology, Pennsylvania State University, ²DFG Center for Advanced Studies "Words, Bones, Genes, Tools", University of Tübingen, ³Research Centre in Evolutionary Anthropology and Palaeoecology, Liverpool John Moores University

It has been hypothesized that human body size sexual dimorphism was reduced via positive selection following the transition from hunting and gathering to agriculture due to a more equal division of labor, shifts in technology, and/or nutritional changes. Alternatively, any recent changes in the degree of human sexual dimorphism could instead reflect genetic drift. Here we apply a genome wide association study (GWAS) approach to study the recent evolutionary history of sexual dimorphism in human body size phenotypes. GWAS can identify genetic loci associated with phenotypic variation; the identified variants can then be analyzed to infer recent evolutionary histories of the corresponding traits. Using GWAS data from the UKBiobank, we identified 147 single nucleotide polymorphisms that are both significantly associated with height variation in either males or females or in both sexes ($P < 1 \times 10^{-13}$) and have a significant sex difference for height ($P < 0.0001$). Using the singleton density score statistic, which quantifies recent changes in the frequencies of alleles underlying polygenic traits, we observed evidence of recent (within ~3,000yr) positive selection ($P < 0.0001$) at these loci, specifically on alleles associated with less sexual dimorphism. This effect was predominantly driven by increases in the frequencies of alleles associated with shorter male stature. In stark contrast, for loci associated with height but not sexual dimorphism there is evidence of recent positive selection on alleles associated with taller height. Our results support the hypothesis of recent positive selection for reduced human body size sexual dimorphism and demonstrate the value of GWAS approaches for testing anthropological hypotheses.

The Penn State University Erickson Discovery, Presidential Leadership Academy Enrichment, and Liberal Arts Enrichment Grants (all to A.M.A.); NIH grant R01-GM115656 (to G.P.); and DFG grant FOR-2237.

Moving through time: Intermediate phalanges from East African early and middle Miocene catarrhines reveal locomotor changes

IRISA D. ARNEY¹, MONTE MCCROSSIN², BRENDA BENEFIT³ and ISAAH NENGO⁴

¹Anthropology, University of Michigan, ²Anthropology, New Mexico State University, ³Evolutionary Anthropology, Duke University, ⁴Turkana Basin Institute, Stony Brook University

A survey of early and middle Miocene East African catarrhine collections indicates intermediate phalanges are one of the most well-preserved yet understudied elements across localities. Here we provide qualitative and quantitative descriptions of several catarrhine intermediate phalanges from the early and middle Miocene. Robusticity indices (RI = base width \times 100 / maximum length) indicate manual intermediate phalanges of *Afropithecus*, *Ekembo heseloni*, and *Equatorius* are moderately robust with index values between 29-37, as in *Colobus*, *Cebus*, and *Nasalis*. Phalanges from Songhor (~19-20 Ma), are more gracile (RI 27-31) than similar sized *E. heseloni*. Curvature indicates two morphs at Songhor. SO 35514 is very curved (included angle = 51°), resembling phalanges from suspensory taxa; while SO 974, 986, and 1966 are less curved (30°-39°), like *Ekembo* and arboreal colobines. SO 35514 could belong to a different taxon than SO 974, 986, and 1966.

At Maboko (15 Ma), a large hominoid manual phalanx (MB 28393), similar in size to *Pan* and RU 151001 (*Ekembo nyanzae*), is attributed to *Kenyapithecus africanus*. It is robust (RI = 37) like RU 151001 (RI = 38), *Pan* and *Mandrillus* phalanges, yet the shaft is straight (21°) like terrestrial *Papio*. Additional small catarrhine phalanges, morphologically distinct from robust, straight *Victoriapithecus* phalanges, can be attributed to *Simiolus* or *Mabokopithecus*. These phalanges are gracile (RI = 24-28) and curved (43°-50°), resembling morphology of brachiating/semi-brachiating taxa.

Results indicate adaptations for more agile forelimb arboreality to at least one taxon at Songhor. Even more derived forelimb agility was present in middle Miocene small-medium apes along with terrestrial adaptations in *Kenyapithecus* and *Victoriapithecus*.

Support was provided by the National Science Foundation, L.S.B. Leakey Foundation, Wenner-Gren Society, National Geographic Society, Boise Fund, and the University of Michigan.

Maternal position within the dominance hierarchy in *Macaca mulatta*: Associations with offspring 2D:4D ratio and growth

JUAN PABLO ARROYO¹, LORENA MADRIGAL¹, REBECCA LONES-KHALFOUNI¹, MANUEL LEBRÓN², MELWEEN MARTÍNEZ² and CARLA ESCABÍ²

¹Department of Applied Anthropology, University of South Florida, ²Caribbean Primate Research Center, Medical Sciences Campus, University of Puerto Rico Rico

The second to fourth digit length (2D:4D) ratio is a sexually dimorphic trait, associated with prenatal exposure to androgens and dominance-rank in several species. Higher-ranking female rhesus macaques have been reported to have lower 2D:4D ratios than lower-ranking females. In this study we assessed if maternal dominance-rank (MDR), maternal received-aggression (RAG) and maternal received-affiliation (RAF) are associated with offspring 2D:4D ratio and growth. Data were collected on dyadic-agonistic and dyadic-affiliative interactions between adult females. Offspring (neonates to 2.5-year-olds) morphometric-weight data were collected twice, 5 months apart. Offspring of high-ranking mothers had higher left-hand 2D:4D (LH-2D:4D) ratios than offspring of middle and low-ranking mothers. MDR was positively associated with LH-2D:4D in males ($p = 0.022$), and both-hand 2D:4D average in males ($p = 0.036$) and females ($p = 0.038$). MDR correlated with increased 5-month BMI change in males ($p = 0.046$), and lower finger trauma ($p = 0.026$) in males and females. RAG correlated with reduced weight-gain in males ($p = 0.046$), and reduced CR-L growth ($p = 0.035$) and higher finger trauma in females ($p = 0.011$). The higher the RAF, the lower the weight ($p = 0.023$) and CR-L ($p = 0.015$) in females. RAF correlated with lower BMI in both males ($p = 0.029$) and females ($p = 0.024$); with lower weight ($p = 0.033$) but higher 5-month weight-gain ($p = 0.006$) and BMI change ($p = 0.004$) in males. RAF correlated with higher right-hand 2D:4D (RH-2D:4D) ratio in females ($p = 0.007$), and a higher RH-2D:4D to LH-2D:4D difference in males ($p = 0.035$). A positive MDR and offspring 2D:4D association is unexpected. Male growth appears to be more susceptible to the effects of MDR, RAG and RAF.

Testing factors influencing the lemur gut microbiome: host genetics or diet?

ABIGAIL E. ASANGBA^{1,2}, MARIAH DONOHUE^{3,4}, ALICIA LAMB^{3,5}, REBECCA J. LEWIS⁶, RANDALL E. JUNGE⁷, MITCHELL IRWIN⁸, STEVEN R. LEIGH⁹, PATRICIA C. WRIGHT^{10,11,12} and REBECCA M. STUMPF^{1,2}

¹Anthropology, University of Illinois at Urbana-Champaign, Urbana, IL, USA, ²Carl R. Woese Institute for Genomic Biology, University of Illinois at Urbana-Champaign, Urbana, IL, USA, ³Ecology and Evolution, Stony Brook University, Stony Brook, NY, USA, ⁴Biology, University of Kentucky, Lexington, KY, USA, ⁵Biology, Clarkson University, Potsdam, NY,

ABSTRACTS

USA, ⁶Anthropology, University of Texas at Austin, TX, USA, ⁷Columbus Zoo and Aquarium, Columbus, OH, USA, ⁸Anthropology, Northern Illinois University, DeKalb, IL, USA, ⁹Anthropology, University of Colorado-Boulder, Boulder, CO, USA, ¹⁰Centre ValBio, Ranomafana, Madagascar, ¹¹Institute for the Conservation of Tropical Environments, Stony Brook University, Stony Brook, NY, USA, ¹²Anthropology, Stony Brook University, Stony Brook, NY, USA

Multiple factors including diet, host genetics, host phylogeny, digestive physiology and habitat have been shown to influence the composition of the host gut microbiome. Previous studies suggest that the gut microbiome composition and function of individuals within the same species may be shaped mainly by environmental factors such as diet, with minor contributions from host genetics. However, studies comparing individuals from different species reveal host genetics and host phylogeny mainly determine the gut microbiome composition and function, with minor contributions from diet. To better elucidate the roles of these factors in affecting the gut microbiome of non-human primates, we compared the gut microbiomes of five closely-related wild lemur species (*Propithecus verreauxi*, *Propithecus diadema*, *Propithecus edwardsi*, *Varecia variegata*, and *Lemur catta*) occupying different dietary niches using data from 16S rRNA gene sequences. Beta diversity measured from unweighted Unifrac distances showed sub-clustering of host species within broader diet clusters. PERMANOVA tests on the distances were statistically significant ($p < 0.001$). Alpha diversity (species richness) showed *P. verreauxi* and *L. catta* with lowest and highest diversities respectively, a possible reflection of diet diversity. LEfSe results indicate that 10 microbial taxa were significantly discriminative among host species whereas 31 microbial taxa were distinguished by diet (omnivory, folivory, and frugivory) indicating that diet, more than host species, was a stronger factor influencing variation in the lemur gut microbiome. Comparative microbiome studies such as this contribute to our understanding of the relative importance of the various factors affecting host-microbiome diversity and function.

We gratefully acknowledge funding from NSF BCS 0820709 and NSF BCS 0935347.

Middle Pleistocene hominin systematics: *Homo heidelbergensis*, *Homo sapiens*, and the species concept revisited

SHEELA G. ATHREYA

Anthropology, Texas A&M University

Efforts at classifying Middle Pleistocene hominins are hampered by the lack of consensus as to how to weight geographical and temporal variation, phylogeny, and morphology. But because scientists are heterogeneous and differ about the species concept, there can be

no global consensus. A shared taxonomy is mostly to achieve other goals, namely: 1) sharing language for transmission of ideas; 2) reflecting the consensus and diversity of interpretations; and 3) developing a classification that allows for inductive reasoning. I propose we shift our focus to these goals. I demonstrate how approaching Middle Pleistocene systematics through the interpretive framework of ethnobiology, which studies folk naming and classification systems, can yield better results. The focus is not on ascertaining "true" evolutionary relationships, but achieving these goals. I review published definitions of Mid-Pleistocene taxa and categorize them, following Berlin's seminal 1973 work, into two levels of cognitive universals: the broader *folk generic* and more restrictive *folk specific* rank. The results demonstrate that our inability to define *H. heidelbergensis* is consistent with other examples of organisms that lack readily perceptible or universally recognized differences among observers. The level of patterning does not allow a folk-species-level distinction, but possesses what other societies name at the folk-generic level. In keeping with global naming systems we should refer to them according to their generic category, with modifiers (e.g., "Middle Pleistocene *Homo*"). Doing so is consistent with all other known taxonomic systems, with observed human capabilities of cognitive differentiation, and is both necessary and sufficient given the current data.

Nonmetric cranial trait expression in pre-contact Southwest Native Americans and modern Asians

MEGAN L. ATKINSON¹ and SEAN D. TALLMAN^{1,2}

¹Anatomy and Neurobiology, Boston University School of Medicine, ²Anthropology, Boston University

Traditionally, pre-contact Native Americans have served as a biological reference in identifying modern Asian individuals for aspects of the biological profile due to their distantly shared genetic history. However, the assumption that pre-contact Native Americans can serve as accurate representatives in cranial nonmetric trait expressions for modern Asian individuals remains largely untested. Therefore, the present study explores craniometric variability between pre-contact Native Americans and modern Asian individuals to ascertain whether population-specific methods should be developed. Nonmetric cranial trait data was recorded on pre-contact Southwest Native Americans ($n = 150$) from the American Museum of Natural History and compared within a nonparametric statistical framework to cranial trait data for modern Thai ($n=150$, Khon Kaen University) and Japanese ($n=150$, Jikei University) individuals. Chi-square analyses indicate that the Native American and Asian groups exhibit significant differences in their nonmetric cranial trait expressions. Of the

35 traits analyzed, 31 (88.6%) differed significantly between the groups. Specifically, 28 traits (80.0%) differed significantly between the males, while 25 traits (71.4%) differed significantly between the females. These differences likely reflect distinct population histories, and the disparities are large enough to conclude that pre-contact Native Americans should not serve as biological references for modern Asian populations when performing ancestry estimations in forensic settings. The present study indicates that Native American and Asian populations are not skeletally homogenous, and as such, it highlights the increasing need for the development of population-specific biological profile methods for Asian populations.

Evolvability and Constraint in Traits of the Primate Vertebral Column with Respect to Functional Trait Complexes

BENJAMIN M. AUERBACH^{1,2} and ELIZABETH R. AGOSTO¹

¹Anthropology, The University of Tennessee,

²Ecology and Evolutionary Biology, The University of Tennessee

Researchers have established genetic covariance of vertebrae with the basicranium, in part related to developmental commonalities in addition to shared biomechanical function. Vertebrae also share functional relationships with the bones of the upper limb, as muscles originate from vertebrae and insert on the scapula and humerus. Such functionally-related traits that are produced through genetic covariance are functional trait complexes (FTCs), in which shared genetic relationships impose constraints in trait responses to directional selection. While other research we have performed has established the basicranium and scapula as a FTC, it is unknown if this complex extends to the vertebrae.

We examine evolvability among basicranial, scapular, and vertebral measurements (cervical and thoracic) from 66 adult *Macaca mulatta*. Measurements were mean-standardized and indices of evolvability were calculated in R following the equations of Hansen and Houle. Higher evolvability measures reflect more independence among traits. Results show the lowest evolvability indices for the scapula with both vertebral regions, as well as the scapula with the basicranium. Significantly higher evolvability occurs between both vertebral regions, and between the basicranium and each vertebral region. This indicates that the scapula forms a FTC with the vertebrae and the basicranium, perhaps related to shared biomechanical functions. In addition, while there are tiered patterns of constraint, we propose all of these elements comprise a FTC, and impose mutual constraints to responses to selection. We find similar

ABSTRACTS

patterns in preliminary analyses of these traits in marsupials (*Petauridae*), which suggests an ancient mammalian origin for genetic covariances among these anatomical regions.

National Science Foundation BCS DDRIG #1825995

Sacroiliac joint fusion in nulliparous and parous females and males

MEREDITH N. AULDS

Geography and Anthropology, Louisiana State University

Previous research shows that sacroiliac (SI) joint fusion is age and sex dependent. Older individuals—specifically starting in the fifth or sixth decade of life—are more likely to develop SI joint fusion. Females have a lower frequency of SI joint fusion than males, perhaps due to pregnancy or parturition. This study examines the relationship between SI joint fusion with both sex and parity status in females. The issue is whether the prevalence of SI fusion in nulliparous females is more similar to that of males or parous females. The sample consists of 46 nulliparous females, 119 parous females, and 158 males from the William Bass Skeletal Collection. Ages of the individuals ranged from 50-89 years. Sex, age, and parity status were self-reported. Results show that the frequency of SI joint fusion is significantly different among males (13.29%), nulliparous females (6.52%), and parous females (0.84%; Fisher's exact test, $P < 0.001$). Pairwise comparison of the three groups for SI joint fusion shows that parous females and males are significantly different ($P < 0.001$), but parous females and nulliparous females ($P = 0.07$) and nulliparous females and males ($P = 0.21$) are nonsignificantly different. Nulliparous females are intermediate in frequency of SI joint fusion between males and parous females which suggests that pregnancy or parturition is involved in lower frequencies of SI joint fusion in parous females.

Is mountain life tougher? Examining differential maximum incisor bending and shearing strength in *Gorilla gorilla* and *G. beringei*

LAUREN N. AUSTIN, JACOB W. MOFFIT and ANDREW S. DEANE

Anatomy and Cell Biology, Indiana University

All gorillas are more folivorous relative to other great apes, however within that group there is considerable dietary variability between *G. gorilla* and *G. beringei*. The former relies heavily on fruiting resources during much of the year and uses terrestrially herbaceous vegetation (THV) to supplement a predominantly frugivorous diet during limited periods of resource scarcity. *Gorilla beringei*, however, more consistently relies on THV year-round owing to the scarcity of fruiting resources at the higher elevations. Although prior

analyses have identified potentially diet specific morphological differences in *G. gorilla* and *G. beringei* incisor crowns (i.e. differences in incisal crown curvature), these differences are not as accentuated as the differences between other closely related taxa with dissimilar diets (i.e. *Ateles* vs *Alouatta*).

This study examines differential patterns of maximum incisor bending strength (MIBS) and maximum incisor shearing strength (MISS) in Gorillas. Regression analyses of four mixed datasets ($n = 187$ individuals; four incisors types) representing all living hominoids and most platyrrhines were used to generate the standardized residuals used to evaluate the relative MIBS and MISS for each taxon. Results indicate that despite having a more traditionally folivorous diet, *G. beringei* has elevated I^2 and I_1 MIBS and MISS relative to *G. gorilla*. This runs counter to observations that more frugivorous primates typically have higher MIBS and MISS relative to more folivorous taxa suggesting that specific aspects of *G. beringei* diet (i.e. elevated pith and bark consumption, increased dietary toughness etc.) are atypical for traditional dedicated folivores and strongly influence *G. beringei* anterior dentition

Ontogeny of vault shape in *Homo erectus* with implications for KNM-ER 42700

KAREN L. BAAB¹ and ALLISON NESBITT²

¹Anatomy, Midwestern University, ²Pathology and Anatomical Sciences, University of Missouri

Although initially assigned to *Homo erectus*, there is now broad agreement that the ecto- and endocranial shape of the 1.5 Myr hominin fossil KNM-ER 42700 fall outside of the bounds of adult *H. erectus*. Its sphenoccipital synchondrosis suggests an older subadult or young adult developmental stage. Yet, its endocranial shape suggests that it is a younger juvenile. This study investigates ontogenetic scaling of the calvaria in *H. erectus* using humans and chimpanzees as models.

We first confirm that the undeformed ectocranial shape of KNM-ER 42700 is distinct from adult *H. erectus*. KNM-ER 42700 shares similarities to KNM-WT 15000 (Nariokotome Boy), but is not intermediate in shape between adult and juvenile *H. erectus* (Modjokerto). The potential impact of development on vault form is complex. Juvenile *H. erectus* are more similar to modern humans in neurocranial shape than are adults. Hence, the intermediate position of KNM-ER 42700 between juvenile and adult *H. erectus* could be due to ontogeny, but may also reflect parallel evolution of a rounder vault. Indeed, the KNM-ER 42700 fossil is positioned closer to the adult distribution of *H. erectus* when the axes are based entirely on the human ontogenetic pattern. We then employed the human, chimpanzee and their common ontogenetic trajectories to generate estimates

of adult and juvenile *H. erectus* vault shape, and assessed their fit based on convergence between estimates and observed morphology. As a final test, we evaluated whether KNM-ER 42700 falls along the *H. erectus* ontogenetic shape trajectory based on the best developmental model.

Grant support was provided by NSF (BCS 1454498, BCS 04-24262, DGE 03-33415, and DBI 96-02234), L.S.B. Leakey Foundation, Wenner-Gren Foundation, Sigma Xi Foundation and the AGEP T-FRAME program (NSF HRD 1311318).

Environmental, but not social cues predict nest site selection and use in a communally breeding primate

ANDREA L. BADEN

Anthropology, Hunter College, CUNY, Anthropology & Biology, The Graduate Center, CUNY, The New York Consortium in Evolutionary Primatology, NYCEP

Nest site selection is at once fundamental to reproduction and a poorly understood component of many organisms' reproductive investment. Here, I describe the nesting behaviors of black-and-white ruffed lemurs, *Varecia variegata*, a litter-bearing primate from the southeastern rainforests of Madagascar. Using a combination of behavioral, geospatial, and demographic data collected from the Mangevo community between July – December 2008, I test the hypotheses that both environmental and social cues influence nest site selection, use, and reuse, and that these decisions ultimately impact maternal reproductive success. Support for these hypotheses was mixed. Nest construction was best predicted by environmental cues, including the size of the nesting tree and density of feeding trees within a 75m radius of the nest, whereas nest use depended largely on the size of the nesting tree and its average distance to feeding trees within 75m. Microhabitat characteristics were unrelated to whether females built or used nests. Social cues, specifically the average distance to conspecifics' nest and park sites, were unrelated to nest site selection or use, but were related to maternal reproductive success; mothers whose litters were parked in closer proximity to others' nests experienced higher infant survival than those whose nests were more isolated. This is likely because nesting proximity facilitated communal crècheing by neighbors. Together, these results suggest a complex pattern of nesting behaviors that involves the strategic placement of nests in areas with high potential resource abundance, nest use in accordance with realized productivity in the area, and communal infant care.

Funding provided by NSF DDIG (BSC-0725975), The Leakey Foundation, US Fulbright Foundation, Primate Conservation, Inc., Primate Action Fund, Rowe-Wright Primate Fund, Stony Brook University, and Hunter College.

ABSTRACTS

Ancient oral microbiome of a fisher-hunter-gatherer community from the Pacific Northwest Coast

ALYSSA C. BADER¹, KATHERINE R. AMATO², J. F. BRINKWORTH¹, KARTHIK YARLAGADDA¹, JEROME S. CYBULSKI³, JOYCELYNN MITCHELL⁴, BARBARA PETZELT⁴ and RIPAN S. MALHI^{1,5}

¹Anthropology, University of Illinois at Urbana-Champaign, ²Anthropology, Northwestern University, ³Research Division, Canadian Museum of History, ⁴Treaty Office, Metlakatla First Nation, ⁵Carl R. Woese Institute for Genomic Biology, University of Illinois at Urbana-Champaign

The microbiome provides a new lens through which to examine human evolution, human-environment interaction, and health. We present the results of a comparative analysis between the oral microbiome of Coast Tsimshian Ancestors and descendants. The Coast Tsimshian have lived in the coastal environment of what is now Prince Rupert Harbour, British Columbia, Canada for at least 6,000 years, based on genomic evidence. Their descendants, including the Metlakatla First Nation, continue to occupy this region. Prior to European colonization, ancestors of the Coast Tsimshian engaged in a fisher-hunter-gatherer subsistence lifestyle. Descendants continue to rely on coastal food resources, in addition to introduced industrialized foods. This study presents a much-needed characterization of the oral microbiome of an ancestral fisher-hunter-gatherer community, and examines more recent evolutionary changes via comparison with descendants who have occupied the same geophysical space through time.

We constructed genomic libraries from ancient DNA preserved in the dental calculus of Ancestors (n=45) and DNA extracted from gumline swabs of descendant participants (n=17). Microbial taxonomic diversity and functional potential was analyzed in conjunction with metadata on oral health, demography, and individual diet and contextualized by community-held knowledge about traditional diet and food culture. Preliminary analyses suggest Ancestors had reduced proportions of Actinobacteria and Firmicutes in their oral microbiome, with elevated proportions of Proteobacteria. Examining the variation between the oral microbiome taxonomic composition of Ancestors and descendants provides new insight to improve our understanding of the biological impact of European colonization on Indigenous communities.

National Science Foundation (NSF BCS-1732263, DGE-1069157), University of Illinois at Urbana-Champaign Graduate College and Department of Anthropology

Arm-swinging and habitat use of the red-shanked douc in the Son Tra Nature Reserve, Vietnam

KATIE E. BAILEY¹, JEFFREY W. WINKING¹, DAVID L. CARLSON¹, TRAN VAN BANG² and HA THANG LONG³

¹Anthropology, Texas A&M University, ²Vietnam Academy of Science and Technology, Southern Institute of Ecology, ³GreenViet Biodiversity Conservation Centre

The doucs (genus *Pygathrix*) are known to use arm-swinging behaviors at higher proportions than other members of the Colobinae subfamily. The arm-swinging of the doucs is kinematically similar to the brachiation of gibbons, though the doucs move more discontinuously and at a slower pace. Previous research in captivity has suggested that habitat constraints are likely what is driving the similar locomotor behavior of doucs and gibbons. Here, we attempt to identify patterns of habitat use as they correspond to the arm-swinging behavior of the red-shanked douc. We predict arm-swinging will occur significantly more on horizontal substrates, in the main canopy, on medium sized substrates (branches), and in old-growth forest, similar to that of gibbons. Data was recording in the Son Tra Nature Reserve, Vietnam between October 2016 and April 2017. The monkeys were filmed most days Monday through Friday using a Canon video camera and data was extracted continuously from all the clips. All data analysis was conducted in R. A generalized linear mixed model (GLMM) was used to analyze all environmental variables. Preliminary results indicate the red-shanked douc arm-swings significantly more on branches, horizontal substrates, in the main part of the canopy, and in old growth forest. This information is critical for understanding and conserving the habitat of the Critically Endangered red-shanked douc.

Primate Conservation, Inc. and Texas A&M University Department of Anthropology

New mandible from Olororgesailie sheds light on Middle Pleistocene human evolution in Africa

SHARA E. BAILEY^{1,2} and RICHARD POTTS³

¹Center for the Study of Human Origins, New York University, ²The New York Consortium in Evolutionary Primatology, ³Human Origins Program, NMNH, Smithsonian Institution

Olororgesailie, Kenya, has previously produced a partial cranium dated to 0.97- 0.90 Ma, attributed to a small *H. erectus* individual. Subsequent excavations in 2017 uncovered additional fossil material in higher strata dated to ~0.615 Ma, consisting of a hemi-mandible comprising the complete left ascending ramus, a distal portion of the left mandibular corpus, and well-preserved M₂ and M₃. The specimen is designated KNM-OG 70780. Although African hominins of similar age are rare, closest in time and geographic proximity

are mandibles from Baringo, Tighennif, and Sidi Abderrahman. Where comparisons are possible, the Olororgesailie mandible shares a number of morphological similarities with these specimens. These include a wide ascending ramus, lack of a retromolar space and, in one case, an asymmetrical mandibular notch. There are differences as well: the ascending ramus of OG 70780 is more vertical and thinner than the Baringo mandible BK 67; the anterior portion of the ascending ramus flares in OG 70780 but is more vertical in Tighennif, and the crest of the mandibular notch (CMN) of OG 70780 joins the condyle more medially whereas the CMN in BK 67 merges with the condyle at its lateral-most border. Dentally, the OG 70780 M₂ is similar in size to the African Middle Pleistocene average, but is squarer. The M₃ is smaller (especially mesiodistally) and more ovoid than the comparative sample. While the Olororgesailie mandible fits in with other African Middle Pleistocene hominins, it also exhibits features attributed to Neanderthals or, potentially, their common ancestor with *Homo sapiens*.

A Critical Review of Diagnostic Criteria Used to Identify Treponemal Infection in Human Skeletal Remains

BRENDA J. BAKER

Center for Bioarchaeological Research, School of Human Evolution and Social Change, Arizona State University

The identification of treponemal infection in skeletal remains of past people has been hindered by the inconsistent use of diagnostic criteria and reference to clinical studies, application of criteria that rely upon nonspecific indicators, and promulgation of "possible" cases despite the absence of a diagnostic pattern of lesions. The ability to discriminate among skeletal manifestations of current variants produced by *Treponema pallidum* subspecies (yaws, bejel, and syphilis) is also debated in the paleopathology literature and must be reconsidered based upon recent advances in immunology and genetics of treponemal infection. The subjectivity in differential diagnoses of treponemal disease has led to publication of numerous suspect cases, thereby contributing to contention surrounding the origin and spread of *T. pallidum*. To move forward, development of a set of best practices for diagnosis of treponemal infection in archaeological and historical human remains is needed, which requires critical evaluation of previously proposed cranial, infracranial, and dental indicators. Lesion specificity (caused by a single versus multiple conditions) and sensitivity (the proportion of those affected who have the lesion) are addressed to consider the ramifications of including only individuals displaying pathognomonic lesions versus those exhibiting lesions with less specificity but greater sensitivity. Assessing the distribution of treponemal disease through time depends upon publications that

ABSTRACTS

(1) provide sufficient information on the archaeological/historical context of the site, its dating, and the sample from which those affected are drawn; (2) report observable and unobservable elements; and (3) include detailed descriptions and clear images with scales.

Missing migrants and the search for identity

LORI E. BAKER

Anthropology, Baylor University

Each year, hundreds of thousands of undocumented migrants cross the US/Mexico border. The migrants, predominately from Latin America, are fleeing extreme poverty and violence to enter a country in which they face political, economic, cultural and social exclusion. It is a dangerous journey, and has resulted in a 5-fold increase in the risk of death since 2000. There are very few federal and state resources that have been allocated to identify the deceased making these individuals even more marginalized in death. Using the information from 110 cases of unidentified migrants exhumed or recovered from South Texas by the Reuniting Families Project, this presentation will outline the resources available for typical forensic cases versus those available for migrant cases. The results will show that many of these cases lacked a basic police report, all of these cases lacked basic forensic investigation and none were examined by a medical examiner, had DNA samples taken, or were entered into any unidentified person database. The US federal system has restrictions that prevent the full utilization of DNA databases to compare family reference samples for foreign relatives. This both hinders identification and reduces the population genetic data that helps to support match probabilities. Forensic anthropologists have led the humanitarian efforts to address this crisis and are compiling data for better identification methods as well as providing scale and needs assessments. In addition, anthropologists have successfully lobbied legislators, educated the public through extensive outreach, and empowered families to help bring dignity to the dead.

Modeling rainforest ecology as a product of local socioeconomic pressures in Masoala National Park, Madagascar

RICHARD J. BANKOFF

Anthropology, The Pennsylvania State University, Intercollege Program in Bioethics, The Pennsylvania State University

Frugivorous primate communities in tropical rainforests are disproportionately affected by the preferential extraction of natural resources for human consumption, most notably canopy-layer (necessary for locomotion, nesting, and dispersal) and fruiting (nutrition) trees. Understanding how local market and subsistence

forces correlate with ecological processes is integral to properly modeling the subtle shifts in forest cover and composition that presage conservation outcomes. The Masoala National Park in Madagascar contains the majority of the species range of highly frugivorous (60-90% of diet) red ruffed lemurs (*Varecia rubra*), a critically endangered primate highly sensitive to anthropogenic disturbance. I tested how variation in human consumption of selected park resources (gathered through interviews) is correlated with changes in the density and diversity of the botanical community of the park around four village sites in two different, internally-comparable biomes (montane vs. coastal rainforest). Forty-four botanical and primatological line transects (mean 675m, mode 1000m) were laid out radially from each village into the park during the July 2017-December 2017 field season. Botanical species distributions were compared in a spatial framework to examine the modularity of particular micro-ecologies and their relation to the park border. The relative contributions of abiotic, biotic, and anthropogenic disturbance have been described using Principal Components Analyses (PCA) and Generalized Linear Models (GLM) to detect subsistence- and economically-motivated covariates of ecological change. Results indicate that tourism-driven economic development is significantly correlated with increased harvest of materials critical to forest structure, while more economically isolated areas display increased consumption of subsistence-associated sustainably harvestable forest products.

Studying trabecular bone tissue structure-function relationship using 3D printing

MEIR M. BARAK and MEHA PATEL

Biology, Winthrop University

Trabecular bone was shown to adjust in response to loading. These structural changes are postulated to optimize trabecular architecture with the principle direction of loading. If this hypothesis is supported, then trabecular structure could help predict joint loading orientations and locomotion behaviors from fossil bones of extinct taxa. However, since each trabecular tissue is unique in structure and since mechanically testing a trabecular sample involves loading until failure, so far it was impossible to test a specific sample multiple times in different directions to find if its optimal mechanical orientation truly correlates with the physiological direction of loading. To answer this question, we have recently introduced a new 3D printing approach, which reproduces a large number of identical trabecular bone replicas and test them in various states and orientations. Using a ProJet 1200 3D-printer we were able to show that we can repeatedly reproduce life-size trabecular replicas with high accuracy, that the stiffness of the printable resin material did not differ significantly between printouts and

that printing layer orientation had a minor effect on the mechanical properties of the trabecular structure printout. Next, we investigated various setups such as comparing the stiffness and strength of the same trabecular structure when loaded on- and off-axis, comparing compressive and tensile stiffness and strength for the same trabecular structure, and the effect of thinning trabeculae on the stiffness and strength of the structure. Our studies demonstrate the potential of 3D-printing in becoming a valuable new tool in physical anthropology research.

This project was supported by SC INBRE grants from the National Institute of General Medical Sciences of the National Institutes of Health and Winthrop University Research Council Grants

Ancient Genomic and Epigenomic Simulation Using the epiPALEOMIX Pipeline

CHRISTOPHER E. BARRETT¹ and JOHN KELLY²

¹Anthropology, University of Kansas, ²Ecology and Evolutionary Biology, University of Kansas

Ancient epigenetics up to this point has largely been experimental both in laboratory protocol, sequencing methods, and bioinformatic analyses. Because ancient DNA (aDNA) recovered from archaeological remains is heavily damaged and fragmented, both by preservation conditions and handling of remains, the use of destructive analytical techniques is not an ideal standard. For these reasons, indirect and less destructive methods are ideal when working with ancient sequences. Fortunately, there are ways to retrieve ancient epigenetic signatures in aDNA by exploiting the extensive damage patterns seen in ancient samples caused by natural post-mortem degradation processes (deamination). These deamination patterns can serve as rough proxies for reconstructing epigenetic marks from aDNA like methylation and nucleosome structure. Individual epigenetic variation is predicated on genetic variation, development, and environmental stress from factors like nutrition, sleep, and drug use.

The best method for reconstructing ancient epigenomic data has yet to be established. The bioinformatic pipeline, epiPALEOMIX, is one published method for analyzing DNA methylation and nucleosome positioning in aDNA at the genomic level. This pipeline has been used to address questions on the temporal, geographical, and preservation range of ancient epigenetic signatures across multiple species including humans. However, the degree of sensitivity in this technique has gone untested. Here, I simulate genomic and epigenomic data to test nucleosome positioning estimates while using different genome read frames than previously considered (147 bp). Modifying the base pair size of the genome read window does affect nucleosome distance estimates.

ABSTRACTS

Hibernation, puberty and chronic kidney disease in hominins from Spain half a million years ago

ANTONIS BARTSIOKAS¹ and JUAN-LUIS ARSUAGA²

¹History and Ethnology, Democritus University of Thrace, ²Instituto de Salud Carlos III de Evolución y Comportamiento Humanos, Centro Mixto Universidad Complutense de Madrid

Both animal hibernation and human renal osteodystrophy are characterized by high serum parathyroid hormone. To test the hypothesis of hibernation in an extinct human species, we examined the hominin skeletal collection from Sima de los Huesos, Cave Mayor, Atapuerca, Spain, for evidence of hyperparathyroidism. We studied the morphology of the fossilized bones by using macrophotography, microscopy, histology and CT scanning. We found trabecular tunneling and osteitis fibrosa, subperiosteal resorption, 'rotten fence post' signs, brown tumours, subperiosteal new bone, chondrocalcinosis, rachitic osteoplaques and empty gaps between them, craniotabes, and beading in ribs mostly in the adolescent population of these hominins. Since many of the above lesions are pathognomonic, these extinct hominins suffered annually from renal rickets, secondary hyperparathyroidism, and renal osteodystrophy associated with chronic kidney disease. We suggest these diseases were caused by non-tolerated hibernation in dark cavernous hibernacula. This is evidenced by the rachitic osteoplaques and the gaps between them mainly in the adolescent individuals along with the evidence of healing. The sublayers in the rachitic osteoplaques point to bouts of arousal from hibernation. The strong projection of the external lip of the femoral trochlea, the rachitic osteoplaques with the empty gaps between them, and the evidence of annual healing caused by non-tolerated hibernation in adolescent individuals, also point to the presence of annually intermittent puberty in this population. The present work will provide a new insight into the physiological mechanism of early human metabolism which could help in determining the life histories and physiologies of extinct human species.

Menstrual cycle variability in rural Bangladeshi women

BAISHAKHI BASU, DARRYL J. HOLMAN, ANWESHA PAN and TANYA T. NGUYEN

Biological Anthropology, University of Washington

Ovarian cycles in women respond to environmental contexts and, in cases of extreme nutritional or psychological stress, can stop temporarily. We examined menstrual cycle variability in 302 married, rural Bangladeshi women. This population is characterized by low socioeconomic status, high disease load, early marriage, high parity, and long periods of lactation. We expected that these women would

experience, on average, longer and more variable menstrual cycles, with increasing variability with age. Participants were surveyed for up to nine months providing bi-weekly questionnaires and urine specimens. We used a parametric hazards analysis, statistically controlling for repeated measures, to estimate parameters of a lognormal distribution of cycle length from 1,289 observed cycles. Covariates included age, categorized into five-year intervals, and breastfeeding. Only about 20% of married women were cycling at 15-35 years; prevalence rose ~50% through 42 years, and was ~80% after age 42. Women aged 15 to 25 experienced, on average, long (>40 days) and highly variable cycles (SD>19). Women over 25 had mean cycle lengths of from 32 to 34 days, with lower variability (SD from 12 to 13). Regular breastfeeding increased the mean and SD of cycle length. We found surprisingly long and variable cycles in Bangladeshi women compared to most previous studies. Young women, in particular, seemed to experience occasional episodes of hypothalamic amenorrhea unrelated to breastfeeding or pregnancy. Relative to young women, small increases in cycle length and variability were seen as women entering the perimenopause.

This research was funded by the American Institute for Bangladesh Studies, Mellon Foundation, NSF (DBS-92-18734, SBR-9600690) and NICHD (R21 HD052081-01A1, 1F32 HD07994).

A meta-analysis of fission-fusion dynamics: towards a standardization of methods to facilitate inter- and intra-species comparisons

CARLY H. BATIST^{1,2} and ANDREA L. BADEN^{1,2,3}

¹Anthropology, CUNY Graduate Center, ²New York Consortium in Evolutionary Primatology, (NYCEP), ³Anthropology, CUNY Hunter College

The term 'fission-fusion' was first introduced by Kummer (1971) to describe the fluid interchanging of subgroups within a primate community. Fission-fusion dynamics (FFD) have now been studied in numerous primate and mammal taxa, but a lack of concise definitions and clear terminology have made inter- and intra-species comparisons infeasible. We conducted a meta-analysis of >200 records in the fission-fusion literature representing 42 primate & mammal species, and collected data on how subgrouping was assessed, what terminology was used, and which subgroup properties were recorded. Sites and research groups differ significantly in their terminologies used (e.g., parties vs. subgroups), and how subgroups are operationally defined (e.g., distance-based, neighbor rule, visibility). Moreover, metrics of the major axes of FFD (e.g., cohesion, composition, temporality) were rarely reported. FFD have been treated as largely unique, but we argue that subgrouping of some kind is commonplace in many primate species.

We can characterize the different "levels" of FFD within primates according to metrics of the aforementioned axes if we can quantify them in similar ways. To determine if within-site variation is truly due to differences in FFD as opposed to the product of different sampling designs, we should test different methodologies within a site to detect potential biases. This can help us analyze both intra-site variation to better understand the social and ecological underpinnings of FFD, and inter-site variation by quantifying differences in data collection protocols.

A Method for Identifying Cold-Induced Activation of Brown Adipose Tissue

VINCENT M. BATTISTA and JIM TORPY

Department of Anthropology, University of Michigan

Brown adipose tissue (BAT) is an energetically-efficient thermogenic form of fat. Inducible BAT, which is found in depots in the upper thorax, can be activated with only a slight drop in ambient temperature. To activate BAT in a clinical setting, human participants have been asked to spend a period of time in a climate-controlled chamber or otherwise to immerse themselves in cold water baths. These methods could be somewhat cumbersome while in the field. Presented is a means of achieving BAT thermogenesis through the use of a Liquid Cooling Ventilation Garment (LCVG). When coupled with thermal imaging, this LCVG approach allows us to track changes in toracic skin surface temperatures (proximal evidence for BAT activation) as they occur in real time. This technique provides a non-invasive and comparatively mild means of inducing BAT thermogenesis, and thus offers new opportunities to explore and quantify various cold-adaptive phenotypes while in the field.

Dental developmental patterns and tissue volume variation along the arcade in Neandertals and Upper Paleolithic humans

PRISCILLA BAYLE¹, THOMAS COLARD^{1,2} and MONA LE LUYER^{1,3}

¹PACEA UMR5199, University of Bordeaux, France, ²PMOI EA4490, University of Lille, France, ³School of Anthropology and Conservation, University of Kent, UK

Differences have been reported between Neandertals and extant humans in their pattern of dental development and tooth tissue proportions along the dental arcade. In this context, the Gravettian child from Lagar Velho, Portugal, has been shown to have a developmental pattern and metamerism variation currently only documented in Neandertals. However, the relationship between these parameters is not fully understood as a larger survey in Late Pleistocene and Holocene humans has not yet been realized. Here we use microCT-based data to finely quantify

ABSTRACTS

these variables and test the link between them in the deciduous and/or permanent dentitions of 13 Neandertal and 5 Upper Paleolithic modern human children of different chrono-cultural contexts from Western Europe. We also incorporate more than 2000 radiographs, 146 CT-scans, and 40 microCT-scans of Holocene children from worldwide origins. When compared to Holocene individuals, Neandertals and Lagar Velho show a delay in incisor relative to molar development that is associated with differences in dentine volume variation along the arcade. Indeed, Neandertals and Lagar Velho show high metameric variation, with particularly large incisor dentine volumes and values closer to Holocene individuals for molars. In contrast, the other Upper Paleolithic individuals, including a Gravettian one, display both comparable developmental pattern and dentine volume variation along the arcade to the Holocene children. Even if future investigations are needed to unlock the genetically- and/or functionally-related factors sustaining this correlation, these results provide insights into developmental processes that are relevant to our knowledge of macro- and microevolution in Late Pleistocene and Holocene populations.

Funding from University of Bordeaux, IdEx Bordeaux, French CNRS, and Région Nouvelle Aquitaine.

Putrid, fermented, spoiled, decayed, let's call the whole thing "off": consumption of putrid meat by Neanderthals

MELANIE M. BEASLEY¹, JULIE LESNIK² and ANGELA PERRI³

¹Department of Anthropology, University of Tennessee, Knoxville, ²Department of Anthropology, Wayne State University, ³Department of Archaeology, Durham University

Elevated $\delta^{15}\text{N}$ values of many Neanderthals has contributed to the widely adopted interpretation of Neanderthals as "top predators". In 2017, Speth proposed that the consumption of putrid meat and fish might be a dietary item that is under-explored in the Upper Paleolithic food menu. We explore the $\Delta^{15}\text{N}$ observed in muscle tissue decomposing during winter of 10 mammals averaging 176 pounds placed on the surface. During the first 40 days when daily temperatures average 9.3 °C, no significant difference is observed from the starting $\delta^{15}\text{N}$ value (mean $\Delta^{15}\text{N} = 0.1\text{‰}$). From day 41-76 (when identifiable muscle tissue was still present), there is a significant increase in $\Delta^{15}\text{N}$ with an average increase of 1.7‰ despite no significant change in the daily temperature average or max daily temperature, 10.0 and 25.6 °C, respectively. In moderately cold weather, mammal muscle tissue consumed within the first 40 days after death, would not increase $\delta^{15}\text{N}$ values of the consumer. In colder weather, it is assumed that during early decomposition the period of stasis in $\delta^{15}\text{N}$ values would exceed 40 days. While Speth (2017) is correct

that Upper Paleolithic hominins could consume putrid meat, the data from our study indicates that the consumption of putrid meat in the first 40 days would not contribute to high $\delta^{15}\text{N}$ values. While ethnohistoric accounts of deliberate putrefaction include intentional burial of carcasses and our study was surface placed mammals, we argue that in significantly colder weather occupied by Neanderthals the lack of $\Delta^{15}\text{N}$ would likely not change if buried.

Timing is everything: Implementing a Life Course Perspective to Investigate Developmental Origins of Health and Disease in a Medieval Italian Skeletal Sample

PATRICK BEAUCHESNE¹, TRENT TROMBLEY², SABRINA C. AGARWAL², KATHERINE KINKOPF², CAROLINE GOODSON³, FRANCESCA CANDILIO⁴, ALFREDO COPPA⁵ and MAURO RUBINI⁶

¹Behavioral Sciences, University of Michigan, Dearborn, ²Anthropology, University of California, Berkeley, ³History, University of Cambridge, ⁴Soprintendenza Archeologia, Belle Arti e Paesaggio per la città metropolitana di Cagliari e le province di Oristano e Sud Sardegna, ⁵Human and Animal Biology, University of Rome La Sapienza, ⁶Anthropological Service, Lazio, Italy

Bioarchaeologists have recently shown increasing interest in the Developmental Origins of Health and Disease (DOHaD) hypothesis as a better way to explain variation in morbidity and mortality in both past and present human populations. We present here an analysis of sex differences using vertebral neural canal data ($n = 70$) as well as prevalence and timing of linear enamel hypoplasias ($n = 51$) from the late medieval rural population of Villamagna, Italy. Vertebral neural canals were measured following standard protocols, with thoracic elements considered separately from lumbar ones as they complete growth at different stages in the life course. Linear enamel hypoplasias were identified macroscopically while a sub-sample of individuals with unworn teeth ($n = 21$) were analyzed for the timing of LEH events by measuring the position of each event on the crown in relation to histological estimates of tooth development. Our results for the transverse measure of vertebral neural canal size suggest that males faced substantial stress in late childhood that is also correlated with an earlier age-at-death. Conversely, we do not see a sex-difference in mortality risk with LEH. These data, taken together, lend support to recent arguments that stress in later childhood and early adolescence may be a better predictor of increased morbidity and mortality than stress events earlier in life. We conclude with a brief discussion of future directions, in particular how interpretations health and stress within the DOHaD framework should grounded in a well-developed biocultural context.

The atlas of the *Australopithecus* specimen StW 573 ("Little Foot")

AMÉLIE BEAUDET^{1,2}, RONALD J. CLARKE³, JASON L. HEATON^{3,4,5}, TRAVIS R. PICKERING^{3,5,6}, KRISTIAN J. CARLSON^{3,7}, ROBIN CROMPTON^{3,8}, TEA JASHASHVILI^{10,3,9}, LAURENT BRUXELLES^{11,12}, KUDAKWASHE JAKATA³, JAKOBUS HOFFMAN¹³, JELLE DHAENE¹⁴ and DOMINIC STRATFORD¹

¹School of Geography, Archaeology and Environmental Studies, University of the Witwatersrand, South Africa, ²Department of Anatomy, University of Pretoria, South Africa, ³Evolutionary Studies Institute, University of the Witwatersrand, South Africa, ⁴Department of Biology, Birmingham-Southern College, USA, ⁵Plio-Pleistocene Palaeontology Section, Department of Vertebrates, Ditsong National Museum of Natural History, South Africa, ⁶Department of Anthropology, University of Wisconsin, USA, ⁷Department of Integrative Anatomical Sciences, Keck School of Medicine, University of Southern California, USA, ⁸Department of Rheumatology, Aintree University Hospital NHS Trust, England, ⁹Molecular Imaging Center, Department of Radiology, Keck School of Medicine, University of Southern California, USA, ¹⁰Department of Geology and Paleontology, Georgian National Museum, Georgia, ¹¹French Institute of South Africa (IFAS), USR 3336 CNRS, South Africa, ¹²French National Institute for Preventive Archaeological Research, France, ¹³South African Nuclear Energy Corporation SOC Ltd. (Necsa), South Africa, ¹⁴UGCT Department of Physics and Astronomy, Ghent University, Belgium

The *Australopithecus* specimen StW 573 ("Little Foot") was discovered in 1997 in Member 2 of the Sterkfontein Formation (South Africa). Besides representing one of the oldest examples of *Australopithecus* in the southern African fossil record, the StW 573 skeleton is remarkable for its exceptional degree of preservation and completeness. In this regard, StW 573 offers the opportunity to shed new light on the poorly known postcranial anatomy and locomotor behaviour of Pliocene hominins. In particular, meticulous excavation and high-resolution micro-CT scanning of the skull revealed a nearly complete first cervical vertebra cemented by breccia to the back of the maxilla. The atlas of StW 573 is missing only the left transverse process and exhibits slight damage to the tip of the right transverse process. Comparative morphological study indicates a combination of human-like (e.g., mildly concave superior articular facets, posterior expansion of the vertebral canal), ape-like (e.g., prominent anterior tubercle, supero-inferior widening of the posterior arch) and unexpected (i.e., absence of prominent tubercles for attachment of the transverse ligament) traits. Since cervical vertebrae play a major role in directing and stabilizing head movement and because they rarely preserve in the fossil record (i.e., this is the first atlas from

ABSTRACTS

Sterkfontein), ongoing comparative morphometric analyses of the atlas of StW 573 will provide new evidence for reconstructing early hominin posture and locomotion.

Funding support provided by Claude Leon Foundation, CoE in Palaeosciences, IFAS, NRF, PAST. We thank the CHPC supercomputing center.

A tale of three monkeys: male-mediated prenatal loss explained

JACINTA C. BEEHNER^{1,2}, MATT N. ZIPPLE³, EILA K. ROBERTS⁴ and SUSAN C. ALBERTS^{3,5,6}

¹Department of Anthropology, University of Michigan, ²Department of Psychology, University of Michigan, ³Department of Biology, Duke University, ⁴Department of Integrative Biology, Michigan State University, ⁵Department of Evolutionary Anthropology, Duke University, ⁶Institute of Primate Research, National Museums of Kenya

Infanticide by males has been the subject of intense empirical and theoretical study for decades. However, a related phenomenon, male-mediated prenatal loss, has received considerably less attention. Male-mediated prenatal loss occurs when inseminated or pregnant females terminate reproductive effort following exposure to a non-sire male, either through implantation failure or pregnancy termination. Male-mediated prenatal loss encompasses two sub-phenomena: sexually selected feticide and the Bruce effect. In this talk, we walk through three different evolutionary scenarios in three species of primate - the yellow baboon, the gelada, and the chacma baboon - to lay out a framework that explains the relationship between infanticide, feticide, and the Bruce effect and describes the proximate and ultimate mechanisms involved for each. We argue that male-mediated prenatal loss may have played a greater role in mammalian social evolution than has previously been documented.

National Science Foundation (BCS-0824592, BCS-0715179, IOS-1255974 to JCB; IOS-1456832 to SCA), National Institute on Aging (R01-AG053330, P01-AG031719 to SCA), Duke University (SCA, MNZ), University of Michigan (JCB), Michigan State University (EKR).

Does learning evolutionary theory within anthropology help students reason about human evolution?

ELIZABETH P. BEGGROW

Center for Life Sciences Education, The Ohio State University

Situated cognition theory sees learning as situated within the context of the social and cultural setting in which it takes place. Consequently, learning evolution within biological anthropology (b.a.) should result in the knowledge acquisition, retrieval and problem solving of evolutionary concepts being situated within the human context. This hypothesis was tested by asking introductory level b.a. (137) and biology (147)

students at a Midwestern university to explain evolutionary change of familiar or unfamiliar traits in either humans or nonhuman taxa and assessing their reasoning patterns. A previously published instrument, the ACORNS, was used to collect data post instruction on basic evolutionary concepts. Responses were scored for the presence of accurate key concepts (KCs) (e.g., variation, heritability, differential reproduction). A Mann-Whitney U test showed no differences for the biology sample between assessments that used human vs. nonhuman taxa, but the b.a. sample had a higher KC score (0.01) for the assessment with nonhuman taxa and used the KC 'differential reproduction' more for nonhuman taxa ($p = 0.024$). Furthermore, a comparison of how familiar and unfamiliar traits in the items affect reasoning patterns found no differences between items for the biology sample, while the b.a. sample had higher KC scores for items that asked about familiar traits in nonhuman taxa ($p = 0.006$). These results suggest that, overall, biology students are able to generalize their knowledge about evolutionary change across contexts more fluidly, while some contextual features appear to impact anthropology students' reasoning patterns, highlighting important implications for b.a. instruction.

This research was funded by the Marilyn Ruth Hathaway Education Scholarship Fund and NSF REESE grant 0909999.

Hominin origins: New evidence from the eastern Mediterranean

DAVID R. BEGUN¹, MADELAINE BÖHME^{2,3}, GEORGE KOUFOS⁴, NIKOLAI SPASSOV⁵, AYLA SEVİM EROL⁶ and ALPER YENER YAVUZ⁷

¹Department of Anthropology, University of Toronto, ²Department of Geoscience, Eberhard-Karls-University, ³Senckenberg Centre for Human Evolution and Palaeoenvironment (HEP), Senckenberg, ⁴Department of Geology, Laboratory of Geology and Palaeontology, Aristotle University of Thessaloniki, ⁵National Museum of Natural History, Bulgarian Academy of Sciences, ⁶Department of Anthropology, Ankara University, ⁷Department of Anthropology, MAKÜ

Great ape fossils, ranging in age from about 9.5 to 7.2 Ma, are known from Bulgaria, Greek Macedonia, Attica and Anatolia. Usually attributed to a single genus, recent analysis confirms the generic distinction of *Graecopithecus* (Attica) and *Ouranopithecus* (Macedonia.) Within Macedonia, the samples from Ravin de la Pluie and Xirochori, both about 9.5 Ma, form a well-defined hypodigm for *Ouranopithecus macedoniensis*. A younger sample from Macedonia but further to the south, Nikiti 1, dated to between 8.5 to 9 Ma, is close in age to Çorakyerler from central Anatolia. Nikiti 1 and Çorakyerler are distinguished from *Ouranopithecus macedoniensis* by larger post-canine teeth, more homomorphic premolars and smaller canines. *Graecopithecus*, from the

7.2 Ma site of Pygros Vassilissis (Attica), has the smallest canine (as suggested by root size), fused premolar roots and the largest molars relative to mandibular corpus dimensions of all eastern Mediterranean great apes. These samples may represent an evolving lineage characterized by increasing postcanine and decreasing canine sizes. We propose two alternative phylogenetic hypotheses. This lineage, linked phylogenetically with the middle and late Miocene dryopiths, may be a terminal representative of the radiation of European Miocene great apes, having survived and adapted to more open conditions in the eastern Mediterranean. Alternatively, this lineage may represent a transition from the stem hominines of central and Western Europe to the earliest known hominins of Africa (e.g. *Sahelanthropus*, *Orrorin*) and as such documents the origin of the hominins in Europe.

DRB is supported by funds from NSERC.

Cranial trauma prevalence in Neanderthals and early Upper Paleolithic modern humans

JUDITH BEIER¹, NILS ANTHES², JOACHIM WAHL^{1,3} and KATERINA HARVATI^{1,4}

¹Paleoanthropology, Senckenberg Centre for Human Evolution and Palaeoenvironment, University of Tübingen, ²Animal Evolutionary Ecology, Institute of Evolution and Ecology, University of Tübingen, ³Osteology, State Office for Cultural Heritage Management Baden-Württemberg, Konstanz, ⁴DFG Center for Advanced Studies 'Words, Bones, Genes, Tools', University of Tübingen

A high frequency of traumatic injuries has been considered common for Neanderthal (NEA) skeletal remains, and is variously attributed to stressful NEA lifestyles, violent behaviors and dangerous hunting practices – in contrast to Upper Paleolithic anatomically modern humans (UPH). However, only few quantitative studies on Paleolithic traumata exist to date and interpretations are mainly based on narrative, case-based evidence. Here, we assess the hypothesis of higher cranial trauma prevalence in NEA compared to UPH. Employing a population-level approach, we compiled an exhaustive database from the literature comprising 114 NEA and 90 UPH specimens (corresponding to 295 NEA and 541 UPH single cranial elements) with and without traumata from sites all over West-Eurasia dating to ca. 80-20 ka BP. We used generalized linear mixed models employing a Markov chain Monte Carlo algorithm to examine how trauma prevalence can be predicted by various variables, including taxon, age-at-death, sex, and skeletal preservation, while accounting for variation between geographic locations and cranial elements. Results show similar overall trauma prevalence in the two taxa, rejecting the hypothesis of higher NEA cranial trauma. Moreover, we found a higher prevalence for males in both taxa

ABSTRACTS

and that trauma prevalence was affected by the preservation of cranial remains. Beyond these similarities, we found age-dependent differences between the taxa, suggesting possible differences in the age of trauma acquisition and/or differential mortality risks of trauma survivors. Our results urge a reconsideration of behavioral and lifestyle attributes thought to underlie the proposed exceptional Neanderthal trauma prevalence.

This research is funded by the German Research Foundation (DFG). We gratefully acknowledge support from the University of Tübingen, the Senckenberg Gesellschaft für Naturforschung and the European Research Council.

The Impact of Industrialisation on London Health

JELENA J. BEKVALAC¹ and GAYNOR A. WESTERN²
¹Centre for Human Bioarchaeology, Museum of London, ²Osteology, Ossafreelance

The Impact of Industrialisation on London Health project is a multidisciplinary research project, funded by the Rosemary Green Grant (City of London Archaeological Trust), investigating the impact of this pivotal period of time on our health through the analysis of changes in trends seen in skeletal pathologies over time, up to the present day. In particular, the research is focussed on identifying the impact of our changing living and working environments that are fundamentally influenced by the process of industrialisation and urbanisation which have critical repercussions for our health. The incorporation of digital imaging technologies into our study has allowed us to enhance our current knowledge of prevalence rates in the past, of diseases important today, such as cancer and osteoporosis, as well as identifying evidence for obesity and metabolic syndrome by identifying hyperostosis frontalis interna (HFI) radiographically. Complementary macroscopic data was also used to study changes in Diffuse Idiopathic Skeletal Hyperostosis (DISH), fractures, rib lesions and caries to enhance our comparative data for trauma, air pollution and diet. The influence of age and sex are examined in relation to changing demographic profiles over time, recognising that the increased longevity experienced in modern populations is a dominant factor in some of the most common diseases seen today. Modern epidemiology also recognises the influence of social status and poverty on disease prevalence in European populations and we also investigate the emergence of social stratification on health outcomes during the Industrial period in London, comparing this to present day health data.

Comparing Evolutionary Models of Primate Hair Color Variation

RACHEL B. BELL¹, BRENDA J. BRADLEY² and JASON M. KAMILAR^{1,3}

¹Graduate Program in Organismic and Evolutionary Biology, University of Massachusetts Amherst, ²Center for the Advanced Study of Human Paleobiology, Department of Anthropology, The George Washington University, ³Department of Anthropology, University of Massachusetts Amherst

Primates are the most colorful mammalian order, yet the evolutionary patterns and processes related to pelage color diversity remain unclear. Here we use phylogenetic methods to examine hair color variation across five body regions for 145 individual primates representing ninety-four species from all major clades. First, we quantify the phylogenetic signal in primate hair coloration for each body region. Next, we compare the fit of three evolutionary models (Brownian motion, Early Burst, Ornstein-Uhlenbeck [OU]) and a null model for each body region. We then test for differences in trait optima and rate of color evolution among catarrhines, platyrrhines, and strepsirhines. Primate torso and hindlimb coloration show little phylogenetic signal. Head and forelimb coloration have higher phylogenetic signals and are more consistently explained by an OU evolutionary model, suggesting stabilizing selection. Despite a weak phylogenetic signal at the order level, sub-order analyses of tail coloration suggest clade-specific selective pressures and may indicate the tail's role in social signaling. Distinct clade patterns in the range of coat variation also emerge: catarrhine and platyrrhine hair color is more variable and generally exhibits higher evolutionary rates than strepsirhine coloration, which falls within a comparatively smaller, lighter range of pigmentation. Divergent patterns of hair color evolution between catarrhines, platyrrhines, and strepsirhines may correspond to clade-level biological differences, particularly visual systems and activity patterns. We demonstrate the independent evolution of pelage coloration between body regions, even between different pairs of limbs. Therefore, multiple selective pressures may differentially shape patterns of pelage coloration across the primate body.

Our research is supported by NSF (BCS #1546730, BCS #1606360), the Wenner-Gren Foundation, The George Washington University, University of Massachusetts, Amherst, Yale University and the Natural Environment Research Council, UK.

A review of prehistoric cannibalism in Europe: choice or necessity?

SILVIA M. BELLO¹, ESTHER HOWE² and JAMES COLE²

¹Dep Earth Sciences, The Natural History Museum, London, ²School of Environment and Technology, University of Brighton, Lewes Road, Brighton, BN2 4GJ, UK

There are many ways in which societies interact with the remains of their dead; among these practices, cannibalism remains an extremely contentious issue within archaeology. Gathering incontrovertible evidence of human body consumption is difficult, but even more controversial can be determining the motivation behind this practice. For our study, we re-evaluated the data presented in the literature of over 60 archaeological sites associated with different species of hominins (*H. antecessor*, *H. heidelbergensis*, Neanderthals and modern humans) for which cannibalism has been previously recognized. For each sample, we considered the distribution and frequencies of cut marks, percussion damage and human tooth marks. We then evaluated the nutritional intake for each site based on a nutritional template that offers a proxy calorie value for the human body. Results show that the frequency of cannibalistic cases through time generally increases, with the higher percentages of cannibalistic groups seen in Neanderthals and modern humans. In the case of modern humans, the association of cannibalism with ritualistic expression also becomes more frequent. Finally, the nutritional value of the cannibalised remains for each site appears significantly lower than that of a range of fauna found within the sites. These results suggest that the motivations behind hominin anthropophagy may not have been purely nutritional. It is proposed here that the comparatively low nutritional value of hominin cannibalism episodes and the higher frequency of cannibalistic sites for Neanderthals and modern humans, support more socially or culturally driven narratives in the interpretation of Palaeolithic cannibalism.

The research work of SMB is part of the "Human Behaviour in 3D" Project, funded by the Calleva Foundation.

Paleoenvironmental studies Tor Hamar, Southern Jordan: Early modern human behavioral adaptability during MIS 3

MIRIAM BELMAKER¹, HERVÉ BOCHERENS^{2,3}, YUICHI NAITO⁴, HALEY D. O'BRIEN⁵, CHRISTOPH WISSING², TORU TAMURA^{6,7} and SEIJI KADOWAKI⁴

¹Department of Anthropology, University of Tulsa, ²Department of Geosciences, Eberhard-Karls Universität Tübingen, ³Senckenberg Center for Human Evolution and Paleoenvironment, Eberhard-Karls Universität Tübingen, ⁴Nagoya University Museum, Nagoya University, ⁵Department of Anatomy and Cell Biology, Oklahoma State University Center for Health Sciences, ⁶Geological Survey of Japan, National Institute of Advanced Industrial Science and Technology, ⁷Department of Natural Environmental Studies, University of Tokyo

Paleoanthropological studies in arid regions of the Southern Levant provide a window into early modern human adaptations post-dating the dispersal from Africa during MIS 3-4. Understanding human adaptations is often

ABSTRACTS

couched as the tempo-spatial position of base-camps along a humid–arid continuum. However, addressing these issues requires local chronologically-constrained environmental data using robust multivariate methods. Here we present a paleoenvironmental study based on faunal composition and paleodietary proxies combined with new OSL dates for the late Pleistocene site of Tor Hamar, Jordan as a mirror into early modern human adaptations during MIS 3.

OSL results indicate layers H-F date to 31-42 ka encompassing Heinrich events 4 and 3 characterized by climatic fluctuations during MIS 3. Faunal composition includes a majority of ubiquitous *Gazelle* sp. and *Capra* sp. However, the presence of mole rat is indicative of a Mediterranean environment close to the site. In contrast, the paleodietary analysis of gazelles suggested a high proportion of C₄ plants with abrasive vegetation in the diet, based on $\delta^{13}\text{C}$ values and tooth wear studies respectively, suggestive of a dry and hot environment.

These results, consistent with other penecontemporaneous sites, point to location of the site within a sharp ecotone. While the rock-shelter was situated in a locally humid landscape, hunting occurred across a wider radius around the site, at times in varying altitudes, and in dryer habitats. Human adaptations during MIS 3 are nuanced and suggest utilization of a wide range of habitats providing a behavioral buffer from fluctuating climatic regimes.

MEXT KAKENHI Grant No. 16H06409

Preliminary analysis of dental pathologies frequencies among individuals at Los Indios archaeological site (AD 600-1200) Santa Isabel, Puerto Rico: considering oral health during the Late Ceramic Age (AD 600-1500)

ARIANA BELTRAN-BURGOS

Anthropology, California State University, Los Angeles

Los Indios archaeological site is in Santa Isabel, Puerto Rico in the southern coast of the island. It is an Ostionoid settlement (AD 600-1200) part of the Late Ceramic Age (LCA) period (AD 600-1500). Ostionoids are the result of the interaction between Saladoid and Archaic groups in the Caribbean. Archaeological evidence recognized the LCA as a transitional period to large complex hierarchical societies with an intensification of agricultural production involving cariogenic food such as maize and manioc. In this research, dental samples of 86 individuals among the total 130 burials were analyzed to explore the relationship between their oral health and the transitional time period. The frequency of total individuals presenting evidence of caries, antemortem tooth loss (AMTL), abscesses and enamel hypoplasia was calculated. Also, the number of teeth

presenting evidence of caries was determined. 66.3 % (57/86) of individuals showed evidence of caries and 13.4 % (170/1273) of teeth presented evidence of caries. Only 8 (8/86 = 9.3%) individuals presented evidence of enamel hypoplasia, 18 (18/86= 20.9%) presented evidence of AMTL and 3 (3/86= 3.5%) had evidence of periapical abscesses. A preliminary analysis suggests that Los Indios inhabitants might have had a marine-based diet. However, the consumption of agricultural products cannot be totally discarded. The relationship between the high percentage of individuals with caries and the low frequency of teeth with caries needs to be further studied. Also, loss of information due to moderate to severe dental wear, and poor preservation of the skeletal material need to be considered.

Urinary oxytocin in capuchin monkeys: Validation and the influence of social behavior

MARCELA E. BENITEZ^{1,2,3}, MEGHAN J. SOSNOWSKI^{1,2,3}, OLIVIA B. TOMEO^{1,2,3} and SARAH F. BROSNAN^{1,2,3,4}

¹Department of Psychology, Georgia State University, ²Language Research Center, Georgia State University, ³Center for Behavioral Neuroscience, Georgia State University, ⁴Neuroscience Institute, Georgia State University

In highly social species, like primates, oxytocin plays an important role in cooperation, and in the formation and maintenance of social relationships. Despite recent interest in the relationship between oxytocin and social behavior in nonhuman primates, relatively little is known about endogenous oxytocin in social New World Monkeys. Here, we investigate the relationship between oxytocin and two affiliative behaviors, grooming and fur-rubbing, in 18 socially-housed capuchin monkeys (*Sapajus apella*). We found that urinary oxytocin increased after capuchins were groomed ($\beta = 0.28$, $t = 2.10$, $p = 0.038$) or participated in a fur-rubbing bout ($\beta = 0.27$, $t = 2.07$, $p = 0.041$). Furthermore, we found that affiliative behaviors fluctuated after fur-rubbing, increasing proximity and contact during ($\beta = 0.69$, $z = 5.75$, $p < 0.001$) and 30 minutes afterwards ($\beta = 0.31$, $SE = 0.14$, $p = 0.026$), but decreasing these behaviors immediately following a fur-rubbing event ($\beta = -0.85$, $SE = 0.24$, $p < 0.001$). This supports previous research that oxytocin may, in fact, initially be related to increased social distance in this species but ultimately function to strengthen social relationships. Overall, these results support a critical role for oxytocin in affiliative behaviors that maintain and strengthen social relationships in capuchin monkeys and highlight the complexity of the interactions among oxytocin, affiliative behaviors, and social bonding.

This research was funded by the National Science Foundation Postdoctoral Research Fellowship (SMA-1214923) and the GSU Brains & Behavior Program

Epigenetic Insights into Early Life Plasticity and Reproductive Function

GILLIAN R. BENTLEY¹, REINHARD STÖGER², RICHARD D. EMES³, BENJAMIN BAR-SADE⁴, KHURSHIDA BEGUM¹, OR EDEN⁴ and PHILIPPA MELAMED⁴

¹Dept of Anthropology, Durham University, UK, ²School of Biosciences, University of Nottingham, UK, ³Advanced Data Analysis Centre, University of Nottingham, UK, ⁴Faculty of Biology, Technion-Israel Institute of Technology

Prior studies on migrant Bangladeshi women to England show early life immunological stress modifies reproductive phenotypes compared to non-migrants. We have validated a rodent model recapitulating these altered phenotypes, and uncovered related molecular and epigenetic mechanisms. Transcriptome analysis of ovaries from stressed mice revealed up-regulated genes that induce follicle growth in the ovary, and repression of genes promoting cell death. Repressed genes include *Srd5a1* (encoding the enzyme 5 α -reductase), down-regulation of which (through increased methylation) matched findings from Bangladeshi migrants obtained using cheek swabs. In mice, expression of *Srd5a1* was also significantly reduced in the hypothalamus, where neurosteroids direct central activation of both the HPG and HPA axes through binding and activating specific neuronal (GABA) receptors. The HPA axis in humans is activated during adrenarche, at approximately age 8, when children attain neurological maturation, signalling onset of middle childhood. Crucially, in prior studies, a threshold for altered reproductive phenotypes in Bangladeshi migrants was also age 8, while Bangladeshi children who moved early to Britain experienced significantly earlier adrenarche. Our studies link central changes in activation and functioning of the adrenal axis with possible epigenetic regulation of *Srd5a1* expression during a crucial developmental window. Changes in activation of hypothalamic control centres (via reduced 5 α -reductase activity) could provide a possible mechanism for alteration in ages of both puberty and adrenarche, as well as modified adult function of these axes. We reveal that epigenetic modifications comprise flexible, regulatory mechanisms mediating phenotypic changes through altered gene expression.

Funding: ESRC/BBSRC, UK

Skeletal remains and historical traces of Ming Dynasty elites in Shaanxi, China

ELIZABETH BERGER¹, WA YE² and LIPING YANG³

¹Lieberthal-Rogel Center for Chinese Studies, University of Michigan, ²Institute for Field Research, University of California, Los Angeles, ³Shaanxi Archaeological Academy

The Yangguanzhai cemetery, near Xi'an, China, has been in use from the Neolithic period through recent historical times. The cemetery includes

ABSTRACTS

22 brick tombs from the Ming Dynasty (1368-1644), many of them multiple burials, belonging to local elites. Four tombs of the Zhang family contain inscriptions of the occupants, as well as their birth, death, and burial dates. Historical records contain information on the Zhang family's residence in the area, and changes in local toponyms, topography, and land use. In addition, an osteobiographical approach to studying the skeletal remains reveals details of their lives that are not recoverable from historical records. For instance, tomb M53 contained a male buried with two females, whose names, ages, and virtues as wives are contained in the tomb inscriptions. Meanwhile, their remains contain the embodied traces of their lives: the skeleton of the wife who died at age 33 shows very few indications of disease or degenerative conditions, while the skeleton of the one who died at 60 shows antemortem loss of most teeth, severe osteoarthritis in most joints, degeneration of the spine, and a chronically dislocated shoulder joint with severe deformation. Additional analysis of all 23 well-preserved occupants of the Ming tombs reveals a relatively high prevalence of trauma, as well as evidence of smallpox, foot binding, osteoarthritis, periostitis, linear enamel hypoplasias, and craniocostosis. This study is intended to model the possibilities of collaboration between bioarchaeology and history, building on the extensive historical, archaeological, and skeletal records of China.

This project is supported by the Shaanxi Archaeological Academy and the Institute for Field Research.

In vitro gene regulatory responses to growth factors in short-statured African rainforest hunter-gatherers

CHRISTINA M. BERGEY¹, KATHLEEN E. GROGAN¹, GENELLE F. HARRISON^{2,3}, VANIA G. YOTOVA³, LUIS B. BARREIRO^{3,4} and GEORGE PERRY¹

¹Departments of Anthropology and Biology, Pennsylvania State University, ²Department of Human Genetics, McGill University, ³Centre de Recherche CHU Sainte-Justine, Université de Montréal, ⁴Department of Medicine, University of Chicago

Body size is a fundamental aspect of biology and health. A considerable portion of the inter- and intra-population variation in human body size and stature is attributable to genetic factors. However, despite recent gains in understanding the genetic underpinnings of this important component of health, the proximate mechanisms that lead to variation in body size are largely unknown. We explored gene expression responses to growth factors in cell lines from individuals from two different populations: Batwa rainforest hunter-gatherers from Southwest Uganda with the "pygmy" phenotype (mean adult stature: males = 152.9 cm; females = 145.7) and their taller subsistence agriculturalist neighbors, the Bakiga

(males = 165.4 cm; females = 155.1). Based on our previous work, the inter-population height difference is at least partly genetically mediated. In the present study, we exposed immortalized lymphoblastoid cells (LCLs) to growth hormone (GH) and insulin-like growth factor-1 (IGF1) and then used RNA-seq to characterize the transcriptome-wide gene expression response at 0, 2, and 6 hours post initial exposure. We also developed and implemented the use of a synthetic antisense oligonucleotide to silence the GH gene and halt endogenous GH production, allowing careful assessment of induced response to exogenous growth factor concentrations. We observe response expression differences in the GH/IGF1 pathway between the populations, with the Batwa having, for example, reduced expression of *SOCS2*, a gene that interacts with growth hormone receptor (GHR) and insulin-like growth factor-1 receptor (IGF1R).

Funding was provided by NIH R01-GM115656, F32 GM125228, and F32 GM123634.

Resilience of the hunter-gatherers of Lagoa Santa, Brazil: a new case of Paleoamerican late survival

DANILO V. BERNARDO¹, PEDRO DA-GLORIA² and WALTER A. NEVES³

¹Laboratório de Estudos em Antropologia Biológica, Bioarqueologia e Evolução Humana, Instituto de Ciências Humanas e da Informação, Universidade Federal do Rio Grande, ²Graduate Program of Anthropology, Federal University of Pará, ³Instituto de Estudos Avançados, Universidade de São Paulo

The contributions of Biological Anthropology are crucial to understanding the occupation of the New World, allowing the proposition of models discussing origin, dispersion, and chronologies of Native Americans. In this context, the investigation of long-term occupations can shed light on the processes of resilience, territorial strategies, and biocultural adaptation of the Native Americans. Here we present a new case of Paleoamerican late survival in South America, based on a new radiocarbon date and the morphology of Lapa do Caetano's skull exhumed in the beginning of the 20th century at Lagoa Santa, Central-Eastern Brazil. We applied multivariate statistical techniques on craniometric measurements in accordance with Howells' protocol followed by tests for the best dispersion scenarios to evaluate the likelihood of the late survival of Paleoamerican morphology. Our results show that Lapa do Caetano' skull is dated to 2120 +/- 30 BP (BETA 396821) and retained the same Paleoamerican morphological pattern found in early skulls in the Americas and in recent crania found in Central-Eastern Brazil. The archaeological data show intermittent hunter-gatherer occupations in the region retaining the same basic strategies of subsistence. These

results suggest strong resilience of these South American hunter-gatherers in both cultural and biological aspects, which have important implications for the models of peopling of the New World. As in previous studies, our investigation shows that models which consider a late survival of the Paleoamerican morphology are better adjusted compared with the models that propose a complete substitution of this early morphology.

Conselho Nacional de Desenvolvimento Científico e Tecnológico – CNPq (Process MCTI/CNPq/Universal 14/2014/461122/2014-6 to DVB) and Fundação de Amparo à Pesquisa do Estado de São Paulo – FAPESP (Process 2013/00069-0 to PD).

Reconstruction of intentional violence in the Central European Early Medieval: perimortem axe skull injuries at Pohansko-Břeclav

MARGIT BERNER¹, JIŘÍ MACHÁČEK² and VLADIMÍR SLÁDEK³

¹Department of Anthropology, Natural History Museum, Vienna, ²Department of Archaeology and Museology, Masaryk University, Czech Republic, ³Department of Anthropology and Human Genetics, Faculty of Science, Charles University in Prague, Czech Republic

Perimortem penetrating skull fractures in archaeological skeletons leave traces that give us clues to reconstruct human activity involved in violent death as well as to identify the weapons or tools used to inflict injuries. In this study, we examined 55 adult individuals from the 2nd church Cemetery of the Early Medieval site at Pohansko-Břeclav (Czech Republic) for signs of cranial injuries in regard to perimortem penetrating skull trauma. In general, evidence of cranial trauma was found in eight individuals (14.5 %). Males (7/32 = 23.3%) exhibited significantly more cranial injuries ($p = 0.043$) than females (1/25 = 4%). Whilst a healed trauma was found in one female (blunt-force trauma) and three males (two blunt-force and one facial trauma), evidence of perimortem and/or multiple skull trauma was found only in males. In three male individuals, we observed depression fractures of special shape, which can be used for a more detailed reconstruction of the type of interpersonal violence. Two skulls revealed one penetration and one cranium three lesions of oval to round shape with sharp edges at the outer table, and irregular edges with chipping on the inner laminar table. Comparison of size and shape of these lesions with the dimensions of different weapons and tools of the Early Medieval archaeological assemblage revealed the hammerhead of axes as the most likely weapon causing these injuries. This kind of intentional violence is unique for the 2nd church Cemetery and was not reported for any of the other seven cemeteries of this site.

ABSTRACTS

Integration of growth in head circumference, body length, and body weight in rural Gambian infants during the first year of life

ROBIN M. BERNSTEIN^{1,2}, ZOFIA STANLEY³, NABEEL AFFARA⁴, DAVID B. DUNGER⁵, KEN K. ONG^{5,6}, ANDREW M. PRENTICE⁷ and SOPHIE E. MOORE^{7,8}

¹Department of Anthropology, University of Colorado Boulder, ²Health and Society Program, Institute of Behavioral Science, University of Colorado Boulder, ³Department of Applied Mathematics, University of Colorado Boulder, ⁴Department of Pathology, University of Cambridge, ⁵Department of Paediatrics, University of Cambridge School of Clinical Medicine, ⁶MRC Epidemiology Unit, University of Cambridge School of Clinical Medicine, ⁷MRC Unit The Gambia, London School of Hygiene and Tropical Medicine, ⁸Department of Women and Children's Health, King's College, London

Relatively large human brains, and their associated high energetic cost, have often been discussed in terms of developmental tradeoffs. These tradeoffs are not constant throughout all of development. The peak metabolic cost of the brain in early childhood is offset by reduced body growth rate, but during infancy, both body weight growth velocity and brain metabolic cost are high and also slowing down. In order to examine the covariation in body and brain growth velocity in the first year of life, we use methods from spatial statistics to estimate a covariance matrix describing the correlation of growth curves between and within subjects across time. We calculated correlations between head circumference, body length, and body weight from measurements of rural Gambian infants enrolled in the HERO-G (Hormonal and Epigenetic Regulators Of Growth) study. We use measurements taken every other day between days 9 and 365 of postnatal life (N=69 (F=36, M=33)). Weight and head circumference were the most highly correlated and in phase of all measurement pairs, with significant correlations spanning lag -10 to 8 days ($r=0.16-0.30$). Only some of these infants show a smoothly decelerating curve of body weight velocity; many others show temporally integrated episodes of body and brain growth faltering and catch-up within the first year of life. This concordance in body weight growth with brain growth during the first year of life, and the potential alteration to energetic costs of development within the context of faltering and rebound, warrants further investigation.

Funded by the Bill and Melinda Gates Foundation (OPP1066932)

Research from records: retrieving and sharing useful data from a non-research database

SHAMSI DANESHVARI BERRY¹ and HEATHER JH. EDGAR^{2,3}

¹Health Informatics and Information Management, University of Mississippi Medical Center,

²Anthropology, University of New Mexico, ³Office of the Medical Investigator, University of New Mexico

A common problem in research is extracting data in an accurate, standardized, time efficient way. This is especially true when useful data were originally collected for a purpose other than research. The New Mexico Office of the Medical Investigator controls such a database, VAST. VAST is associated with a dataset we are making available for research in the New Mexico Decedent Image Database (NMDID). NMDID provides free access to 15,249 whole body CT scans and 57 associated metadata variables from VAST.

We encountered several challenges associated with merging these data sources. For example, sex can be listed as "M/m/male/Male." As data complexity increases, data recovery becomes less accurate. To address this, the NMDID utilizes data standards derived from anthropology, medicine, and other fields. For instance, the field "substance usage" was standardized using the International Classification of Diseases. Where there were no appropriate standards, modifications or new standards were generated. VAST also includes many free-text fields, each encompassing substantial, varied information. We implemented Canary for natural language processing (NLP) to retrieve these data. This effort resulted in drug prescription information on decedents as well as environmental conditions of the cadaver. Manually reviewing the record to extract prescriptions and conditions would take approximately 5 minutes per case, totaling 1250 hours for this dataset. NLP allowed completion of this work in 50 hours. The CTs and associated metadata in NMDID can be used to address research questions in fields such as anatomy, growth and development, pathology, public health, and forensics.

Funded by National Institute of Justice 2016-DN-BX-0144. Statements made are solely the responsibility of the authors.

South African hominin dental biomechanics

MICHAEL A. BERTHAUME^{1,2,3} and KORNELIUS KUPCZIK²

¹Department of Bioengineering, Imperial College London, ²Max Planck Weizmann Center for Integrative Archaeology and Anthropology, Max Planck Institute of Evolutionary Anthropology, ³Department of Anthropology, Durham University

Dietary reconstructions of *Australopithecus africanus* and *Paranthropus robustus* point towards overlapping, but distinct, dietary ecologies, with *A. africanus* consuming more savanna resources, using its incisors more, and eating foods that wore its molars less. Morphologically, *P. robustus*'s larger chewing muscles and relatively larger, thicker enameled molars have led some to argue *P. robustus* consumed foods that required a higher bite force. If so, it is reasonable to assume

P. robustus's molars were more efficient at breaking foods down. Here, we quantify molar function using 32 3D printed replicas of LM₂s (n=17 *A. africanus*, n=15 *P. robustus*) exhibiting low levels of wear and a universal tester. Teeth fractured gelatin blocks, and the force and energy to fracture was recorded/calculated (n=5 trials/tooth). A Bayesian mixed effect linear model was used to test for differences in force and energy while normalizing for the random effects of multiple trials and dental wear. *Paranthropus robustus* required 27% more force and 17% more energy to fracture the gelatin blocks, presumably because *A. africanus*'s molars concentrate energy around a crack tip, instigating crack initiation, more efficiently than *P. robustus*. These results indicate that, for a given diet, *P. robustus* would require larger masticatory muscles to produce a higher bite force/more energy to break down the foods, and thicker enamel to resist these forces. The differences observed here suggest *P. robustus* may have consumed foods for which reducing bite force/energy were not important, or that the changes in craniomandibular and dental complexes do not represent dietary adaptations.

We thank the Max Planck Institute of Evolutionary Anthropology and Max Planck Weizmann Center for funding this research.

Frailty and Survivorship in Medieval Poland: A Comparison of Urban and Rural Populations

TRACY K. BETSINGER¹, SHARON N. DEWITTE², HEDY JUSTUS³ and AMANDA M. AGNEW⁴

¹Anthropology, SUNY Oneonta, ²Anthropology, University of South Carolina, ³SNA International, ⁴Skeletal Biology Research Lab, Ohio State University

Early medieval Poland (10th-12 centuries AD) experienced substantial change, including increasing urbanization, which has been associated with detrimental health effects, such as higher rates of infectious disease due to population crowding. This may lead to higher rates of mortality and lower survivorship, impacts from which rural populations may have been buffered due to their lower population density. Skeletal samples from medieval urban and rural Polish populations provide an opportunity to test the hypothesis that urban inhabitants experienced lower survivorship and a higher risk of mortality than their rural counterparts. To test this hypothesis, demographic data from urban Poznań (n=98) and from rural Giecz (n=246) were analyzed using Kaplan Meier survival analysis, a semi-parametric Cox proportional-hazards model, and fully parametric Siler and Gompertz hazards analysis. Analyses including all individuals as well as adults of each sex reveal no differences in survivorship between urban and rural inhabitants. Analyses of adults (18+ years) similarly reveal no significant difference in urban and rural survivorship. However,

ABSTRACTS

analysis of nonadults, reveal that rural children have higher survivorship than urban children. None of the semi-parametric or fully parametric hazards analyses reveal any significant difference in risk of mortality between rural and urban inhabitants using the entire dataset or any subset thereof. These results suggest that rural vs. urban dwellings did not impact the overall survivorship and risk of mortality once people reached adulthood. For nonadults, living in urban centers apparently reduced survivorship, perhaps because of increased exposure to and easier spread of infectious disease.

Assessing striae of Retzius periodicity nondestructively using perikymata counts and distribution in two new populations

BARBARA J. BETZ, MACKIE C. O'HARA and LEIGH OLDERSHAW

Anthropology, The Ohio State University

To accurately assess the timing of linear enamel hypoplasia (LEH) defects, it is necessary to accurately estimate striae of Retzius periodicity for each individual. Previous studies using mandibular canine samples from medieval Denmark and modern New Zealand, United Kingdom, and southern Africa have found an inverse relationship between striae periodicity and the total number of striae in imbricational enamel (analogous to total number of perikymata). Some have further proposed that a simple calculation can be developed for nondestructively estimating periodicity based on the range of perikymata counts in deciles six to nine. In an effort to test this inverse relationship in additional populations, high definition tooth crown replicas and histological thin sections of mandibular canines from Neolithic Çatalhöyük ($n=15$) and from a modern New York, NY cadaver sample ($n=4$) were used to assess periodicity and perikymata distributions. Populations were analyzed separately and perikymata were counted within deciles of crown height. Results showed substantial overlap between perikymata counts for teeth of different periodicities. Relationships between periodicity and perikymata counts within specific deciles also showed substantial overlap. Possible explanations for such mixed results compared to previous studies may include preservation of the material, sex, and inter-population variation, as well as number and severity of LEH defects in certain deciles.

An experimental investigation of asymmetrical Paleolithic wooden spear tips: expediency or design?

REBECCA BIERMANN GÜRBÜZ and STEPHEN J. LYCETT

Department of Anthropology, The University at Buffalo, State University of New York (SUNY), Buffalo, NY 14261

Paleolithic wooden spears provide rare but unique insights into early hunting technology. Examples from Schöningen (Germany) indicate that spear tips were sometimes asymmetrical. Possible reasons for this could be related to placing the tips in harder portions of wood, away from the center of the stave used. Alternatively, a more parsimonious possibility is that asymmetrical tips could be more efficiently produced (i.e., took less time to make) than symmetrical ones. Here, we experimentally investigated two different manufacturing processes, producing asymmetrical and symmetrical spear tips, while also testing the influence of biometric factors on spear-tip manufacturing efficiency (measured by time). Two groups of 20 participants each sliced wooden dowels using finger-held steel blades, in order to standardize cutting conditions. Each participant's grip and pinch strength were measured. One group sliced the wooden dowel into an asymmetrical shape (slicing only on one side of the dowel), while the other group created a symmetrical shape (slicing on all sides of the dowel). Based on time taken, results demonstrated no significant difference in efficiency between symmetrical and asymmetrical spear-tip manufacture. Conversely, biometric characteristics present a more dominant influence in explaining time variation, specifically that pinch strength was found to be significantly related to time. These results demonstrate that the biomechanical properties are the main driver in time differences rather than task variation (asymmetrical versus symmetrical spear tips). These results also indicate that the asymmetrical tips of spears at Schöningen were not simply the incidental by-product of a more efficient manufacturing process.

The sensitive camel and the wishing troll: Paint chips redefining arbitrary categories of skin pigmentation in anthropological education

ADAM BIERNASKI and LANA WILLIAMS

Anthropology, University of Central Florida

Imagine a learning experience that promotes an open and personal discussion into the phenotypic variation of skin color and the categories assigned to them. Armed with nothing but their skin pigment and a matching free paint chip from the local hardware store, students are able to redefine the parameters of skin color and racial discourse by utilizing an arbitrary system unassociated with social status or human biology. Students are encouraged to engage in external research, match their skin tone to any one of thousands of available paint hues, and engage in critical online discussions with their classmates. When introducing this exercise, students are encouraged to consider the creation of whiteness and the use of skin color as a visual indication of racial profiles. With these considerations, the students create their own skin color classification

based on their paint chip names such as Level Up, Cappuccino, or even Wishing Troll. These arbitrary categories are often constructed based on anything from geographic locations to food - no more factual than color equating to race. By engaging in this personally reflexive exercise, students are temporarily placed outside their cultural confines where different perspectives on color, race, and their worldview can be fostered. This free activity has been successfully implemented in distance learning courses and is readily adaptable for classroom settings. Response to this exercise has been overwhelmingly positive and has engaged more students per semester than any other discussion in the class supporting its effectiveness as a learning tool.

Primate Communities and Atmospheric CO₂ in the Plio-Pleistocene of east Africa

MARYSE D. BIERNAT^{1,2} and KAYE E. REED^{1,2}

¹School of Human Evolution and Social Change, Arizona State University, ²Institute of Human Origins, Arizona State University

The shift from woody cover, or forested areas, to open grasslands in east Africa over the past 5 million years has been a central concept in the study of human evolution. Vegetation structures in particular are highly susceptible to changes in atmospheric CO₂ (pCO₂). Grasses (C₄ plants) are adapted to low CO₂ concentrations while shrubs and trees (C₃ plants) are more adapted for higher CO₂ concentrations. Thus, the relationship between pCO₂ and vegetation can be exploited to understand past environments. Previous research has shown that ungulate taxa are sensitive to changes in pCO₂ as the vegetation that they rely on change in response. Since primates are thought to be dependent on specific vegetation, this project investigates the relationship between primate species and global atmospheric CO₂ changes in the Plio-Pleistocene of east Africa. From 22 sites across east Africa, pCO₂ values and presence/absence data on primate species were compiled. Species richness and diversity indices were calculated for each site and a linear model was employed to ascertain the relationship between primate diversity and pCO₂. While pCO₂ values have been significantly increasing over the past 5 million years, no significant relationship can be determined between pCO₂ and primate species diversity. These results may indicate that primates might have been more able to adapt to changing environments than other mammalian clades (i.e. ungulates). Functional trait data in relation to pCO₂ may yield more significant results concerning primate diversity in the Plio-Pleistocene and further uncover the context of hominin evolution.

ABSTRACTS

Translating unique variants: the classroom, the courtroom, and the dinner table

ABIGAIL W. BIGHAM

Anthropology, The University of Michigan

Patterns of genetic diversity are critical for deciphering human origins, understanding normal phenotypic variation, and identifying genetic risk factors for complex diseases. The overwhelming majority of this genetic diversity is shared among global human populations. Nonetheless, some genetic variants are unique to individual populations. Unfortunately, these population specific variants have been misinterpreted by some as evidence in support of the genomic basis of race. Understanding what private alleles reveal about particular populations and perhaps more importantly with respect to race, what they do not, is central to deconstructing ideas of racial categorization. Anthropological geneticists are well positioned to address unique variants in a variety of forums. Here, I will discuss the global distribution of population specific variants, how they arise, and how they are maintained in a population. I will then go on to address strategies for translating unique variants across different audiences, from the undergraduate classroom to the dinner table with friends and family.

Epigenetic predictors of pubertal timing

ALEXANDRA M. BINDER

Epidemiology, University of California, Los Angeles

Puberty represents a critical period of hormone-sensitive development that shapes life-long disease susceptibility. Among women, early age of menarche is associated with a greater incidence of type 2 diabetes, cardiovascular disease, and cancer. Over the last century, there has been a global trend towards earlier onset of menarche and breast development. Little is known about the potential contributors to this secular trend and how pubertal timing programs long-term modifications in disease risk. Epigenetic modifications may provide a biomarker of early life exposures and shifts in gene regulation that alter physiologic development. Dr. Binder will discuss her research into relationships between specific patterns of DNA methylation and pubertal development among a longitudinal cohort of girls in Santiago, Chile. She will detail observed associations between reproductive maturation and epigenetic aging, an indicator of biologic aging and predictor of cancer risk and mortality rate. In this cohort, accelerated epigenetic aging during adolescence was associated with an earlier age of menarche and faster progression through puberty. Shifts in epigenetic aging were also correlated with changes in the developing breast structure. Dr. Binder will discuss the reproducibility of these

findings across international cohorts, and guide consideration of DNA methylation assay timing when investigating critical windows of susceptibility.

These investigations were supported by Public Health Service grant NIH/NCI R01CA158313 (to Dr. Karin Michels), and the Breast Cancer and the Environment Research Program award NIH/NCI/NIEHS U01ES026130 (to Dr. Michels).

Isotopic perspectives on the shep-herd relationship at two Hellenistic (ca. 323 – 31 BCE) settlements in Thessaly, Greece

KATHERINE G. BISHOP¹, SANDRA GARVIE-LOK¹, MARGRIET HAAGSMA² and SOPHIA KARAPANOU³

¹Anthropology, University of Alberta, ²History and Classics, University of Alberta, ³Ephorate of Antiquities, Diachronic Museum in Larissa, Greece

Part of understanding human lives is establishing how humans interact with their animals. Isotope analysis has become an increasingly used tool for assessing how humans managed animals over space and time. In areas where the extent of management is debated, stable isotope analysis of microsampled animal teeth provide useful insight into the diet and mobility of herders and their animals. Current research on ancient pastoralism in Thessaly, Greece, is divided over the presence, prevalence, and effects of seasonal livestock movement (transhumance). We present the first isotope-based approach to this problem, and examine shepherding at two Hellenistic (323 – 31 BCE) settlements in Thessaly. A sample of 12 sheep and goat third molars was collected from sites at Farsalos and Kastro Kallithea. Intra-tooth variation of carbon ($\delta^{13}\text{C}$), oxygen ($\delta^{18}\text{O}$), and strontium ($^{87}\text{Sr}/^{86}\text{Sr}$) isotope values was measured from microsampled dental enamel to examine diet, seasonality, and mobility of sheep and goats. Based on the $\delta^{13}\text{C}$ values, all animals were eating C_3 plant sources. The $\delta^{18}\text{O}$ and $^{87}\text{Sr}/^{86}\text{Sr}$ results indicate multiple management styles including (1) local grazing with no significant movement; (2) local grazing at variable water reservoirs, (3) non-local grazing at various locations, and, (4) transhumance. Our analysis represents the first documented case of transhumance in Greek antiquity. Each management style has corresponding impacts on ancient economy, human ecology, land-use, and human-animal relationships. Our research contributes to the growing literature on ancient animal management, provides useful information for modelling ancient practices, and connects the recent ethnographic past with the deep past.

Funding was provided by the Social Sciences and Humanities Research Council of Canada, various sources at the University of Alberta, the Killam Trusts, and the Canadian Association of Physical Anthropology.

Human Eco-immunology in the Field: Measuring multiple dimensions of immune function with minimally invasive, field-adapted techniques

AARON D. BLACKWELL^{1,2} and ANGELA R. GARCIA^{2,3}

¹Dept. of Anthropology, Washington State University, ²Dept. of Anthropology, University of California, Santa Barbara, ³Center for Evolution and Medicine, Arizona State University

Immune function is multifaceted and characterizations based on single biomarkers may be uninformative or misleading, particularly when examined across ecological contexts where single biomarkers may reflect different processes. However, measuring the many facets of immunity in the field can be challenging, since many measures cannot be obtained on site, necessitating sample preservation and transport. Moreover, immunity is best measured in blood, since measures in urine, feces, and saliva often reflect conditions in the bladder, gut, and mouth, rather than systemic conditions. Here we assess current state-of-the-art methods for measuring immunity, focusing on measures that require a minimal blood sample, obtained from a finger prick, which can be: 1) dried on filter paper, 2) frozen in liquid nitrogen, or 3) stabilized with chemical reagents. Stable protein products, such as immunoglobulins and C-reactive protein are reliably measured in dried blood spots. Because less stable proteins, e.g. cytokines, may be problematic to measure, even in fresh blood, mRNA from stabilized blood may provide a cleaner measure of cytokine gene expression. Gene methylation assays or mRNA sequencing also allow for the quantification of many other parameters, including the inference of leukocyte subsets. Finally, components of cellular immunity can be quantified using flow cytometry on frozen samples, so long as careful freeze-thaw techniques are exercised. We provide examples of how combining these techniques provides an improvement over single-marker studies, allowing for a more nuanced understanding of how social and ecological variables are linked to immune measures and disease risk in diverse populations and settings.

Hellman Family Faculty Fellowship

Presence of Lingual Cuspule and paraconid on one Archaic period individual from the Ohio Valley

ERIN C. BLANKENSHIP-SEFCZEK

Anthropology, The Ohio State University

Molar cusps are useful for discussing evolutionary changes and determining affilial relationships; however, some of these traits are underrepresented in the literature. The Lingual Cuspule and paraconid are two molar traits considered near absent in modern human populations. The Lingual Cuspule has only been

ABSTRACTS

reported once before, on the distolingual surface of the first molar of an adult male in an African population. The paraconid was thought to have been lost in primate evolution beginning in the Oligocene (34-23 MYA). Both traits were found on the mandibular third molars of one adult male from the late Archaic (2500-500BC) site of Shick in Hancock County, Ohio. This site is far removed from the African population where the Lingual Cuspule was previously identified. Additionally, in the example presented here, the accessory cusp is located on the mesiolingual surface indicating the possibility for the Lingual Cuspule to be expressed in multiple locations on the lingual surface, and on different molar teeth. It is possible the low-reporting rates of this trait are due to mis-identification of other known traits, including the MMTP. Even with clarification, the occurrence of the Lingual Cuspule would likely remain rare. As for the paraconid, there are examples of non-human primate molars with this trait, but there are no reported cases appearing in hominins. The expression of a paraconid in modern humans could suggest secondary evolution. Further reporting and descriptions of both traits are necessary to discuss the evolutionary implications in modern humans.

Ohio State University Alumni Grant for Graduate Research and Scholarship Ohio State University, Department of Anthropology, Larsen Research Grant

Estimating Sex Using the Human Mandibular Canine

BRITTNEY L. BLEVINS

Department of Geography and Anthropology, Louisiana State University

Sexual dimorphism can be quantified in human mandibular canines; therefore, these teeth can be used to estimate sex of skeletonized individuals. This study complements and expands on previous research by comparing mesiodistal diameter (MD), buccolingual diameter (BL), and dental indices (including crown area, crown module, and crown index) of human mandibular canines. Measurements were taken from a sample of skeletal individuals from the Terry Collection (n=651), the Maxwell Museum of Anthropology Skeletal Collection (n=61), and a random sample of dental casts from the James K. Economides Orthodontic Case File (JKE, n=599), for a total of 641 males and 597 females. Both left and right-side canines were measured, and statistics were conducted separately to avoid double counting individuals. Using ANOVA, a significant difference was seen between males and females for left and right BL measurements ($p < .0001$), indicating that males have significantly larger BL measurements of the mandibular canine than females from the study sample. Significant differences were seen between males and females for left and right MD measurements only when the JKE individuals were excluded from analyses

($p < .0001$). Additionally, all calculated dental indices show statistically significant differences between males and females ($p < .0001$). Logistic regression equations for left and right sides was created to estimate sex based on measurements from either the left or right mandibular canine that correctly estimates the sex of individuals in up to 66% of cases for the left canine. This method may be useful for estimating sex in forensic and bioarchaeological cases when traditional methods are unavailable.

This research was funded in part by a Robert C. West Graduate Student Field Research Award from the Department of Geography and Anthropology at Louisiana State University.

The Influence of Habitual Activities and Lifelong Occupations on Morphological Measures of Skeletal Robusticity

LYDIA BLIZZARD¹, HARRISON DEAN¹, HALEY E. HORBALY¹ and MARK HUBBE^{2,3}

¹Department of Anthropology, University of Tennessee, Knoxville, ²Department of Anthropology, The Ohio State University, ³Instituto de Arqueología y Antropología, Universidad Católica del Norte, Chile

Previous studies have identified relationships between skeletal robusticity and environmental factors, specifically habitual activity patterns. While most studies have analyzed this relationship from the perspective of cross-sectional properties, few have explored activity's effects on morphological measures of robusticity. In this study, reported lifelong occupation and habitual activities of 120 individuals are used as proxies for activity level. The occupational data reported from the 120 individuals were scored on a scale of one to five, with five being the most rigorous activity. Likewise, the habitual activity data were scored on a scale of one to three, with three also being the most rigorous. Morphological sex estimation scores for the cranium, os coxa, and distal humerus were used as measures of robusticity. Activity levels and sex estimation scores were compared to test the association between skeletal morphology and habitual activities/occupations. Results indicate there is no significant difference in cranial or pelvic robusticity among groups of different activity levels ($p > 0.05$). There are, however, significant differences in the olecranon fossa shape and depth ($p < 0.01$) and the angle of the medial epicondyle of the humerus ($p < 0.01$). This could be due to a preference for arm use, underlying sexual dimorphism in occupations and habitual activities, or could reflect the involvement of the elbow joint in a wide range of activities. Overall, this study shows that activity level has limited effects on the morphological robusticity of the skeleton.

Intra-annual variation in diets of Plio-Pleistocene papionins from Kenya

SCOTT A. BLUMENTHAL^{1,2}, THURE E. CERLING³, KENDRA L. CHRITZ^{1,4}, JULIA A. LEE-THORP² and FREDRICK MANTH^{1,3,5}

¹Department of Anthropology, University of Oregon, ²Research Laboratory for Archaeology, University of Oxford, ³Department of Geology & Geophysics, University of Utah, ⁴National Museum of Natural History, Smithsonian Institution, ⁵Earth Sciences Department, National Museums of Kenya

The well-documented expansion of C₄ vegetation in eastern Africa since the Pliocene is accompanied by increasing consumption of C₄ resources by members of at least four orders of mammals, including Primates. Previous research on the evolution of C₄ feeding has focused on inter-individual dietary variation, and it is critical to investigate aspects of within-individual niche flexibility. To address diet change within the lifetimes of extinct papionin individuals, we used laser ablation stable isotope analysis to measure carbon isotopic variation along the growth axis of enamel strips (2.6-9.9 mm in length) exposed in broken fossil teeth (n=22). Among *Theropithecus* (n=18), intra-tooth $\delta^{13}\text{C}$ ranges vary from 1.1‰ to 5.1‰ (mean range = 3.1‰) reflecting significant diet changes on intra- and inter-annual time scales. In contrast, our preliminary analysis of non-*Theropithecus* papionins (n=4) demonstrates lower intra-tooth $\delta^{13}\text{C}$ variability (mean range = 1.3‰), indicating unexpectedly low intra-individual diet flexibility despite significant inter-individual $\delta^{13}\text{C}$ variation. These results demonstrate that laser ablation can be used to detect significant isotopic variation within individual fossil monkey teeth, and that conventional sampling methods can mask significant intra-tooth isotopic, and thus dietary, variability. Despite indications that fossil *Theropithecus* was a C₄ specialist, we find that diets flexibly included significant amounts of C₃ resources from ca. 4.0-1.0 Ma. The evolution of the diets of *Theropithecus*, and perhaps other primates, must be understood in the context of seasonal-scale shifts between C₃ and C₄ resources, which can influence selective pressures associated with resource availability, nutritional balance and competitive interactions.

We thank the Natural Environment Research Council (NE/P013376/1) for funding.

Effects of domestication and selective breeding on coat coloration in alpacas through exon 4 analysis of agouti gene

EMMA K. BLYSTONE

Anthropology, Binghamton University

Alpacas were domesticated ~6000 years ago in the Andes, and are one of the most color-variable mammals. Genetic studies of domestication provide insight into human and animal coevolution. This study aims to analyze how domestication and selective breeding have

ABSTRACTS

affected the expression of coat coloration. The agouti gene encodes for the agouti signaling protein (ASIP), which functions as an antagonist to the melanocortin 1 receptor – a protein involved in regulating mammalian hair and skin color. This study examined a 57 base pair deletion located on exon 4 of the agouti gene coding for the last 40 amino acid residues that make up the C-terminal portion of ASIP. Forty-eight animals were selected for genetic analysis based upon variation in primary and secondary coat coloration. Gel electrophoresis was used to identify an indel in exon 4. Samples would either show one or two alleles. Heterozygous individuals contained a short and long allele (n=20), while homozygous individuals had one long allele (n=28). Preliminary analysis showed that no individuals were homozygous short, as expected given the deleterious nature of this genotype. There is no significant association between coat color and exon 4 of the agouti gene (ChiSq= 0.928, p=0.818). This research is part of a concerted effort to genotype candidate genes for coat color in alpacas, to provide greater insight into the evolution of alpaca coat coloration, and how domestication can select for different phenotypes. Once genotypes for coat coloration have been established, we can estimate how long ago these mutations occurred.

Sex-biased admixture and geographic mating structure shape genomic variation in Cape Verde

KATYA BOBREK¹, SANDRA BELEZA² and AMY GOLDBERG³

¹Anthropology, Emory University, ²Genetics, University of Leicester, ³Evolutionary Anthropology, Duke University

Cape Verdeans are descendants of Portuguese colonizers and West Africans brought as slaves in the 1400s. Previous analyses found that genetic ancestry recapitulates historic patterns, with ~57% of Cape Verdean ancestry tracing to relatives of modern West Africans. Here, we use genome-wide SNP data from 564 unrelated individuals spanning the islands of Cape Verde to infer the impact of sex-specific mating patterns on the distribution of genetic ancestry within and between islands. Specifically, we used a model-based approach to compare X-chromosomal and autosomal ancestry, examining if levels of sex-biased admixture differed by island. Our analyses support the hypothesis that sex bias occurred during the founding of Cape Verde. European men and African women contributed significantly more than their counterparts, with a ratio of mean X-chromosomal to mean autosomal African ancestry of ~1.26. Both the global ancestry and level of sex bias differed between islands. Next, we looked for differences in mating patterns and migration rates within and between islands using the distribution of genomic regions shared identically-by-descent. The southern islands have

lower between-island IBD, consistent with historical evidence of an older shared history and less recent migration between the islands. The north-west islands, which were more recently colonized and are geographically closer together, show high rates of cross-island mating and overall small effective size. Our work provides insight into the fine-scale demography of an understudied population. More generally, this work demonstrates the utility of genetic data to study the dynamics of colonization and social structure.

Characterization of the microbiome in the AIDS-resistant natural host Sooty mangabey monkey (*Cercocebus atys*)

RACHELE M. BOCHART¹, STEVEN E. BOSINGER², JOYCE COHEN¹, GREGORY THARP², SHERRIE JEAN¹, ADAM ERICSEN², BHAVANI MADETI² and MARIA CRANE¹

¹Division of Animal Resources, Yerkes National Primate Research Center, Emory University School of Medicine, ²Division of Microbiology & Immunology, Yerkes National Primate Research Center, Emory University School of Medicine

Unlike HIV-infected humans, the African sooty mangabey avoids AIDS-like disease progression despite high viral loads. Our previous studies have identified that a primary tissue site differentiating the pathogenic versus non-pathogenic outcome in SIV infection is the gastrointestinal mucosa. Distinct from non-natural macaque species, we discovered that African natural host species retain mucosal integrity, do not exhibit luminal microbiota translocation, and harbor a mutation in TLR4 which dampens signaling to bacterial LPS and TLR4 ligands. Collectively, these data demonstrate that the gastrointestinal environment and mucosal immunity play a strong role in determining disease outcome. In this study, we examined the microbiome of a captive mangabey colony at Yerkes National Primate Research Center and its relationship to SIV status in comparison with rhesus macaques. Matched samples from naturally infected SIV positive and negative animals were collected for 16S ribosome-based taxonomic characterization of host-resident microbes. When comparing SIV status of the natural host our results showed microbiome stability with infection, which contrasts the non-natural host species. Specifically, with SIV infection, sooty mangabeys revealed stability of potentially SIV pathogenic genera that have shown to modulate mucosal inflammation and immune activation, which may further potentiate disease progression. Furthermore, we evaluated the impact of the environment on microbiome comparing mangabeys housed in indoor-caging with semi-natural outdoor colonies. This comparison recapitulated evidence of microbiome differences seen with

increased levels of captivity. This study describes a potentially beneficial evolutionary adaptation between host immunity and microbiome resulting in control of chronic SIV infection.

The Yerkes NHP Genomics Core is supported in part by ORIP/OD P51OD011132.

Variation in Maturation Timing Influences Interpretations of the Juvenile Skeleton

MELANIE E. BOEYER^{1,2} and DANA L. DUREN^{1,2}

¹Department of Orthopaedic Surgery, University of Missouri, ²Department of Pathology and Anatomical Sciences, University of Missouri

The juvenile skeleton develops in a predictable pattern to reach adult morphology. The stages of maturation, particularly those related to epiphyseal fusion, have been used extensively to approximate the age of an individual or to reconstruct life histories from skeletal remains in archaeological or forensic contexts. Similar assessment methods in living children through radiographic observation inform delays or accelerations in somatic maturation. However, the timing and tempo of skeletal changes, including epiphyseal fusion, varies among past and present populations and is also highly variable within relatively homogeneous groups. For the present analysis, we examined variability in epiphyseal fusion timing in the hand-wrist. Using radiographic data from 1,292 children from the Fels Longitudinal Study, we recorded the chronological age (CA) at which epiphyseal fusion was initiated and completed in the distal radius and elements of the third ray. Once initiated, the process of fusion typically lasts less than 20 months, but the age range over which initiation can occur spans approximately 8.80 years in boys and girls (CA 11.53–20.12 and 8.98–18.00 years, respectively), and the timing of fusion completion spans 10.23 years in boys and girls (CA 13.36–22.06 and 10.98–22.72 years, respectively). The 1st and 3rd quartiles for these traits overlapped by as much as 0.96 years. Results of this study can be used in refining interpretations of life history parameters and age estimates in past populations. Importantly, characteristics of children at the extremes of the distribution provide insights into the biological factors underlying epiphyseal fusion variability.

This work was supported by grants from the National Institutes of Health (R01AR055927; R01HD012252; F31HD091939).

Pulling teeth: Dental avulsion at Kulubnarti, Sudan, in regional context

KATELYN L. BOLHOFNER¹ and BRENDA J. BAKER²

¹Department of Sociology, Anthropology, and Social Work, Texas Tech University, ²School of Human Evolution and Social Change, Arizona State University

ABSTRACTS

Dental avulsion, the intentional removal of one or more teeth, has been documented among Sudanese groups from the pre-Mesolithic period to the present. Avulsion in this region typically involves removal of permanent incisors, though removal of deciduous canine buds causing interruption of permanent canine development also has been demonstrated. The pattern of dentition removed and any association of avulsion with the sex of individuals appear to vary through time, leading to difficulty in interpreting the purpose of the practice. We present evidence of avulsion in individuals from two cemeteries dating to the Early Christian period (ca. A.D. 550-800) at Kulubnarti in northern Sudan.

All individuals with permanent incisors (those 6-7 years and older) and observable dentition were examined using diagnostic criteria for avulsion developed previously by the authors. Eleven of 154 (7.1%) individuals exhibit avulsion, a slightly lower frequency compared to other Meroitic (ca. 350 B.C.-A.D. 350) to Christian period samples. The youngest affected was 14-15 years old. A higher percentage of avulsed maxillary incisors than expected for the region is found at Kulubnarti (6 of 11; 55%). Five of 11 (45%) exhibit avulsion of mandibular teeth, but no individual shows avulsion involving both arcades. At Kulubnarti, avulsion of the central incisors (n=9; 82%) is a hallmark of dental modification, in contrast to other samples from the Middle Nile region where mandibular lateral incisors were more commonly avulsed. Close contextual examination of the new evidence for avulsion at Kulubnarti offers additional insight into dental modification through time in Sudan.

Hidden in plain sight: the persistence of racemaking in contemporary population genomics

DEBORAH A. BOLNICK

Department of Anthropology, University of Connecticut

One of the central narratives of our discipline has long been that biological anthropology experienced a paradigm shift around racial thinking in the mid-20th century. At this time, the narrative suggests, the study of race was abandoned for the study of populations, a focus on classification and typology was replaced with a focus on variability and the processes that produce it, and assumptions about stasis and the fixity of traits gave way to evolutionary frameworks and investigations into how individuals and groups change over time. These shifts had a significant impact on research undertaken over the last 70 years, especially in conjunction with technological advances during this period. Together, these developments have played a critical role in shaping contemporary understandings of human genetic variation as well as the nature and meaning of race.

However, while our field has advanced in important ways, aspects of racial thinking have persisted, hidden in plain sight. There are a plethora of ways in which antiquated ideas about race still permeate biological anthropology, so that race is continually being made and remade anew through contemporary scientific practice. In this presentation, I focus on the persistence of racemaking in human population genomics. Drawing on recent studies of both ancient and present-day populations, I show how assumptions about stasis, isolation, purity, and the association between sociopolitical and genetic categories are embedded in contemporary genomic research, reifying and reinscribing ideas of race. I also suggest alternative approaches to help us move away from the molecular (re) production of race.

New associated immature postcranial remains of *Homo naledi* from the Dinaledi Chamber, South Africa

DEBRA R. BOLTER^{1,2} and MARINA C. ELLIOTT¹

¹Evolutionary Studies Institute, University of the Witwatersrand, ²Anthropology, Modesto College

A minimum of 15 *Homo naledi* individuals, based on dental remains, has been recovered from the Dinaledi Chamber, Rising Star Cave, South Africa. The individuals span all age classes—infant to old adult - although most bone and teeth elements are commingled and unas-sociated. The Dinaledi fossils date to Middle Pleistocene—236,000-335,000 years ago, a poorly understood time in hominin evolutionary history. In 2018 we reported on an instance of articulated lower limb elements for an older juvenile individual (now referred to as Dinaledi Hominin 7 (DH7)). Here, we report on a second older juvenile whose right femur was found in articulation with pelvic remains. These elements include *in situ* associations of three elements, with field numbers U.W. 101-938a immature right femur, U.W. 101-938b unfused femoral head epiphysis, and U.W. 101-938c right acetabular fragment. When permanently accessioned, U.W.101-938c was identified as a partial ischium, superior aspect, and was renumbered U.W. 101-1754. In the lab, U.W. 101-1755 right partial ischium, inferior aspect, was refitted to U.W. 101-1754 (VanSickle et al., 2017), for a nearly complete ischial lunata surface. These findings contribute to our growing understanding of post-cranial ontogenetic adaptations in *H. naledi*, and to the investigation of the evolution of life stages in these recently extinct hominins.

Human Walking Behavior

AZARIEA BONNER-HARRIS¹ and CARA WALL-SCHEFFLER^{1,2}

¹Biology, Seattle Pacific University, ²Anthropology, University of Washington

Recent studies have clearly shown that environmental cues influence gait changes in walking humans. Here we test how people adjust their walking behavior to maximize survivorship during risk-taking behavior. Video data were collected over the course of eighteen months at four different urban intersections in which people were crossing streets against lights (i.e. jaywalking) with the potential for oncoming car traffic to hit them. The footage was analyzed using the software, Kinovea. Five independent variables were selected for analysis: two relating to the situation (i.e. crosswalk length and traffic heaviness), and three relating to the decision making of the walker (i.e. whether s/he had a load, was jaywalking, and whether s/he made surrounding checks before crossing). We collected data on 1,517 people crossing streets. The analysis revealed that single pedestrians increased their speed while jaywalking (p=0.006) and checked their surroundings more often (p=0.001). Additionally, pedestrians who walked in groups were less likely to jaywalk (p=0.013) and did not adjust their speeds when they did jaywalk (p=0.001). Pedestrians who were carrying some type of load also did not adjust their speed when they jaywalked. Taken together, these findings further support ethnographic literature claiming that group walking is often for safety, and that walking alone increases vigilance.

Mortuary practices' archaeology seen under a multivariate perspective: case study of southern Brazilian shellmounds

ANA CLAUDIA A. BORELLA and DANILO V. BERNARDO

Laboratório de Estudos em Antropologia Biológica, Bioarqueologia e Evolução Humana, Instituto de Ciências Humanas e da Informação, Universidade Federal do Rio Grande

The comprehension and the investigation of the archaeology of mortuary practices plays a central role to the understanding of the symbolic universe and the social organization of human populations. In this context, the study of the relationship between mortuary variability (defined as degree of variation in funerary practices, or mortuary treatment patterns, within one society), social complexity and environmental conditions can lead to the comprehension of biocultural adaptations of past societies. In order to investigate the relationship between social aspects and ecological factors, here we present a study carried on over archaeological data of burials of 168 individuals distributed along 16 archaeological shellmounds builders' sites, the Sambaquis, in the southern Brazilian shore. The Sambaquis have been studied even before the beginning of formal archaeological research in Brazil and are characterized by the large number of human burials, which allowed several studies of their funeral practices. To reach our goal we assembled

ABSTRACTS

a dataset composed by 31 categorical variables describing the funerary characteristics of the 168 subjects. The dataset was analyzed by statistical multivariate techniques resulting in a clustering of four types, or patterns, of burials in these 16 sites. All subjects were classified under these four-type patterns, resulting in an index of variability for each archaeological site analyzed. According with our results, the intra-site variability is generally minor than the extra-site variability, suggesting that cultural and symbolic aspects can be the principal responsible rather than ecological factors to the choices of mortuary practices in these populations.

Conselho Nacional de Desenvolvimento Científico e Tecnológico – CNPQ Process MCTI/CNPq/Universal 14/2014/461122/2014-6 to DVB and Process PIBIC/CNPq/FURG 103271/2017-1 to ACAB

Quantitatively designing and testing the effects of data-driven interventions to address lemur-hunting in Madagascar

CORTNI BORGERSON¹, BENOEL RAZAFINDRAPAO², DELOX RAJAONA² and BE JEAN RODOLPH RASOLOFONIAINA²

¹Anthropology, Montclair State University, ²Masoala, Madagascar

Madagascar is renowned for its primate biodiversity, yet nearly all species of lemur are now threatened with extinction. During four years (2015-2018) we conducted extensive monthly surveys of endangered lemurs, habitat, hunting behavior, socioeconomics, and human health and nutrition across 18 sites on the Masoala Peninsula of Madagascar. During this time, we acquired rigorous quantitative data on lemur hunting and how hunting affects both lemur and human populations. We found that the best predictor of lemur trapping was food insecurity. Child malnutrition and food insecurity were high across the peninsula. Further, few alternatives to wild meats were available in adequate supply and many were highly volatile. Thus, most households hunted wildlife and these meats significantly improved child health and nutrition. In order to reduce the unsustainable hunting of threatened lemurs, we co-designed, with local communities, an effort to increase the affordability, accessibility, and quality of sustainable sources of animal-based foods in three test communities where forests contributed greatly to food security. While the project is still underway, early results from annual surveys of both test and control sites suggest a reduction in both the hunting of endangered species and animal-based

food insecurity within test communities. Yet, there is still much to be done. Here we discuss the project, its successes and challenges, our approach for the future, and what lies ahead for both the lemurs and people of Madagascar.

This research was funded by grants from the National Geographic Society Conservation Trust (C280-14 and C021-17) and the National Science Foundation SBE-IBSS Postdoctoral Research Fellowship (1513638).

Glandular microbiomes vary by species and host traits in wild and captive lemurs

SALLY L. BORNBUSCH¹, LYDIA K. GREENE^{1,2}, RACHEL L. HARRIS¹ and CHRISTINE M. DREA^{1,2,3}

¹Department of Evolutionary Anthropology, Duke University, ²University Program in Ecology, Duke University, ³Department of Biology, Duke University

The gut microbiome has received warranted attention for its role in primate health; however, myriad other microbiomes across primate body sites (e.g. mouth, skin, genitals, and scent glands) are no less significant to host well-being and behavior. Although commensal skin and vaginal microbiomes have been linked to host species identity, sex, social status, and hormone concentrations, glandular microbiota, and their potential contribution to olfactory signals, via fermentation, remain poorly understood. Given the prominent role of olfaction and glandular scent marking in strepsirrhines, lemurs are particularly well suited to studies of glandular microbiomes. Here, we examine the glandular microbiomes of wild sifakas and woolly lemurs and captive ring-tailed lemurs across scales – from species, to conspecifics of different sex or social status, to individuals and their unique glands. We collected swabs from multiple species- and sex-specific glands, sequenced 16S rRNA amplicons, and used published bioinformatics and statistical pipelines to explore variation in glandular microbiomes. We find that glandular microbiomes of lemurs varied significantly by species, by sex, by gland, and by social status, with some patterns persisting in both wild and captive animals. Interestingly, we found that the sternal glands of male sifakas, which produce a testosterone-mediated visual signal of rank, harbor significantly different consortia between stained (dominant) and unstained (subordinate) males, suggesting an underlying hormonal mechanism for sternal microbiome selection. Beyond addressing the relevance of microbiomes to olfactory communication and social behavior, this study illustrates the potential richness of information to be gained through the study of diverse microbiomes.

Micro- and macro-wear of human dental enamel. A materials science perspective

OSCAR BORRERO-LOPEZ¹, ANTONIA PAJARES¹, PAUL J. CONSTANTINO² and BRIAN R. LAWN³

¹Materials Science and Engineering, Universidad de Extremadura, ²Department of Biology, Saint Michael's College, ³Materials Measurement Laboratory, National Institute of Standards and Technology

The microwear markings observed on the surface of fossil teeth are a powerful tool for the reconstruction of diet. This work intends to contribute to the multidisciplinary knowledge of dental microwear by modelling it using contact mechanics. The principal outcomes of such analytical modelling are the ability to (i) infer bite forces, and (ii) categorise wear as mild (controlled by deformation), or severe (controlled by fracture), from the size of observed pits and scratches. Macrowear is subsequently modelled as accumulation of individual microwear events. This approach enables assessments of the effects of tooth geometrical variables and chewing habits on enamel wear. Micro- and macro-wear models are validated by comparison with experimental data from *in-vitro* microindentation and wear tests conducted on human teeth. Implications in evolutionary biology are discussed, with special attention to the particles that are most deleterious for tooth wear.

This study was supported by Junta de Extremadura, Spain, and FEDER/ERDF funds (grant IB16139).

Gestation length in African and Asian colobines

CAROLA BORRIES^{1,2}, CARRIE S. MONGLE² and ANDREAS KOENIG^{1,2}

¹Anthropology, Stony Brook University, SUNY, ²Interdepartmental Doctoral Program in Anthropological Sciences, Stony Brook University, SUNY

Although Colobini (African colobines) and Presbytini (Asian colobines) share key traits, including relatively small neonates and anatomical adaptations for folivory (e.g., sacculated stomach), previous reports have documented longer gestation lengths in Colobini compared to Presbytini. This seems to suggest improved maternal energy in Presbytini facilitating faster fetal growth and a shorter gestation length. To assess the validity of the difference in gestation length between the two tribes, we compiled data from the literature with an emphasis on distinguishing how conceptions (i.e., the beginning of gestation) were determined. If changes in hormone levels, swelling or mating patterns were analyzed, we labeled the data as 'accurate' (13 species). If observed mating was used or methods were undisclosed, data quality was labeled as 'unclear' (16 species). We analyzed the 'accurate' and 'unclear' gestation length data separately in relation to adult female body mass within

ABSTRACTS

a phylogenetic framework. In both datasets, the pGLS regression was significant, but R-squared values were low, indicating a small effect size. Importantly, however, the overall pattern was reversed. While in the 'unclear' dataset gestation length in most Colobini was longer (Colobini: 178-200 days, Presbytini: 150-200 days), in the 'accurate' dataset it was longer in all Presbytini (Colobini: 152-169 days; Presbytini: 195-212 days). The differences between Asian and African colobines were significant only for the 'accurate' data and when intercept and slope were both considered (pANCOVA, $P = 0.03$). Thus, methods matter and unexpectedly revealed that gestation length in Colobini is in fact shorter (not longer) than in Presbytini.

A virtual assessment of the proposed suprainiac fossa on the early modern European calvaria from Cioclovina, Romania

ABEL M. BOSMAN¹ and KATERINA HARVATI^{1,2}

¹DFG Center for Advanced Studies: "Words, Bones, Genes, Tools", Eberhard Karls University of Tuebingen, ²Paleoanthropology, Senckenberg Center for Human Evolution and Palaeoenvironment, Eberhard Karls University of Tuebingen

The calvaria from Cioclovina (Romania) has been argued to possess a mixture of Neanderthal and *H. sapiens* autapomorphic traits, including a suprainiac fossa, making it important in the discussion on Neanderthal and *H. sapiens* hybridization. However, its supranuchal morphology has only been evaluated with a qualitative analysis of the ectocranial surface. A detailed study of the internal anatomy of the Cioclovina supranuchal region is thus of particular interest.

We investigated these internal structures by using computed tomography and calculating their respective relative contributions to total cranial vault thickness. These measurements were combined with published data and evaluated with a principal component analysis (PCA).

Our results show that the internal morphology of the Cioclovina supranuchal region is characterized by superficial resorption present on the outer layer of the external table. Neither the diploic layer nor the external table decreases in relative thickness in the region of the proposed depression. Furthermore, in the PCA, the Cioclovina specimen falls within the convex hull of recent modern *H. sapiens*. These results indicate that the supranuchal morphology of the Cioclovina specimen does not correspond to the external and internal morphology of the typical Neanderthal suprainiac fossa. Together with earlier results, there is little phenotypic evidence that Cioclovina can be considered a *H. sapiens* / Neanderthal hybrid.

Our study demonstrates the usefulness of this method in assessing proposed Neanderthal-like suprainiac depressions in Upper Paleolithic and other fossil specimens.

This research was funded by the German Research Foundation (DFG FOR 2237: Project "Words, Bones, Genes, Tools: Tracking Linguistic, Cultural and Biological Trajectories of the Human Past").

A Push for Trans-inclusive Language in Forensic Anthropology

FATIMAH A. BOUDERDABEN

Anthropology, Entomology, Texas A&M University

While distinct differences between sex and gender have been known to the anthropological community for some time, the presence of trans-exclusive language in academic writing is still a problem. With the current violent climate in America, it is becoming increasingly likely that forensic anthropologists will encounter a case involving a transgender individual. Utilizing gendered language in forensic anthropological writing when the identity of the decedent is unknown presumes the gender of the said decedent which is inherently trans-exclusionist. Since a forensic anthropologist cannot estimate gender, this practice is also erroneous.

This research paper tackled the question of how common trans-exclusive language is in forensic anthropological writing. It was hypothesized that gendered language would be consistently used in forensic anthropological literature in reference to unidentified remains and sex estimation techniques. This was tested by searching for and analyzing articles relating to sex estimation and unidentified remains from the Texas A&M University libraries database, the "Criminal Justice Abstracts." A total of 611 articles found and an evaluation of the abstracts of those articles resulted in 98 articles being further evaluated.

The purpose of this study was to uncover the true frequency of trans-exclusive language in forensic anthropological writing and propose a solution. It was found that approximately 49% of the articles further evaluated used some sort of trans-exclusive language. The solution proposed in this paper to reduce this error rate is the implementation of gender-neutral language in forensic anthropological writing. This practice benefits both the individual being identified and the anthropological community.

Analysis of cortisol levels from archaeological hair from the medieval nubian population of kulubnarti

GRACE B. BOWLAND¹, DENNIS VAN GERVEN¹ and ROBIN M. BERNSTEIN^{1,2}

¹Anthropology, University of Colorado, Boulder,

²Institute of Behavioral Science, University of Colorado, Boulder

The glucocorticoid cortisol is linked with physical or perceived environmental stressors and analysis of cortisol is often used to assess effects of stressors such as malnutrition, illness, and trauma. Cortisol can be obtained from many sources for short term analysis including saliva, blood and feces, but hair provides both a noninvasive and reliable method for measuring time-averaged cortisol levels, as the hormone is incorporated into the hair shaft during hair growth. Hair cortisol analysis has been used with archaeological remains dating back to AD 1000. Here, we report the results of analysis of hair samples taken from 89 individuals from the early Medieval to late Feudal Nubian site (AD 1100–AD 1400) of Kulubnarti. These remains were excavated from two cemeteries, designated R and S, at the site of Kulubnarti, Nubia. Individuals ranged in age from 2 to 45+ years and were categorized as Early childhood ($n=36$), Later childhood ($n=25$), Adolescent ($n=11$), and Adult ($n=12$). Using this cross-sectional sample, we describe the age-related pattern of hair cortisol concentrations (HCC) in relationship to previously published information on stress and life history in these individuals. Across the whole sample, mean HCC was 29.48 pg/mg ($SE=1.92$, range 7.48-111). Our results show that HCC peak during early childhood and decrease during adolescence and into adulthood, consistent with similar patterns documented in contemporary populations. While absolute HCC decreased with age, variation in HCC increased with age from early ($SD=0.196$) and later ($SD=0.218$) childhood to adolescence and adulthood ($SD=0.272$).

Funded by the Department of Anthropology and College of Arts and Sciences, University of Colorado Boulder.

Measuring enthesal morphology of the opponens pollicis muscle in digital and physical specimens of *Homo sapiens*

LUCYNA A. BOWLAND¹, MATTHEW W. TOCHERI^{2,3} and CALEY M. ORR^{4,5}

¹Anthropology, University of Arkansas,

²Anthropology, Lakehead University, ³Human

Origins Program, National Museum of Natural

History, Smithsonian Institution, ⁴Cell and

Developmental Biology, University of Colorado

School of Medicine, ⁵Anthropology, University of Colorado Denver

Entheses are the sites where soft tissue inserts into bone, and have long been used in anthropology to infer activity within past populations. As the use of three-dimensional (3D) data becomes more commonplace within anthropology, the question of how reliable this technology is for capturing enthesal development becomes more relevant. The limits of data derived from 3D virtual renderings remains to be determined, and this question is vital to any research efforts going forward within anthropology. The opponens pollicis muscle flange, located on the pollical

ABSTRACTS

metacarpal, offers an ideal test for this question because of its robust expression within *Homo sapiens*. This project tests for possible discrepancies between measurements of the opponens pollicis flange taken from 3D virtual renderings (derived from laser scans) versus measurements derived from physical remains from an adult sample of *H. sapiens*. Measurements taken include breadth of the metacarpal base and head, length of the shaft, and radial projection of the opponens pollicis flange. Measurements of 3D virtual renderings were taken using the measurement tool in the Geomagic program, while corresponding measurements of the physical specimens were taken using a set of digital calipers. Preliminary results show slight differences in measurements taken between the two methodologies, highlighting the need for further research into different data collection methods. Additionally, obtaining accurate measurements of the opponens pollicis flange has important implications for understanding the evolution of the modern human thumb and the origin of tool use and manufacture within fossil hominins.

Funding provided by National Science Foundation (BCS-1539741) (CMO).

Residual Rickets and Respiratory Disease in Rural and Urban Post-Medieval London

DEREK A. BOYD

Anthropology, University of Tennessee, Knoxville

Vitamin D deficiency is a pervasive health problem among individuals of all ages in rural and urban communities around the world. Recent clinical and bioarchaeological research has demonstrated a relationship between vitamin D deficiency and respiratory disease in age cohorts spanning the life course. Because several studies have linked early-life metabolic insults to adult morbidity and mortality in the past, this study sought to investigate the long-term health consequences of childhood vitamin D deficiency on adult respiratory health in three skeletal assemblages representing affluent rural and urban communities from post-Medieval London. Estimations of age-at-death and biological sex, as well as macroscopic evidence of residual rickets, rib periostitis, and maxillary sinusitis were recorded for 601 adults using data available online from the Wellcome Osteological Research Database curated by the Museum of London. Common odds ratios (OR_c) revealed that whether an individual came from an urban or rural assemblage had no effect on their age-specific odds of presenting residual rickets (OR_c=0.90, 95%CI:0.46-1.78), rib periostitis (OR_c=1.20, 95%CI:0.59-2.43), or maxillary sinusitis (OR_c=1.02, 95%CI:0.38-2.68). Moreover, none of the individuals presented both residual rickets and rib periostitis, although three individuals presented both residual rickets and maxillary sinusitis. These results provide preliminary evidence that early life vitamin D deficiency

may be implicated in the development of upper respiratory tract infections in adults; however, the adults examined here were from affluent backgrounds, and whatever effect urbanization may have had on the relationship between childhood vitamin D deficiency and adult respiratory health in the past requires further investigation.

Testing hypotheses about the relationships between diet and the primate torso: Implications for human evolution

EVE K. BOYLE¹ and SERGIO ALMÉCJA^{1,2,3,4}

¹Center for the Advanced Study of Human Paleobiology, Department of Anthropology (CASHP), The George Washington University, ²Division of Anthropology, American Museum of Natural History, New York, NY, ³New York Consortium of Evolutionary Primatology (NYCEP), ⁴Institut Català de Paleontologia Miquel Crusafont (ICP), Cerdanyola del Vallès, Barcelona, Spain

Torso differences between *Australopithecus* and *Homo* are often claimed to reflect a reduction in gut size following an increase in diet quality in the latter genus. This hypothesis emerges from the fact that animals that primarily eat green plants exhibit relatively larger guts than animals that rely on prey, and the assumption that torso form reflects accommodations for differently sized guts. However, recent studies show that other factors might influence primate torso morphology (e.g., body mass).

This study uses a series of multiple phylogenetic generalized least squares (PGLS) regressions to test the relationships between different aspects of torso morphology, body mass, diet, and locomotion. Iliac flare, ilium width, bi-iliac breadth, and lumbar spine length were measured in 48 anthropoid species, and ribcage breadth was measured in 30 species. Available data for diet (percent time feeding on food categories), body mass, locomotion (frequency of observed locomotor modes) and gut size (digestive tract surface area) were collected from the literature. Models of different complexity were fitted and compared using Akaike Information Criterion (AIC) weights.

Results indicate that body mass is often the only significant predictor variable and many models are improved by including locomotion. In cases where including diet yields a best-fitting model, it is often not the expected items (green plants, prey) that covary with morphological variables, but other diet items (seeds, flowers). More specific studies investigating the relationship between extant primate torso morphology and diet are necessary before posing scenarios of human diet evolution based on the hominin fossil record.

Funding provided by NSF (GRF; BCS 1316947), the Wenner-Gren Foundation (Dissertation Fieldwork Grant), the Agencia Estatal de Investigación (CGL2017-82654-P; AEI/FEDER EU), the Generalitat de Catalunya (CERCA Programme), and GWU.

Musculotendinous changes associated with hindlimb bone elongation in the Longshanks mouse

MADISON M. BRADLEY¹, SARAH MOORE¹ and CAMPBELL ROLIAN²

¹Department of Anthropology and Archaeology, University of Calgary, ²Department of Comparative Biology and Experimental Medicine, University of Calgary

Primates adapted for specialized locomotion such as jumping or cursoriality tend to have longer, more gracile hindlimbs. These primates often have parallel changes in their muscular anatomy, including relatively longer elastic elements in the distal hindlimb extensors. Elongation of elastic elements allows for energy savings during cursoriality and power amplification during jumping. It is not known if, and how, distal muscle-tendon units respond to selection for longer hindlimbs within populations. We hypothesized that within a population, the proportion of muscular and tendinous elements of the ankle extensors would differ according to hindlimb length. Using Longshanks, a strain of mice selectively bred for increased tibia length, and random-bred control mice, we examined how distal muscle-tendon units changed in response to tibial elongation. We used diffusible iodine contrast enhanced micro-CT to quantify the gastrocnemius muscle and calcaneal tendon unit in both sedentary mice and mice trained to jump. Longshanks had 5-11% longer gastrocnemius muscles (ANOVA $p < 0.005$) and 9-27% longer calcaneal tendons (ANOVA $p < 0.01$) than controls, regardless of exercise treatment. However, the ratio of gastrocnemius to calcaneal tendon length was not significantly different between strains. There was no evidence for power amplification in the jumping Longshanks mice despite their longer calcaneal tendons. This study shows that while selection for tibial elongation can cause changes in the geometry of the associated muscle-tendon unit, these changes alone do not significantly alter locomotor performance. Thus, there was likely direct selection for elastic elements, either through energy savings or increased performance, in jumping species.

Nutritional balancing and composition varies with infant age in wild mother orangutans (*Pongo pygmaeus wurmbii*)

TIMOTHY D. BRANSFORD^{1,2}, SRI SUCI UTAMI ATMOKO³ and ERIN R. VOGEL^{1,2}

¹Anthropology, Rutgers, the State University of New Jersey, ²The Center for Human Evolutionary Studies, Rutgers, the State University of New Jersey, ³Biological Sciences, Universitas Nasional Jakarta

In the peat-swamp forests of Indonesia, the availability of habitat macronutrients varies with fruiting cycles of tree species, creating an ever-changing nutritional landscape for orangutans to navigate. Mother orangutans nurse their infants

ABSTRACTS

for up to nine years, spanning these unpredictable periods of fruit scarcity. Yet, little is known about how mother orangutans modulate their foraging behavior to buffer their infants from variable nutrient and overall energy availability. Here, we build on previous work and begin to answer this question by examining if a mother orangutan's nutritional strategy varies significantly with the age of her infant. We calculated macronutrient balance (protein vs. non-protein energy; P:NPe) for full-day follows from 15 years of data (n=2075; 2003-2018) on mothers with dependent offspring in the Tuanan research area, Central Kalimantan, Indonesia. Using GAMMs with fruit availability as a fixed effect, we found that a mother's P:NPe ratio decreased significantly as her infant aged (p=0.041). A mother's highest protein intake was when her infant was 12-18 months old (p=0.0005), a time when infants first start incorporating solid food into their diet. Inversely, total nonstructural carbohydrate intake was highest when a mother had older infants (p=0.0003), and her P:NPe ratio was lowest when her infant was 4-5 years old (p=0.0002). By the time an orangutan is five years old, she will travel independently with her mother and primarily eat solid food while supplementing with milk. Therefore, mothers are less behaviorally constrained with older infants and can afford to seek out more preferred foods like fruit.

This project was funded by the United States Agency for International Development, National Science Foundation, The Center for Human Evolution Studies, and the American Society of Primatologists.

Morphological integration and modularity in the humerus of modern humans

MARIANNE F. BRASIL

Human Evolution Research Center, Department of Integrative Biology, University of California, Berkeley

Much of the research focusing on integration in the human skeleton has focused on craniodental anatomy, at least in part because of its relevance to human evolution and taxonomy, coupled with the cranium's import for sensory functions and the dentition's import for food processing. Comparatively fewer studies have been undertaken on human postcranial anatomy, although recent studies have focused on specific skeletal regions, including the vertebral column, pelvis, scapula, long bones, hands, and feet.

This study focuses on the humerus to assess how metric features are interrelated. Fifteen linear humeral measurements were collected following established osteometric standards. The measurements capture total length, as well as midshaft and end dimensions. Data were collected from adult modern human skeletons (N=103 individuals; n=51 females, n=52 males), across four population groups: Zulu

(n=34), Portuguese (n=28), Egyptian (n=22), and Jordanian (n=19). A bivariate correlation analysis was run for each pair of measurements to produce a correlation matrix.

The matrix reveals patterns of correlation that are consistent with expectations based on developmental and functional factors. Dimensions are strongly correlated within and between the proximal and distal ends, whereas shaft cross-sectional dimensions have stronger correlations with each other than with other metrics. Measurements of length are moderately correlated with end dimensions, and to a lesser degree with shaft cross-sectional dimensions. These relationships have implications for how we interpret variation across modern humans, and even more so in the fossil record where the evidence is much more scarce and variation more irregularly sampled.

This study was supported by the National Science Foundation DDRIG-1732221 and the Portuguese Studies Program at UC Berkeley. MFB was supported by the University of California Berkeley Chancellor's Fellowship.

Studying oral health status in Pre-Hispanic and Colonial indigenous individuals from Central Mexico through paleogenomics

MIRIAM J. BRAVO LÓPEZ¹, VIRIDIANA VILLA ISLAS¹, AXEL SOLÍS GUZMÁN¹, ELIZABETH CAMPOS MEJÍA², ALBERTO HERRERA MUÑOZ², JORGE GÓMEZ VALDÉS³ and MARÍA C. ÁVILA ARCOS¹

¹Population & Evolutionary Genomics Lab, International Laboratory for Human Genome Research, ²Centre INAH Querétaro, Centre INAH Querétaro (National Institute of Anthropology and History), ³Postgraduate Studies Division, National School of Anthropology and History, UNAM

Genome-wide studies of ancient pathogens have proven instrumental in both identifying and characterizing past human infectious diseases. To gain insights into the human infectious disease in indigenous populations in Mexico, we analyze seven Pre-Hispanic teeth samples and twenty-nine Colonial teeth samples from Central Mexico. We generated low-depth shot-gun sequencing data from these two sample sets and used KRAKEN to compare the reads to a database constructed from complete bacterial, archaeal, and viral genomes in RefSeq. The taxonomic assignments specific to known pathogenic species were evaluated in more depth. Interestingly, one individual from the pre-contact period had a high fraction of reads assigned to *Tannerella forsythia*, a Gram-negative anaerobic bacteria involved in periodontal disease and associated with the progression of cardiovascular disease. Furthermore, four individuals from Colonial period also yielded reads matching to the *T. forsythia* genome in important amounts. Mapping these data to the *T. forsythia* KS16 genome revealed the characteristic patterns

of damage expected of ancient DNA, thus supporting its ancient nature. Undoubtedly, the drastic changes that took place as a result of colonization also influenced the type of diet and lifestyle of the native population, and consequently, their oral health. Further phylogenetic and comparative genomic analyses of *T. forsythia* spanning this transition will help to understand the evolution of their pathogenicity, and opens up questions regarding past lifestyle, diet and genetic makeup of pathogens and hosts for both time periods.

Wellcome Trust, CONACYT

Factors influencing the strength, equality, and stability of male chimpanzee social bonds at Gombe National Park

JOEL BRAY^{1,2} and IAN C. GILBY^{1,2}

¹School of Human Evolution and Social Change, Arizona State University, ²Institute of Human Origins, Arizona State University

Male chimpanzees form strong, equitable, and stable social bonds, which are hypothesized to assist in rank acquisition and reproductive success. But how do bonds vary over the entire course of adulthood, and do the factors influencing bonds vary between populations? We extend previous studies, using 35 years of behavioral data (N = 26 individuals) from Gombe National Park and statistical methods (additive and multiplicative random effects models) that control for the non-independence of dyads. Maternal brothers, dyads similar in age, and dyads dissimilar in rank had stronger bonds, as defined by a composite index based on party association and grooming rate. A significant interaction between age similarity and maternal kinship demonstrated that these effects were primarily driven by maternal brothers similar in age exhibiting stronger social bonds. Maternal brothers, dyads similar in both age and rank, and dyads with stronger bonds groomed more equitably; again, an interaction between maternal kinship and age similarity was significant. After controlling for age, rank, and kinship, the strength of male social bonds was predicted by the equivalent index up to five years prior, indicating that social bonds were stable, community-wide, for at least five years. Additionally, maternal kinship and lifetime grooming equality were the strongest predictors of a dyad's longest bond, based on three methods for estimating bond duration (max duration: 9 to 13 years, varying by method). Between-population differences are discussed in the context of demographic variation, and we examine circumstances leading to the formation and dissolution of stable bonds.

Funding provided by the Jane Goodall Institute, the National Science Foundation, the National Institutes of Health, the Leakey Foundation, and the National Science Foundation Graduate Research Fellowship.

ABSTRACTS

Estimating the minimum number of individuals (MNI) from a looted, commingled context in Hualcayán, Peru

EMILY A. BRIGGS¹, KELSEY C. JORGENSEN², REBECCA E. BRIA¹ and EMILY A. SHARP³

¹Department of Anthropology, University of Minnesota, ²Department of Anthropology, Wayne State University, ³School of Human Evolution and Social Change, Arizona State

For looted bioarchaeological sites, evaluating the minimum number of individuals (MNI) and mean number of elements (MNE) can provide a critical source of demographic information when human remains have been de-contextualized. This study used three different methods: traditional MNI (White 1953), zonation method (Knüsel and Outram 2004), and landmark method (Mack *et al.* 2015) to calculate the MNE and MNI, and compare the degree of difference between these three methods. The human remains used for analysis were excavated from Andean chullpas on the outskirts of Hualcayán, Peru dating to 200-700 CE. Chullpas are above-ground tombs built to house mummies from associated kin groups, and are often looted by contemporary locals seeking to sell ceramic and textile artifacts. Resultantly, when the mummy bundles are unwrapped, human skeletal remains become fragmented and are scattered outside of the chullpas. Results from this analysis indicate that the three MNI methods produce similar estimations only when skeletal remains that are highly fragmented (<25% present) are excluded; with MNI of 7 (White), MNI of 7 (Knüsel and Outram), and MNI of 7 (Mack *et al.*). When highly fragmented and remains are included, MNE and fragmentation estimates range more drastically, from 8 to 59 and 60, respectively. Excluding bones prone to fragmentation produces more consistent results, however, the disadvantage lies in its unfaithful representation of the amount of human remains in a commingled assemblage. Until a better method is devised, the more systematic traditional and landmark methods were easier to apply in this type of context.

The evolution of human neutrophilia and the functional divergence of a bactericidal cell in primates

JESSICA F. BRINKWORTH^{1,2}, KATHRINE VAN ETEN¹, PRIYA BHATT¹, KEATON MCCLURE⁴, MIKE WOO¹, NEGIN VALIZADEGAN¹, SUVANTHEE GUNASEKERA¹, YARAVI SUAREZ¹ and BRIAN ALDRIDGE³

¹Department of Anthropology, University of Illinois Urbana-Champaign, ²Institute for Genomic Biology, University of Illinois Urbana-Champaign, ³College of Veterinary Medicine, University of Illinois Urbana-Champaign, ⁴Department of Molecular and Cell Biology, University of Illinois Urbana-Champaign

A distinctive and evolutionary puzzling feature of human immunity is neutrophilia. A short lived, highly reactive cell, neutrophils are important limiters of bacterial pathogens. Human proportions of neutrophils (50-70% of circulating leukocytes) are energetically costly. Neutrophils are replaced every 6-8 hours, typically die as an antimicrobial strategy, cause considerable bystander tissue damage during infection and seem to contribute to major human diseases (sepsis, asthma). Most other primates and mammals maintain immunocompetence with considerably fewer neutrophils (20-40% circulating leukocytes). Human neutrophilia may be the outcome of evolutionary alterations to neutrophil responses such that higher numbers of the cell have to circulate to maintain host protection. To address this possibility, we analyzed transcriptomic, and cell physiological responses of human, rhesus macaque and common marmoset neutrophils. Cells were isolated via a density gradient, and stimulated with 1ng-1ug of lipopolysaccharide (LPS) from *Escherichia coli* or the bacteria itself (MOI 10:1) for 1-3 hours. Transcriptomic responses were captured by RNA sequencing, and cell physiological responses [phagocytosis, apoptosis, extracellular trapping (NETing)] by fluorescent microscopy. Species strongly differed in transcription of genes in innate immune and cell trafficking pathways. Primates exhibited considerable NETing and apoptosis sensitivity to even subclinical doses of LPS, but humans displayed a unique suite of neutrophil antimicrobial responses - phagocytosing and apoptosing more, while NETing less than other primates. Importantly, genes involved in these activities appear to be under selection in primates. These results pair with neutrophil activities in human-specific pathologies and suggest that important neutrophil antimicrobial strategies have evolutionarily diverged in humans.

University of Illinois at Urbana-Champaign, Department of Anthropology.

Osteometric sorting of metacarpals and metatarsals in commingled human skeletal assemblages

KRISTEN A. BROEHL
Anthropology, University of Nevada, Reno

Commingling can significantly impede analyses in bioarchaeology and forensic anthropology. Osteometric sorting helps individuate skeletal remains, but few studies have included hand and foot elements in their sorting frameworks despite numerous contexts where these elements comprised a major portion of an assemblage. Therefore, this study derives the data needed for osteometric pair-matching of metacarpals and metatarsals. A sample (n=86) from the University of New Mexico's documented osteological collection acted as a reference for calculating average left-right differences and standard deviations for

measurements (length, maximum length, inter-articular length, head width, base width) on the metacarpals and metatarsals. In an independent test sample, use of the derived osteometric data with a standard sorting formula for combined measurements led to correctly excluding 74.6-89.8% of potential matches, depending on the digit.

The derived data was then used to sort the Point San Jose Collection to clarify context. The collection's association with a military hospital from the 1870s in San Francisco shows medical origins, but commingling obscures the exact purpose since it is difficult to identify complete individuals versus discrete body parts. Pair-matching metacarpals was used as a proxy for estimating skeletal completeness. Osteometrics excluded 59.3-73.6% of potential matches, and visual methods helped sort those remaining. High numbers of pair-matches showed the remains were likely cadavers rather than surgical waste, thereby improving interpretations of the collection, including the social circumstances surrounding its discard. This research shows that osteometric sorting of metacarpals and metatarsals is successful and useful in anthropological analyses.

Funded in part by CSU, Chico Research, Scholarship, & Creative Activity.

Crown shape analysis of the maxillary dentition of *Homo naledi*

JULIET K. BROPHY^{1,2}, DARRYL J. DE RUITER^{2,3} and LEE R. BERGER²

¹Geography and Anthropology, Louisiana State University, ²Evolutionary Studies Institute and Centre for Excellence in PaleoSciences, University of the Witwatersrand, ³Anthropology, Texas A&M University

The phylogenetic status of *Homo naledi* is currently unresolved. The identification of similarities/differences and consistent patterns of change in occlusal morphology has proven to be useful for deciphering phylogenetic relationships among taxa. A crown shape analysis was performed on the Dinaledi maxillary P³, P⁴, M¹, M², and M³ using Elliptical Fourier Function Analysis. The Dinaledi fossils were compared with teeth from hominins classified as *Australopithecus africanus*, *A. robustus*, *Homo sp.*, *H. erectus*, *H. habilis*, and *H. rudolfensis*. All of the teeth were size standardized in order to assess shape. Principal component analyses were performed on the amplitudes of the digitized teeth. The results indicate that there is considerable overlap of the crown outline shapes within each tooth type. These results are not inconsistent with previous work on maxillary postcanine dentition. The maxillary M1s are the most informative tooth type for this sample. *Homo naledi*, *H. rudolfensis*, and *H. erectus* first molars plot in the negative half of PC2, likely reflecting the distal displacement

ABSTRACTS

of the lingual cusps, in particular the hypocone, giving the teeth a skewed contour; the angles formed at the hypocone and paracone are more acute in these teeth than those that have a positive PC2. *Australopithecus robustus*, *A. africanus*, and *H. habilis* plot mainly in the positive half of PC2 which is due to the more squared crown shape without a skewed contour. While the maxillary teeth in this sample are useful for assessing similarities between taxa, the mandibular teeth appear better for discriminating between groups.

Functional adaptation of trabecular bone in the Human mandibular condyle in relation to diet

ELLA J. M. BROWN¹ and JAY T. STOCK^{1,2}

¹Department of Archaeology, University of Cambridge, ²Department of Anthropology, Western University

The trabecular structure of the human skeleton develops in relation to mechanical stimuli. Mandibular shape and size variation has been attributed to changes in mechanical loading related to diet, and more specifically, the transition from hunter-gathering to agriculture. This study tests whether variation in diet and loading influences trabecular bone in the mandibular condyle among different human populations that have varied subsistence practices.

We compare semi-nomadic pastoralists and agriculturalist populations from Northern Africa and Britain. Analysis consisted of volumetric measurements of trabecular bone in the condyle, including bone volume fraction (BV/TV), connective density (Conn.D) and degree of anisotropy (DA), which all contribute to the mechanical strength of bone. Data was collected via the Nikon XTH 225 ST HRCT Scanner at the Cambridge Biotomography centre and analysed via BoneJ.

Results showed differences in the degree of anisotropy and connective density between all populations that related to differences in subsistence. There were also site specific differences between the medial and lateral areas of the condyle. A greater degree of anisotropy was noted in the medial side of the condyle compared to the lateral among all populations. This suggests that the direction of loading during mastication follows the same pattern for different diets, but the toughness of the food leads to changes in the density and anisotropy of mandibular trabecular bone. Differences in trabecular bone morphology also correlate with cortical bone shape, suggesting that the interaction between genetic constraint and skeletal plasticity in relation to diet is complex.

This study was funded by the Cambridge AHRC Doctoral Training Partnership and the Isaac Newton Trust.

Orangutan Nesting Behavior in Gunung Palung National Park, West Kalimantan, Indonesia

LAURA A. BRUBAKER-WITTMAN¹, ANDREA BLACKBURN¹, ANDREA L. DIGIORGIO¹, FAYE S. HARWELL¹, ERIN E. KANE¹, TRI WAHYU SUSANTO² and CHERYL D. KNOTT¹

¹Anthropology, Boston University, ²Biology, National University of Indonesia

Nesting behavior is unique to the great apes among primates and has wide ranging implications for understanding socioecology and conservation. While much is known about nesting in gorillas, chimpanzees, and some orangutan populations living in disturbed forest and peat swamp, the nesting behavior of orangutans living in primary forest is poorly understood. We studied the nesting behavior of Bornean orangutans (*Pongo pygmaeus wurmbii*) in Gunung Palung National Park, West Kalimantan, Indonesia, using observations of 4,526 nesting events collected between October 1994 and September 2018, testing hypotheses about nest height. We found a significant effect of age/sex on nest height ($F(3)=106.1$, $p<0.001$). Post-hoc comparisons (adjusted α -level= 0.008) showed that flanged males nested significantly lower than all other age/sex classes ($p<0.001$) while females nested significantly lower than juveniles and unflanged males ($p<0.001$). Flanged males and females tended to nest lower in the canopy when alone than in the presence of other orangutans (males: $F(3)=24.25$, $p<0.001$; females: $F(3)=5.83$, $p=0.001$). Our results help demonstrate that across forest types, flanged male orangutans prefer to nest lower in the canopy while all other age- and sex-classes prefer higher canopy positions for nesting. Furthermore, our finding that solitary individuals nest lower than individuals near other orangutans suggests that nesting higher in the canopy may allow individuals to space their nests optimally when in proximity of other orangutans. These results have significant conservation implications, as logging and deforestation fundamentally change the forest structure, disrupting the canopy and making preferred nesting locations unavailable.

National Science Foundation (BCS-1638823, BCS-0936199, 1540360, 9414388); National Geographic Society; US Fish and Wildlife (F15AP00812, F12AP00369, 98210-8-G661); Leakey Foundation; Disney Wildlife Conservation; Wenner-Gren Foundation; Nacey-Maggioncalda Foundation; Conservation, Food and Health

The Effect of Polycystic Ovarian Syndrome (PCOS) on Bone Mineral Density

SARAH BRUCKLER¹ and MEGAN MOORE²

¹Department of History and Philosophy, Eastern Michigan University, ²Department of Sociology, Anthropology, and Criminology, Eastern Michigan University

The effect of Polycystic Ovarian Syndrome (PCOS), a common endocrine disorder, on the human female skeleton is not well known. PCOS is characterized by symptoms, such as excessive sex hormones, insulin resistance, and weight gain, all of which are correlated to increased bone mineral density (BMD). However, common comorbid conditions like menstrual dysfunction and autoimmune hypothyroidism are correlated to decreased BMD. This pilot study compares cranial and total BMD of non-smoking subjects (aged 18-45 years) with PCOS ($n = 10$) with healthy, age and BMI-matched controls ($n = 5$) using full body, DEXA scans. A significant correlation between age and cranial BMD ($r = 0.644$; $p = 0.009$) was detected in the PCOS sample that was not detected in the control sample. Additionally, a correlation between cranial BMD and total BMD was observed in the control sample ($r = 0.800$; $p = 0.050$), but not the PCOS sample ($r = 0.135$; $p = 0.590$). Finally, no significant correlation between cranial BMD and BMI was observed in either sample. The results of this study suggest that women with PCOS may reach peak bone mass at a later age than women without the disorder, that PCOS has a systemic effect on BMD, independent of weight, and that cranial vault BMD is a useful metric for determining illness-related effects on systemic BMD. While an expanded study is necessary to confirm the conclusions of this study, it is useful for understanding the utility of DEXA technology in determining the systemic effects of disease on BMD.

This research was sponsored by the Senior Honors Thesis Award granted by the Eastern Michigan University Honors College.

A cautionary theory: Learning from the origins of allometric scaling

ALEX B. BRUMMER¹, JULIA D. MONK² and ADAM B. RODDY²

¹Institute for Quantitative and Computational Biology, University of California, Los Angeles, ²School of Forestry and Environmental Studies, Yale

A central goal in organismal and evolutionary biology is to define the rules that govern all living organisms in order to understand similarities and differences between organisms. One mathematical theory commonly used for this purpose is 'allometric scaling'. Its origins dating back two centuries lie in comparisons of ratios brain size and body size, and these early studies were commonly used to affirm the preconceived superiority of white males. Eventually, these comparisons of ratios per individual developed into linear regressions across multiple individuals, giving rise to the modern form of allometric scaling. Though allometric scaling has been essential in providing deep insights into the evolution of biological form and function, its history is fraught with examples of racist and sexist

ABSTRACTS

ideology, which persist to this day. In this talk I will elucidate the advancement of allometric scaling, highlighting its historical misapplications in an effort to understand why there is such a recurrence in thought and to serve as a warning for current and future applications of the theory to the study of cities and cultures.

Do polyspecific associations influence nutritional intake of female redbtail monkeys (*Cercopithecus ascanius*)?

MARGARET A. H. BRYER^{1,2} and JESSICA M. ROTHMAN^{1,2,3}

¹Anthropology Program, The Graduate Center of the City University of New York, ²New York Consortium in Evolutionary Primatology, ³Department of Anthropology, Hunter College of the City University of New York

Primate group living carries costs and benefits that grow more complex with polyspecific associations. Though several sympatric monkey species feeding and traveling together as mixed-species groups may reduce predation risk and increase access to food, feeding competition may also increase. We quantified the potential nutritional costs of polyspecific association for forest living redbtail monkeys (*Cercopithecus ascanius*) in Kibale National Park, Uganda. The majority of our female redbtail monkey focal follows collected 2015-2016 included polyspecific association (>70%), defined as a heterospecific(s) <20 meters. Redtail monkey digestible energy intake did not differ by proportion of day spent in polyspecific association with blue monkeys (*Cercopithecus mitis*), mangabeys (*Lophocebus albigena*), or both frugivorous heterospecifics ($p = 0.48$). All observations of interspecific aggression during female redbtail monkey feeding involved redbtail monkeys receiving and fleeing from aggression, indicative of a previously proposed interspecific hierarchy in which redbtail monkeys are at the bottom. However, the number of aggressive events received from other frugivores by redbtail monkeys did not affect redbtail daily digestible energy intake ($p=0.21$). These findings suggest that redbtail monkey diverse diet and ability to switch foods reduces feeding competition during frequent polyspecific association. Nutritional costs of polyspecific association depend not only on dietary overlap, but also dietary flexibility of species involved.

This study was funded by NSF BCS 1540369 (DDRI Bio Anth), NSF BCS 1521528, NSF BCS 0922709, and NSF DGE 0966166 (NYCEP IGERT).

Are we what we eat? Regional diet, but not climate, shapes cranial morphology in Jomon foragers

LAURA T. BUCKLEY^{1,2,3}, ISABELLE DE GROOTE⁴, YUZURU HAMADA⁵ and JAY T. STOCK^{1,6,7}

¹Department of Archaeology, University of Cambridge, UK, ²Department of Anthropology,

University of California, Davis, USA, ³Department of Earth Sciences, Natural History Museum (London), UK, ⁴School of Natural Sciences and Psychology, Liverpool John Moores University, UK, ⁵Section of Evolutionary Morphology, Primate Research Institute, Kyoto University, Japan, ⁶Department of Anthropology, Western University, London, Canada, ⁷Max Planck Institute for the Study of Human History, Jena, Germany

Understanding the interplay of factors affecting human phenotypes is a long-standing challenge, and climate and diet have long been appreciated as key influences on cranial morphology. The effects of these factors are rarely compared within a single, variable population, however. Jomon prehistoric foragers inhabited the Japanese Archipelago throughout its considerable climatic range and developed sophisticated subsistence practices suited to habitat diversity. We used 3D surfaces and landmark geometric morphometric techniques to analyse relationships between cranial shape, climate (temperature and precipitation), and diet among the samples of Jomon. We also compared covariation between cranial shape and climate in Jomon to our previous research demonstrating covariation between climate and cranial shape in macaques throughout Japan. Following previous, archaeologically-based schemes we divided Japan into four dietary regions. In contrast to strong evidence for climatic adaptation in macaques, Partial Least Squares analysis of Jomon crania shows no significant relationship between shape and climate. Canonical Variates Analysis, however, shows a large, significant difference in cranial shape between dietary groups of Jomon. Climatic variation sufficient to influence cranial morphology in a non-human primate does not impact Jomon cranial phenotype. Disparity in the covariates of cranial shape between humans and non-human primates suggests humans are buffered from moderate climatic stress by their behaviour. In the absence of climatic selection, differences in behaviour such as diet may shape human morphology. These results contribute to our understanding of the relative importance of selective pressures shaping human phenotypes and of biological versus behavioural adaptive strategies during human evolution.

This work was supported by the European Research Council (AdaPt Project: FP7-IDEAS-ERC 617627)

The Antiquity of Treponemal disease in the Asia-Pacific regions: Implications for settlement history

HALLIE R. BUCKLEY¹, MELANDRI VLOK², KATE DOMETT³, HIEP HOANG TRINH⁴ and MARC OXENHAM⁵

¹Anatomy, University of Otago, ²Anatomy, University of Otago, ³College of Medicine and Dentistry, James Cook University, ⁴Department of Prehistoric Archaeology, Vietnam Institute of Archaeology,

⁵School of Archaeology and Anthropology, The Australian National University

The impact of infectious disease on human populations during the prehistory of the Asia-Pacific Islands has received less attention than other regions of the world. Here, we review published accounts of treponemal disease in this region from biocultural and ecological perspectives. We also present new findings from the Neolithic period cemetery of Man Bac in northern Vietnam (human ribs dated on four individuals to 3951-3620 cal BP, 95.4%) that includes a well-preserved young adult male (Burial MB05M20) with diagnostic lesions indicative of treponemal infection. No reliable published prehistoric cases of treponemal disease exist for mainland South East Asia (MSEA) or island South East Asia (ISEA). Despite early European contact accounts of an almost ubiquitous presence of treponemal disease in Polynesia, the earliest skeletal evidence of probable yaws (*T. pallidum pertenuis*) in the Pacific islands is from Micronesia c.800 A.D. There are no cases of Lapita period (3300-2500 B.P.) treponemal disease or pre-Lapita (3500 BP-400 A.D.) Micronesian samples. What, then, was the route of entry into the Pacific, and when did this occur? From craniometrics and aDNA, the people of Man Bac have been differentiated into two groups; the original Australo-Papuan people and East Asian immigrants. MB05M20 was from the latter group, possibly heralding the introduction of the disease into Southeast Asia. The presence of treponemal disease in northern Vietnam pre-dates the arrival of Lapita into the Pacific islands, is potentially significant for understanding its antiquity in Southeast Asia, and provides context for the later introduction of the disease to the Pacific.

Partially Funded by a Royal Society of New Zealand Marsden Fund

The uncertainty of the potto and exudate-feeding in Lorisidae

ANNE BURROWS^{1,2}, ADAM HARTSTONE-ROSE³, LEANNE T. NASH⁴, MARY T. SILCOX⁵, KEEGAN R. SELIG⁶ and SERGI LÓPEZ-TORRES⁶

¹Department of Physical Therapy, Duquesne University, ²Department of Anthropology, University of Pittsburgh, ³Department of Biological Sciences, North Carolina State University, ⁴School of Human Evolution and Social Change, Arizona State University, ⁵Department of Anthropology, University of Toronto Scarborough, ⁶Institute of Paleobiology, Polish Academy of Sciences

Molecular studies indicate monophyly of Lorisidae with *Arctocebus/Perodicticus* [Perodictinae] and *Loris/Nycticebus* [Lorinae]. Lorinae includes a small-bodied insectivore (*Loris*) and a larger-bodied obligate, gouging exudativore (*Nycticebus*). *Arctocebus* is a small-bodied insectivore and the larger-bodied *Perodicticus* (the potto) consumes fruits and gums (exudates) at

ABSTRACTS

least seasonally. Questions persist about the role exudate-feeding may have played in the evolution of lorises and how pottos may access and incorporate gums into their diets. The present study was designed to evaluate morphological evidence for exudatory in *Perodicticus*. Caliper measurements were collected from the toothcomb, upper canines, first upper and lower premolars, and the last lower molar of the skulls of *Loris* spp. (n=19), *Nycticebus coucang* (n=61), *Arctocebus* spp. (n=8), and *Perodicticus* spp. (n=40). Mean scaled differences were compared among the four groups using Bonferroni corrected one-way ANOVA's ($\alpha < 0.05$). For some of these taxa, differential enamel thickness in the lower canine, used to represent the toothcomb, was examined via Micro-CT scans. We found that the toothcomb and molars of *Perodicticus* most closely resemble those of the obligate, gouging exudatory *N. coucang*. *Arctocebus* and *Loris* did not differ significantly from one another in dental morphometrics. The distribution of enamel thickness in the toothcomb of *Perodicticus* also suggests that it consumes gums and could gouge similarly to *N. coucang*. Thus, both subfamilies yield an analogous suite of interspecific dental differences. More definitive evidence of gouging should be sought for *Perodicticus* but present results may indicate that gouging and/or exudatory was basal within Lorisidae.

Opening Adult Learners Up to New Ideas Using Museum Experiences

NICOLE M. BURT

Human Health and Evolutionary Medicine,
Cleveland Museum of Natural History

Engaging adults and teaching them new information can be challenging (Becker Patterson, 2018), but it is crucial if we want an engaged science literate public. Museums are on the forefront of an informal education revolution targeting both children and adults (Rogoff et al., 2016). Informal learning is a key method for effectively introducing new ideas to adults and creating an atmosphere where learners can control their learning trajectory. When learners control the direction of their engagement, it is important to create novel interactions that engage while simultaneously pushing people outside of their comfort zones. This is a strategy for teaching politically charged topics such as bioethics, evolution, and climate change. As a curator, I regularly provide adult education experiences to the lay public and as continuing education for professionals. Using examples of short and long format biological anthropology adult programs taught at the Cleveland Museum of Natural History, I will detail how novel locations and experiences can be used to open adult learners up to new ideas and challenging content. The method involves teaching with hands on material and a

pedagogy focused on discourse. While the focus is on museum programming, the methods used to create an educational dialogue can be used in any non-traditional learning environment.

Becker Patterson, M. (2018). The forgotten 90%: Adult nonparticipation in education. *Adult Education Quarterly*, 68(1), 41-62.

Rogoff, B., Callanan, M., Gutierrez, K., Erickson, F. (2016). Chapter 11: The Organization of Informal Learning. *Review Research Education* 40: 356-401.

Ontogenetic processes in the nasal cavity among Alaskan Inuits: Implications for respiratory adaptations in cold-dry environments

LAUREN N. BUTARIC¹, SCOTT D. MADDUX², CHRISTINA L. NICHOLAS³ and ANDREJ EVTEEV⁴

¹Department of Anatomy, Des Moines University, ²Center for Anatomical Sciences, University of North Texas HSC, ³Department of Orthodontics, University of Illinois at Chicago, ⁴Anuchin Research Institute and Museum of Anthropology, Lomonosov Moscow State University

Tall-narrow nasal cavities among cold/dry populations likely reflect air-conditioning processes. However, the ontogenetic processes shaping adult internal nasal morphology remain unknown. This study investigates the ontogenetic basis of nasal cavity size and shape in Alaskan Inuits. Thirteen coordinate landmarks outlining nasal shape were collected from computed-tomographic data of mixed-sexed adults (n=39) and subadults (n=41) from Pt. Hope, Alaska, as well as comparative West-African adults (n=48). A canonical variates (CV) analysis indicates regional differences along CV1 (70.26%) and age-related differences along CV2 (22.083%). CV1 tracks anterior nasal cavity height and breadth, with ANOVA results indicating that all Alaskan age-groups exhibit significantly taller/narrower nasal cavity shapes compared to West African adults (all *P-values* < 0.001). CV2 tracks nasal height and choanal shape: younger individuals (0-5.9yoa) present with relatively shorter nasal heights and posteroinferiorly-placed choanal margins compared to their older counterparts. Reduced major axis regressions indicate that while CV1 is not related to nasal size ($r^2=0.024$; $P=0.08$), CV2 maintains a stronger, negative correlation ($r^2=0.369$; $P<0.0001$). Overall, analyses suggest that functionally important aspects of Inuit nasal shape appear early in development (0-5.9yoa), well before attaining adult nasal size (15-20yoa). Further, morphology associated with age-related size appears to predominantly impact the interplay between nasal height and choanal positioning, rather than nasal breadth dynamics. These preliminary results ultimately indicate that the tall-narrow nasal cavities conducive for air conditioning processes in cold-dry environments

are established early in ontogeny, providing further support that the nasal cavity maintains an important adaptive role in thermoregulatory processes.

3D Morphometric Analysis of Cranial Variation at the Egyptian Colonial Site of Tombos in Nubia

MICHELE R. BUZON, MELISSA G. TORQUATO and ERIK R. OTÁROLA-CASTILLO

Department of Anthropology, Purdue University

Archaeological excavations at the site of Tombos, located at the Third Cataract, have expanded our understanding Egyptian colonial presence in Nubia during New Kingdom. Previous bioarchaeological analyses have shown that cranial characteristics of individuals from Tombos reflect Egyptian and Nubian morphology. This study uses 3D geometric morphometrics to advance the examination of cranial morphological variation at Tombos. We analyzed cranial morphology based on distinct burial classification: New Kingdom-Egyptian middle-class Chamber tombs, New Kingdom-Egyptian elite Pyramid/Chapel tombs, and Late New Kingdom through 3IP/Napatan Tumulus burials. We placed landmarks using GULmorph, a new software package in the R programming environment called. We recorded 94 standard osteometric landmarks from 31 specimens to complete the analysis. Procrustes ANOVA revealed statistically significant differences in cranial shape between burial types ($F = 2.1647, P < 0.001$). To further explore this result, we conducted post-hoc pairwise comparisons using the Bonferroni correction ($\alpha = 0.0167$). These tests demonstrated that there was a significant difference between the chamber and pyramid groups ($F = 2.4491, P < 0.009$) and the pyramid and tumulus groups ($F = 3.2273, P < 0.001$), but no significant difference between the chamber and tumulus groups ($F = 1.5898, P < 0.024$). These results suggest that the people buried in elite Egyptian style pyramid tombs separated themselves from the Nubian style tumulus graves. It is possible that Egyptians who interacted with the local Nubians as well as their offspring were buried in the middle-class chamber tombs.

This research was supported in part by the National Science Foundation grants 0917815 and 1359210 and the National Geographic Society Committee for Research and Exploration.

Dental macrowear, diet and anterior tooth use in *Ptilocolobus badius* and *Colobus polykomos*

GRACE V. CALHOUN¹, EMMA M. LAGAN¹, DEBBIE GUATELLI-STEINBERG¹, PAUL E. MORSE² and W. SCOTT MCGRAW¹

¹Anthropology, The Ohio State University,

²Evolutionary Anthropology, Duke University

ABSTRACTS

Inferences about diet and feeding behavior from macrowear in extinct taxa hinge on the strength of associations between diet and dental wear patterns in extant taxa. Two similarly-sized colobine species living sympatrically in the Ivory Coast's Tai Forest and that differ significantly in both diet and oral processing behavior provide an opportunity to explore the reliability of such associations. We tested the hypothesis that *Colobus polykomos*' aggressive processing of tough, hard *Pentaclethra macrophylla* pods manifests in greater anterior tooth wear relative to that observed in *Ptilocolobus badius* which does not exploit this resource. We assessed rates of anterior tooth wear in a sample of 10 adult *C. polykomos* and 19 adult *P. badius* from naturally deceased specimens collected from the Tai Forest. We compared differences in ratios of dentin exposure to total occlusal area between anterior and posterior teeth of these species. Mann-Whitney *U* tests reveal that the ratios of averaged first and second incisor wear to first molar, second molar, and third molar wear in *C. polykomos* are significantly greater than those of *P. badius* for each interspecific comparison (*p*-values for Mann-Whitney *U* tests range from 0.036 to <0.001). These results indicate that known differences in diet, food material properties, and oral processing behaviors are reflected by increased incisal wear compared to molar wear in *C. polykomos* relative to that of *P. badius*. These observations support the use of differential macrowear along the tooth row for informing inferences of diet and food processing behavior in extinct primates.

Changes in costovertebral joint anatomy have been selected for in humans and increase ventilation during endurance running

WILLIAM E. CALLISON, NICHOLAS B. HOLOWKA and DANIEL E. LIEBERMAN

Department of Human Evolutionary Biology, Harvard University

Humans differ from apes in being adapted for endurance activities like long-distance running, which requires increasing oxygen intake as much as 80-fold from approximately $0.084 \text{ L}\cdot\text{min}^{-1}\cdot\text{kg}^{-1}$ to $6.1\text{--}6.9 \text{ L}\cdot\text{min}^{-1}\cdot\text{kg}^{-1}$ of body mass. How and when did humans evolve these impressive capabilities? Here we experimentally test the hypothesis that the human thorax evolved derived features to enable inspiration of large amounts of air for sustained periods of time. Using 3D morphometrics, we also test the hypothesis that these features first appear in the genus *Homo*, and evolved convergently in other mammals adapted for cursoriality. To test the first hypothesis, we used 3D kinematics of the thorax and spirometry to compare how much tidal volume during running increases from thoracic and diaphragmatic movements in humans as well

as goats and dogs, the latter of which is also a cursor. While we found that all three species use diaphragmatic breathing to increase tidal volume with increased aerobic demand, humans expand the thorax by as much as 14% via dorsoventral and mediolateral expansion. In contrast, dogs supplement diaphragmatic breathing with just dorsoventral expansion and goats rely solely on diaphragmatic ventilation. 3D analyses of the costovertebral joint indicate that thoracic movements in species adapted for high aerobic activity are facilitated by concavo-convex costovertebral joint morphologies. While australopiths have ape-like joint morphologies, evidence for derived concavo-convex costovertebral joints is present in *Homo erectus*. These results support the hypothesis that the genus *Homo* was selected for endurance in part by supplementing diaphragmatic ventilation with thoracic ventilation.

Surveying Portugal residents' view on the creation and dissemination of three-dimensional replicas of human skeletal remains

VANESSA CAMPANACHO^{1,2,3} and FRANCISCA ALVES CARDOSO^{3,4,5}

¹CIAS - Research Centre for Anthropology and Health, University of Coimbra, ²CEF - Centre for Functional Ecology - Science for People & the Planet, Forensic Anthropology and Paleobiology, University of Coimbra, ³LABOH - Laboratory of Biological Anthropology and Human Osteology, CRIA - Centro em Rede de Investigação em Antropologia, FCSH, Universidade NOVA de Lisboa, ⁴CNRS, EFS, ADES, Aix Marseille Univ, ⁵Cranfield Defense & Security, Cranfield University

Due to the recent accessibility to surface scanning technology a surge in the production of three dimensional (3D) digital replicas of human skeletal remains has occurred. Some of those 3D models are easily accessible online. Consequently, ethical concerns about the unrestricted online dissemination and access of digital replicas of skeletal remains have been grown. These concerns are largely unexplored in Portuguese society, thus an online survey was conducted among Portugal residents aiming to understand their perception on how these models are created, used and shared. The survey is composed by 20 non-mandatory questions, and still ongoing with data here presented being only preliminary. To date 144 individuals, aged between 18 and 69 years old, have participated, most of which were females (56.9%). Half of the participants have visualized a 3D model of skeletal remains; nonetheless, only 12.9% of them have created a 3D model. Largely, the results suggest that Portugal residents agree with the dissemination of 3D digital replicas of human bones, with 87.3% of the participants being willing to allow for their skeleton and that of family members to be digitized after death. Though, the majority considered that the 3D model should be of restricted access and always

associated to a description/context. It is noteworthy the low number of participants, which may be indicative of a lack of interest on the subject. But it may also suggest a low self-assessment on their credibility to express an opinion on the topic.

Shaping voids and building bridges: towards an ethic and legal framework and societal approach to Portuguese human identified skeletal collections (HISC) (Dr Francisca Alves Cardoso - FCT IF/00127/2014)

Differentiating human skeletal remains through energy dispersive X-ray fluorescence (EDXRF)

KATHRYN CAMPEAU

Anthropology, University of Toronto

The ability to differentiate individuals from commingled skeletal remains is critical in forensic and archaeological contexts for identification purposes (forensics) and to determine the demographics of an assemblage (archaeological) (Byers, 2011). Factors affecting the chemical composition of bone include: age, sex, diet, disease, geography and medical treatment (Byrd & Adams, 2016; Nganvongpanit et al., 2016; Bocca et al., 2018). Consequently, an individual's bones should have a unique elemental "fingerprint" that could be used to discriminate between individuals. EDXRF is a quick and non-destructive technique which produces an elemental characterization of samples analyzed. Remains of three known individuals from a southern Italy Iron Age burial site were analyzed to determine if inter-skeletal elemental variation (between individuals) is greater than intra-skeletal variation (within an individual). Fifty various bone samples were analyzed for each individual. Multivariate statistics, Principal Component Analysis (PCA) and Linear Discrimination Analysis (LDA), were used to interrogate EDXRF data. Results showed greater elemental variation inter-skeletally. LDA analysis had a correct classification rate of 98.6% in ascribing bone samples to an individual. This study also examined remains of three other semi-commingled individuals from a Southern Italy Iron Age site. LDA analysis on sorted fragment data produced a classification rate of 94.6%. The most influential components in discriminating the remains were the ratios of Pb/Ca, Zn/Fe, and Sr/Pb. These results illustrate the potential of this non-destructive method of analysis to discriminate small and fragmented commingled remains, providing a timely and cost effective alternative to current techniques.

ABSTRACTS

Integrative archaeometrical and osteological approach suggests violent deaths for Dutch colonizers in 17th Century Northeastern Brazil

ANDRE LUIZ CAMPELO DOS SANTOS, HENRY SOCRATES LAVALLE SULLASI and SERGIO FRANCISCO SERAFIM MONTEIRO DA SILVA
Archaeology, Federal University of Pernambuco

The outcomes of the European colonization of the Americas have been an important research area in Archaeology, Anthropology, and History. One particular challenge is to construct the contexts of how the early colonizers lived and died. To partially answer this question, we conducted a taphonomic analysis on 28 17th Century human skeletons found at the Centre of Recife, Pernambuco, Brazil. This collection is relevant because the working archaeological hypothesis is that these individuals may be associated with the Dutch West India Company (WIC), which operated in Northeastern Brazil between 1630 and 1654. Specifically, we hypothesize that these remains may represent the transition between the Dutch and the Portuguese occupations. To characterize the necrology of the remains, we conducted an osteological analysis that identified perimortem and antemortem lesions in the skulls of 5 individuals. Specifically, we found that the lesions are located in neurocranium and facial bones, measuring from 22 mm to 130 mm in length, from 1 mm to 50 mm in width, and associated with piercing-cutting and sharp instruments such as swords and bayonets, with and without bone remodeling. We further analyzed these lesions using a X-Ray Fluorescence (XRF) instrument and found that they harbor significantly higher concentrations of the Iron element than the unaffected areas. Overall, our results suggest that these individuals may have been exposed to violent events associated with the forms of resistance during the Dutch occupation. Our work also shows that the XRF technique can contribute to the delineation of both archaeological and forensic contexts.

This research is funded by Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPQ) from Brazil.

New ages for old primates: a revised geochronology for the highly endemic late Uintan and early Duchesnean assemblages from the Devil's Graveyard Formation of West Texas

CHRISTOPHER J. CAMPISANO^{1,2}, ALAN L. DEINO³, CHRISTOPHER J. LEPRE^{4,5} and E. CHRISTOPHER KIRK^{6,7}

¹Institute of Human Origins, Arizona State University, ²School of Human Evolution and Social Change, Arizona State University, ³Berkeley Geochronology Center, Berkeley Geochronology Center, ⁴Department of Earth and Planetary Sciences, Rutgers University, ⁵Paleomagnetism Lab,

Lamont-Doherty Earth Observatory, ⁶Department of Anthropology, University of Texas at Austin, ⁷Jackson School Museum of Earth History, University of Texas at Austin

Few North American terrestrial Eocene primate localities have the potential to be directly dated by radiometric techniques, with most dated via a combination of biostratigraphy and paleomagnetic analyses. The primate-bearing Devil's Graveyard Formation (DGF), located in the Trans-Pecos volcanic field of West Texas, preserves numerous airfall and reworked tephra suitable for ⁴⁰Ar/³⁹Ar analysis. Building upon recent research that establishes an age of 45 Ma and older for the early Uintan primate localities (biochrons Ui1a and Ui1b) of the DGF, a series of new ⁴⁰Ar/³⁹Ar ages and paleomagnetic analysis place the late Uintan localities (biochron Ui3) at approximately 44.5 Ma and at the base of Chron C20n, establishing them as possibly the oldest Ui3 localities. Additionally, new dates on tephra bracketing the Skyline channels provides a much-needed revised age for *Mahgarita stevensi* of approximately 41.5 Ma, confirming an early/earliest Duchesnean age. In contrast to the early Uintan primate assemblage in the DGF, which includes no locally endemic taxa, the late Uintan and early Duchesnean localities includes a highly endemic primate assemblage. An in-progress revision of the DGF primates indicate that six of the seven primate taxa recorded from the late Uintan and early Duchesnean localities are endemic. Additionally, the endemic *Mescalerolemur horneri* (Ui3) and *Mahgarita stevensi* (Du), re-dated here, are the only two non-notharctine adapiform species described from North America. Both taxa are more closely related to Eurasian and African adapiforms than to North American notharctines, providing further evidence of faunal interchange between North America and Asia in the Middle Eocene.

Social relationship quality vs quantity: Which is a better predictor of survival in female baboons?

FERNANDO A. CAMPOS^{1,2}, ELIZABETH A. ARCHIE³ and SUSAN C. ALBERTS^{2,4}

¹Department of Anthropology, University of Texas at San Antonio, ²Department of Biology, Duke University, ³Department of Biological Sciences, University of Notre Dame, ⁴Department of Evolutionary Anthropology, Duke University

In humans, a strong link between social relationships and all-cause mortality cuts across geographic, gender, and socioeconomic lines: people with stronger or more supportive social relationships live longer than people who lack such relationships. Recent studies have revealed strikingly similar patterns in nonhuman primates and other social mammals, suggesting not only a common evolutionary origin but also shared biological mechanisms. Debate about the

underlying mechanisms has focused on whether structural (e.g., number of partners) or functional (e.g., relationship quality) aspects of social bonds are better predictors of fitness. Here, we use fine-grained longitudinal data on social relationships and lifespan of 276 adult female baboons (*Papio cynocephalus*) (N = 2,037 female-years) to model and compare the effects of social bond quality, frequency, and number of grooming partners on adult female survival while controlling for social status, group size, and observer effort. Using time-varying Cox proportional hazards models, we find that greater relationship quality with partners of both sexes, larger numbers of partners of both sexes, and higher interaction frequency with male partners all significantly predict longer lifespan ($p < 0.01$). The best single predictor is number of grooming partners, and the overall best model includes both number of partners and relationship quality, which have independent, significant effects on survival ($\Delta AICc = 30$ compared to next-best model). These findings advance our understanding of how social relationships affect survival throughout the aging process, and they clarify the specific aspects of sociality that are most important predictors of lifespan in adult female baboons.

This research was funded by the National Institutes of Health, the National Science Foundation, the Leakey Foundation, and the Max Planck Institute for Demographic Research.

Morphological affinities of Plio-Pleistocene hominins and its phylogenetics implications: a phenetic multivariate exploratory analysis

TAMIRES C. CAMPOS¹, DANILO V. BERNARDO¹ and TATIANA F. DE ALMEIDA²

¹Laboratório de Estudos em Antropologia Biológica, Bioarqueologia e Evolução Humana, Instituto de Ciências Humanas e da Informação, Universidade Federal do Rio Grande, ²Laboratório de Genes do Desenvolvimento, Departamento de Genética e Biologia Evolutiva, Instituto de Biociências, Universidade de São Paulo

In despite of the extensive scientific production about human evolution, considered as the study of the lineage comprising species more closely-related to modern humans than to chimpanzees, a definitive hominin cladogram is far from a consensus. Part of this can be addressed by taphonomy factors, that shuffles and comminutes the fossil record, including here the new discoveries that need to be taxonomically understood. Other part of this assessment can be attributed to the own nature of cladistic analysis which depends on the complex identification of plesiomorphic and apomorphic states, which is particularly potentiated when the object of study is fossil. Assuming that the use of general resemblance to infer evolutionary relationships among taxa is still a legitimate tool, mainly when it is done in parallel to cladistic analysis, we present

ABSTRACTS

here a study about the morphological affinities of Plio-Pleistocene based on a phenetic multivariate analysis applied to the metric data obtained in the specialized literature and in the organized dataset as the Human Origins Database, for example. In this way we performed different sets of analysis covering morphological data of skull, mandible, tooth and members of 12 different hominin taxa explored quantitatively by Principal Component Analysis and Clustering Analysis, followed by matrices comparison of geographical distance, chronological and technological to evaluation of parsimony. In despite of the missing data in all specimens, our results show that the more parsimonious phylogeny is the one that consider closest relationships among *Homo habilis* with other australopithecines than with other representatives of genus *Homo*.

Investigating dietary properties and the feeding ecologies of lemurs in human-maintained habitats

STEPHANIE L. CANINGTON and JONATHAN M.G. PERRY

Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine

Captivity is informative for understanding the behavioral flexibility of species to different feeding ecologies. Although food selection is constrained by availability, comparing material properties of foods consumed in different artificial environments provides an additional method for investigating "feeding" adaptation and flexibility in lemurs. Using focal animal sampling, we tested material properties of the foods consumed by *Lemur catta* (RTL) and *Propithecus coquereli* (sifaka) at the Duke Lemur Center (DLC; $n=2;2$) and Maryland Zoo (MZ; $n=2;2$).

Diets of focal animals were operationalized using Dietary Diversity Indices (\sum Food Species in a Category / Total Species Consumed). For analyzing food challenge, we gathered data on energy release rate ("toughness": J/m^2) via wedge ("W") and scissors ("S") tests using a Lucas Scientific FLS-1 property tester.

RTL at MZ ate no leaves, however, RTL at DLC (as in the wild) ate many species (82% of species in the diet) of foraged ground foliage, tree foliage, and vines within a wide range of toughness ($S=141-812 J/m^2$). At MZ, RTL predominantly ate fruit (67% of consumed species; $W=50-314 J/m^2$), partly overlapping with DLC RTL. The diversity of leaves eaten by sifaka at DLC (56% of consumed species; $S=101-948 J/m^2$) mostly overlaps with their RTL conspecifics. Sifaka at MZ ate only one kind of leaf: sumac ($S=196 J/m^2$), as well as very tough non-leaf foods (e.g.,

acorn squash, $W=769 J/m^2$). Given the opportunity to forage (e.g., DLC), lemurs (even somewhat frugivorous ones like RTL) choose a variety of foods - including tough items.

No funding agencies to report.

Regulatory Constraint During Human Knee Evolution Underlies Osteoarthritis Risk

TERENCE D. CAPELLINI, DANIEL RICHARD and EVEYLN JAGODA

Human Evolutionary Biology, Harvard University

The unique biomechanical characteristics associated with human bipedalism are reflected in knee morphology, which results from genetic changes in the regulatory control of development and growth. During human evolution, variants influencing adaptive knee morphology increased in frequency, however, at some loci, deleterious, small effect regulatory variants also increased via piggybacking on selected haplotypes. These deleterious variants likely contribute to modern osteoarthritis predisposition, although those regulatory variants present in regions of drift may as well. We examined both possibilities by profiling chromatin accessibility during mouse knee chondrogenesis and by integrating these data with datasets derived from comparative genomics, positive selection scans, functional genomics, and GWAS. We identified thousands of distal femur-specific, proximal tibia-specific, and shared knee regulatory sequences, each showing enrichment for activity during human embryogenesis and adulthood. Interspecies sequence analyses revealed expected patterns, such that shared elements showed higher primate conservation than bone-end-specific elements. Human knee elements were also enriched for nucleotide acceleration and involvement in delayed ossification and growth plate fusion. Intraspecies analyses on humans, chimpanzees, and gorillas, revealed a unique pattern of evolutionary sequence constraint in humans, such that bone-end-specific elements displayed lower variation than shared elements, patterns not found in apes. On this backdrop, we found that variable human knee sequences were enriched for osteoarthritis GWAS variants and were depleted for evidence of positive selection, instead identifying with drift processes. In sum, evolutionarily-tolerable regulatory variants (i.e., ones that drift) may underlie osteoarthritis occurrence especially as they provide the genetic background upon which intrinsic and extrinsic factors operate.

This study was funded via grants from the NIH NIAMS (1R01AR070139-01A1) and NSF (BCS-1518596).

Enamel proteome sequences from Dmanisi (Georgia) enable molecular phylogeny beyond the limits of ancient DNA preservation

ENRICO CAPELLINI¹, FRIDO WELKER^{2,3}, JESPER V. OLSEN⁴, DAVID LORDKIPANIDZE⁵ and ESKE WILLERSLEV^{1,6}

¹Centre for GeoGenetics, Natural History Museum of Denmark, University of Copenhagen, ²Natural History Museum of Denmark, University of Copenhagen, ³Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology, ⁴Novo Nordisk Foundation Center for Protein Research, University of Copenhagen, ⁵Georgian National Museum, ⁶Department of Zoology, University of Cambridge

We ignore how species who faced extinction earlier than one million years (Ma) ago are genetically related to the living ones because ancient DNA fully, and irreversibly, degrades after $-0.5-1$ Ma. Here we show that this limit can be overcome by using proteomics to: (i) sequence million years-old proteins extracted from fossil dental enamel, (ii) measure evolutionary changes in amino acid sequences, and (iii) reconstruct evolutionary histories beyond the limits of ancient DNA preservation. Deep-time palaeoproteomics enables: (a) unprecedented access to genetic evidence from epochs still considered impossible to routinely access by biomolecular investigation, and (b) molecular-based investigation of major evolutionary processes so far intractable for molecular phylogenetics, potentially including those of relevance to palaeoanthropology.

Dental enamel is the hardest tissue in vertebrates, frequently recovered and identified at palaeontological sites. Teeth are therefore a key piece of evidence for fossil mammalian ecology and evolutionary studies. We present a novel analytical approach using high-resolution, high-sensitivity tandem mass spectrometry (MS) to reconstruct protein sequences from fossil dental enamel. From most of the specimens analysed, extended stretches of amelogenin, enamelin, and ameloblastin were identified in enamel samples. Glutamine deamidation, a spontaneous modification extensively observed in ancient samples, was surprisingly high. This observation is a strong indicator of the authentic ancient endogenous origin of the sequences retrieved. Enamel proteins are not expressed in other tissues, they never appear among regular random laboratory contaminants, and they are not detected in ordinary saliva proteomes.

E.C. is supported by a research grant (17649) from VILLUM Fonden. Work at the Novo Nordisk Foundation Center for Protein Research is funded in part by the Novo Nordisk Foundation (NNF14CC0001).

ABSTRACTS

Geographic variation in long bone growth and age estimation of juvenile skeletal remains

HUGO FV. CARDOSO¹, CHARLOTTE PRIMEAU², LOUISE HUMPHREY³, LESLEY HARRINGTON⁴, EMILY HOLLAND⁵, LUIS RIOS⁶, MENNO HOOGLAND⁷, LAURE SPAKE¹, JENNIFER NELSON⁴ and ELLIE GOODERHAM¹

¹Department of Archaeology, Simon Fraser University, ²Division of Cancer, University of Dundee, ³Department of Earth Sciences, The Natural History Museum, ⁴Department of Anthropology, University of Alberta, ⁵Department of Anthropology, Brandon University, ⁶Department of Paleobiology, Museo Nacional de Ciencias Naturales-CSIC, ⁷Department of Archaeology, Leiden University

The accuracy of juvenile age estimation methods based on long bone length is known to be tied to the similarity between the method's reference sample and the target population. This similarity has been most often described in terms of "biological/genetic proximity" or ancestry, and is the basis for advocating population- or country-specific methods. The similarity of ontogenetic environments, however, has been less explored as the source for this variation. The purpose of this paper is to examine and explore the sources of variation in growth in long bone length in a geographically and temporally diverse sample of individuals originating from 18th to 20th century Europe. The diaphyseal length of the 4 long bones were collected from a sample of 399 known-age juvenile skeletons, aged between birth and 12 years. The data combines anatomy- and cemetery-based reference collections in Portugal, Spain, Italy, Greece, France, The Netherlands, Switzerland, the UK and Sweden. Unstandardized residuals from the best-fitting equation of long bone length regressed against age were used to quantify growth status of the different sub-samples relative to the average of the overall sample. Results show that differences in growth between the different sub-samples generally reflect secular change between temporally distant populations, but also differences in socioeconomic development between contemporary nations. These findings have important implications for age estimation, by illustrating that there is a large amount variation within one single, broadly defined population ("Europeans") and that such variation is likely to derive from different ontogenetic environments.

This project was partly funded by the Social Sciences and Humanities Research Council of Canada

Revisiting Herto: New evidence and perspectives on *Homo sapiens* from Ethiopia

YONATAN SAHLE¹, YONAS BEYENE², ALBAN DEFLEUR³, BERHANE ASFAW⁴, GIDAY WOLDEGABRIEL⁵, WILLIAM K. HART⁶, LEAH E.

MORGAN⁷, PAUL R. RENNE⁸, JOSHUA CARLSON⁹ and TIM D. WHITE¹⁰

¹DFG Center for Advanced Studies: Words, Bones, Genes, Tools, University of Tübingen, Germany, ²French Center for Ethiopian Studies, Addis Ababa, Ethiopia, ³Laboratoire de Géologie, ENS, CNRS UMR 5276, Lyon, France, ⁴Rift Valley Research Service, Addis Ababa, Ethiopia, ⁵Six (6) Salako Way, Santa Fe, NM 87506, ⁶Department of Geology and Environmental Earth Science, Miami University, Oxford, OH, USA, ⁷U.S. Geological Survey, Denver Federal Center, Denver, CO, USA, ⁸Berkeley Geochronology Center and Department of Earth & Planetary Science, University of California, Berkeley, CA, USA, ⁹Human Evolution Research Center and Department of Integrative Biology, University of California, Berkeley, CA, USA, ¹⁰Human Evolution Research Center and Department of Integrative Biology, University of California, Berkeley, CA, USA

Research at localities in the radioisotopically dated Upper and Lower Herto Members of Ethiopia's Bouri Formation provides new data that complement and extend reports of fossils and artifacts first published by the Middle Awash research project in 2003. The new archaeological and paleontological data are from sediments dated to the later Middle Pleistocene, a time that witnessed the emergence of *Homo sapiens* anatomy, distinctive behaviors, and technologies traditionally characterized as the "Middle Stone Age." Results of revisits to Herto reported here include the *in situ* recovery of a stone tool assemblage from the Upper Herto Member, from sediments deposited on the margin of a freshwater lake where large mammals were butchered ~160 ka. This spatially and stratigraphically controlled lithic assemblage includes artifacts normally typologically attributed to both African Acheulean and Middle Stone Age industries or techno-complexes. At Herto and elsewhere anatomical and technological change did not conform to simple, progressive "transition-to-*H. sapiens*" models. Rather, emergence of various attributes is now documented to have been temporally and spatially more complex than traditionally conceptualized. The Herto paleoanthropological record is an expanding paleoanthropological resource base that provides unique perspectives on human emergence in Africa. We evaluate several recent claims involving inferences derived from evidence made available by the Omo Kibish, Baringo Kapthurin, Ologesailie, and Jebel Irhoud occurrences in light of our new archaeological data. In this way, the continuing Herto research contributes to elucidating the timing and patterns of technological, behavioral, and anatomical change in Africa during the evolution of our species.

Patterns in and determinants of cortical thickness and rigidity in the femoral diaphysis of Holocene *Homo sapiens*

KRISTIAN J. CARLSON^{1,2}, ADAM A. KOLAWA¹, KIMBERLEIGH A. TOMMY², MARK R.

DOWDESWELL³, NICHOLAS B. STEPHENS⁴, LILY J. DOERSHUK⁴, JAAP P.P. SAERS⁵, JAY T. STOCK^{5,6}, TIMOTHY M. RYAN⁴, ADAM D. GORDON⁷ and TEA JASHASHVILI^{8,9}

¹Department of Integrative Anatomical Sciences, Keck School of Medicine, University of Southern California, ²Evolutionary Studies Institute, University of the Witwatersrand, ³School of Statistics and Actuarial Science, University of the Witwatersrand, ⁴Department of Anthropology, Pennsylvania State University, ⁵Department of Archaeology, University of Cambridge, ⁶Department of Anthropology, Western University, ⁷Department of Anthropology, University of Albany, SUNY, ⁸Molecular Imaging Center, Department of Radiology, Keck School of Medicine, University of Southern California, ⁹Department of Geology and Paleontology, Georgian National Museum

There is a consensus that modern humans have undergone postcranial gracilization since the Late Pleistocene. There have been hints of greater complexity in this temporal trend, according to several recent studies of human cortical and trabecular bone in various skeletal elements. Here we evaluate the femoral diaphysis in a quasi-continuous fashion in order to visualize and quantify cortical bone distributions characterizing four diverse modern human samples. We test whether factors such as activity levels or patterns, geography, subsistence strategy, or substrate, among others, may affect patterns in cortical bone distributions.

Using image data acquired through medical and high-resolution computed tomography, we digitally quantify cortical bone from 20% to 80% diaphyseal length in modern human femora representing North American and African groups. We measure cortical thickness and second moments of area around and along the diaphysis. We use color maps to visualize and qualitatively evaluate observed patterns in the sample, and penalized discriminant function analyses to quantitatively evaluate these patterns between groups.

Among the intrinsic and extrinsic (e.g., environmental and behavioral) factors we consider, activity patterns are able to differentiate not only cortical thickness or second moment of area magnitudes characterizing individual groups, but also the relative locations where groups express high levels of cortical thickness or greater rigidity. When applied to a larger sample of Holocene humans that more faithfully reflects inherent human variability, these findings, and this approach in general, offer a unique opportunity to further understand complexity in the trend towards gracilization of the modern human skeleton.

NSF BCS-1719140, NSF BCS-1719187, NRF-DST (South Africa), ERC under European Union's Seventh Framework Programme (FP/2007–2013)/ERC Grant Agreement n.617627, RCUK/BBSRC grant BB/R01292X/1, USC Provost grant for Nikon Metrology XTS225ST micro-CT.

ABSTRACTS

Extreme endurance running alters the gut microbiota

RACHEL N. CARMODY¹, EMILY M. VENABLE¹, ANDREW S. BOLZE¹, LAUREN CHRISTOPHER¹, BRYCE A. CARLSON², MONICA P. LOUIS³ and THEODORE GARLAND, JR.³

¹Department of Human Evolutionary Biology, Harvard University, ²Department of Anthropology, Purdue University, ³Department of Biology, University of California Riverside

The gut microbiome contributes importantly to the human energy budget, but almost all studies of these effects to date have manipulated energy intake rather than expenditure. Probing whether high energy expenditure elicits increased or decreased microbial contributions to energy gain affords insight into the fundamental nature of human-microbial interactions and their evolutionary significance. To explore how high energy expenditure shapes the gut microbiota, we performed 16S rDNA sequencing on fecal samples collected from high-running and limited-running cohorts of humans and mice. Our human cohorts consisted of ultra-marathoners participating in the 2015 Race Across the USA (n=9), averaging a marathon a day from coast to coast, and co-traveling race staff with minimal to moderate running experience (n=4). Our mouse cohorts consisted of artificially selected hyper-running Hsd:ICR mice (n=42) and normal-running genetic controls (n=42), with half of each group given exercise wheels and all maintained under identical dietary and environmental conditions. Hyper-running mice with wheel access (p=0.001) as well as human ultra-marathoners (p=0.010) exhibited significant differences in gut microbial community structure compared to limited-running controls, and compared to baseline, controlling for covariates. Notably, in both host species, high-runners exhibited higher relative abundances of Firmicutes and lower Bacteroidetes (both LDA_{3.0}, LEfSe), a phylum-level microbial profile linked to increased energy uptake in the colon. Our emerging results suggest that gut microbial responses to high levels of energy expenditure may buffer host energy balance, lowering barriers to intensive aerobic activity in hominins past and present.

This study was supported by the William F. Milton Fund and the Harvard Department of Human Evolutionary Biology.

Captive chimpanzees (*Pan troglodytes*) demonstrate contagion in spontaneous scratching behavior

ERICA A. CARTMILL^{1,2}, DANIEL M.T. FESSLER¹, BRITTANY N. FLORKIEWICZ¹, AUSTIN GANE¹ and KELSEY RYAN¹

¹Anthropology, UCLA, ²Psychology, UCLA

Contagious behaviors are behaviors in which the probability of performing an action increases after witnessing it in others. Such behavioral contagion

has been documented in several mammalian species. In humans, yawning, smiling, laughing, and scratching are all thought to be contagious. Researchers have proposed that contagious behavior is linked to empathy (or precursors thereof). For that reason, understanding its evolution and distribution across other species is particularly relevant to the study of cognitive evolution in the human lineage. Contagious scratching can be explained either in terms of transmission of anxiety (and thus related to empathy), or in terms of cues used to calibrate ectoparasite defenses (and thus unrelated to empathy). Although it has been investigated in several non-human species, the results are mixed. The only previous study in non-human apes used an experimental paradigm in a laboratory setting and found that the probability of scratching did not increase after watching a video of another ape scratching. We conducted 31 hours of focal observation of captive chimpanzees housed in a large social group at the Los Angeles Zoo and tested for contagion in spontaneously-occurring scratching events. Using a binomial regression, we found that chimpanzees were significantly more likely to scratch in the five seconds after witnessing another scratch than they were during baseline observations. As distance from the initial scratching individual increased, probability of contagion decreased. As visual attention to the initial scratching individual increased, probability of contagion increased. Our results provide the first observational evidence for naturally-occurring contagious scratching in chimpanzees.

Length variation in the upper limbs and hands of modern Thai skeletons

D. TROY CASE¹ and KRISTEN R. R. SAVELL²

¹Dept. of Sociology & Anthropology, NC State University, ²Dept. of Biology, Sacred Heart University

Although relative bone length has long been an area of interest in biological anthropology, comparison of length relationships in the bones of the limbs with those of the hands and feet is considerably rarer, especially in adults. Given that such comparisons can provide insight into the development of individual bones and morphogenetic fields, we investigated length variation in the long bones of the arm and hand (humerus, radius, metacarpals, and phalanges of rays 1, 3, and 5) in 192 modern Thai skeletons of known sex.

Principle components analysis identified two significant components (varimax rotated), one most strongly focused on the metacarpals, but also on the humerus and radius in both sexes, and another most strongly focused on the middle phalanges but including the proximal phalanges in both sexes. These two components account for 76% of the variance in males and 80% in females. They mostly distinguish the arm and palm from the digital bones. Coefficients of

variation were also calculated for each bone, but showed no significant differences throughout the limb and hand except for intermediate phalanx 5. Pearson's correlation analysis suggests that the radius shows more similarity in length to the metacarpals than does the humerus, but this similarity weakens within the fingers in a distal direction, particularly in females.

These results suggest that metacarpal length demonstrates a stronger relationship with the proximal elements of the arm than with the digits, potentially highlighting regional developmental differences. This study also highlights some similarities that may relate to morphogenetic fields.

Data collection for this project was funded by a 2013 Fulbright Teacher-Scholar Grant to Thailand.

In vivo bending deformation of the human lumbar spine during axial loading: Implications for hominin postural adaptation

ERIC R. CASTILLO and DANIEL E. LIEBERMAN
Human Evolutionary Biology, Harvard University

How do variations in posture affect the human spine's resistance to bending forces during loading? Previous studies have shown that lumbar lordosis influences patterns of postural change during axial loading, but few studies have explored the spine's load-deformation relationship *in vivo*. In this study, changes in lumbar curvature were measured during a series of weight vest experiments. Infrared cameras captured 3-D positional data from spinal markers attached on the spinous processes of T12-S1 to measure lumbar posture. Increasing loads from 0-30% body mass were applied in 5% increments to a weight vest for 2 minutes per trial while participants stood in a neutral posture. A curved beam model was used to estimate bending stress and strain of the lumbar spine as a single functional unit. MRI scans prior to the experiments were used to correct externally measured changes in spinal shape for internal anatomical structure. Results suggest naturally straighter lumbar spines are stiffer: sagittal bending resistance was inversely associated with unloaded lordosis, explaining 52% and 64% of the variation in flexural bending stiffness and elastic modulus, respectively (p<0.0001). On average, lordosis tended to decrease during loading, but naturally straighter spines tended to deform by straightening while naturally curved spines tended to become more curved. Straighter lumbar spines also tended to show less time-dependent postural variability during a loading trial (p<0.01). These results collectively suggest that fossil hominin species with consistently low degrees of lumbar lordosis may have been better adapted for greater stability and lower injury risk while carrying loads.

This work was supported by the Wenner-Gren Foundation (grant #8757) and Harvard University.

ABSTRACTS

Consistent sex differences in stone play and stone tool use in free-ranging Balinese long-tailed macaques

CAMILLA CENNI¹, CHLOË INDIA WRIGHT¹, NOËLLE GUNST¹, I NENGAH WANDIA² and JEAN-BAPTISTE LECA¹

¹Psychology, University of Lethbridge, ²Primate Research Center, Udayana University

Sex differences in tool use behavior have been widely reported in several primate species, with a male bias towards a predisposition for percussive actions, considered a key feature in the evolution of technical intelligence in the hominin lineage. However, little is known about how such sex differences develop and whether similar sex-related specializations exist in object play, an activity hypothesized to facilitate the emergence of tool use in animals and humans. To address these questions, long-tailed macaques (*Macaca fascicularis*) are an ideal primate model because stone tool-assisted percussive foraging is habitual in some populations of this species, whereas other populations exhibit a culturally-transmitted stone-directed form of object play, known as stone handling (SH), whose repertoire includes pounding a stone onto another. We compared sex differences in the spontaneous expression of SH and the experimentally-induced performance of stone tool-assisted foraging behavior, with a focus on percussive actions, in free-ranging provisioned long-tailed macaques in Bali, Indonesia. Preliminary results showed strongly male-biased percussive SH, and a similar trend emerged from a pilot experimental phase of stone tool use. By providing insights into the evolution of sex-typical interests and specialization in object play and tool use in non-human primates, our research may contribute to elucidate the origins of the division of labor in early humans.

NSERC and the University of Lethbridge Research Fund

Measuring attack on self: The current state of minimally invasive biomarkers for autoimmunity

TARA J. CEPON-ROBINS

Department of Anthropology, University of Colorado, Colorado Springs

Autoimmune disorders (e.g., Rheumatoid Arthritis, Type 1 Diabetes, Inflammatory Bowel Disease) occur when the immune system produces antibodies that attack self-produced cells/tissues as though they were foreign antigens. Autoimmune disorder prevalence is on the rise all over the world, including among populations undergoing economic development. Understanding why autoimmune disorders are becoming more prevalent relies on research among transitioning populations, as well as more traditionally living populations for baseline comparisons. Assessing prevalence of autoimmunity among these populations can be difficult

due to invasive blood/tissue sampling and limited access to medical equipment for storage and analysis. The development of minimally invasive, field-friendly techniques for understanding autoimmunity among traditionally living and transitioning populations is crucial for documenting local, national, and global changes to health.

The present study analyzes the state of technologies currently being used in Biological Anthropology for assessing autoimmune disorder prevalence and risk-factors among hard-to-reach populations. Studies on autoimmunity among these populations published within the last 10 years were reviewed. Methodologies used varied widely in suitability for field settings. On the more field-friendly end of the spectrum are measures that are gathered via minimally-invasive methods (e.g., finger-prick blood samples, stool samples) and either stored easily (e.g., dried blood spots) or analyzed immediately in the field using point of care testing (e.g. rapid tests). These methods are discussed in more detail and new field friendly methods are introduced that are currently in development. More work is needed to create and employ minimally invasive methods for measuring autoimmunity in field settings.

Life history parameters recorded in dental cementum

PAOLA CERRITO^{1,2}, SHARA E. BAILEY^{1,2}, BIN HU³ and TIMOTHY G. BROMAGE⁴

¹Center for the Study of Human Origins, Department of Anthropology, New York University, ²New York Consortium in Evolutionary Primatology, NYCEP, ³Biomaterials & Biomimetics, New York University College of Dentistry, ⁴Department of Biomaterials, New York University College of Dentistry

Tooth cementum, the connective tissue anchoring mammalian teeth within their alveolar socket, grows continuously, throughout the individual's life. Studies have observed its biannual increments of contrasting brightness, which have been used to estimate season and age at death in multiple species. Moreover, reproductive events have been inferred from the relative thickness of the bands in two mammalian species. The aim of this project is to test the hypothesis that life history variables affect cementum microstructure in a way that can be discerned via light microscopy and that can be correlated with the age of the individual. Thin sections of donated male and female *H. sapiens* teeth with known age and life history parameters were prepared for circularly polarized light (CPL) imaging. Digital micrographs were acquired. In all samples a small number of bands with contrasting brightness were observed in CPL. Previous work suggests that these correspond to changes in crystal orientation and/or size. Using FIJI® we measured the thickness of each band and estimated the age of the individual corresponding to the time when the bands were

formed by establishing proportional relationships with the total thickness of the cementum. We confirmed that the bands correspond to reproductive events and menopause (with an average error of ± 2 years) in females, and observed that in males they correlate with skeletal maturity and, perhaps, somatic/physiological aging (~50 years of age). This methodology has the potential to inform us on the timing of life-history events in archaeological and paleoanthropological contexts.

Impacts of Thoracic Kyphosis Relative to the Midfacial Skeleton

KRISTYNA L. CEUNINCK¹, TRI TRAN², ADAM ENGEL², WILLIAM SENSACOVIC² and JOHN STARBUCK¹

¹Department of Anthropology, University of Central Florida, ²Department of Radiology, Florida Hospital

Kyphosis is a spinal condition that includes forward rounding of the spine from vertebral wedging of five degrees or more. Morphological integration (MI) refers to the fact that parts of complex organisms do not vary randomly and instead display degrees of interdependence that are thought to occur from shared genetic or developmental origins, and/or functional demands. Since the skull rests atop of the vertebral column, posture can influence skull development and craniofacial anatomy. Because kyphosis alters posture and ambulatory mechanics, patterns of MI between the skull and spine of affected individuals likely differ from unaffected individuals. We test the hypothesis that individuals with kyphosis exhibit statistically significant MI differences relative to controls for thoracic vertebral and midfacial measurements. Using Amira software, six anatomical landmarks were identified on the T6 vertebrae and the midfacial skeleton, respectively, of CT images of adult kyphotic ($n=15$) and control ($n=19$) samples. A Euclidean Distance Matrix Analysis (EDMA) of MI was carried out using XYZ landmark coordinates by calculating correlation values for paired linear distance measurements (one vertebral and one midfacial) separately for both samples. Only 35 of the 225 (15.56%) correlation differences were statistically significant. Patterns of variation among these significant correlation differences were explored by examining sample directionality of differences, sign patterns, and strengths. These results are important for identifying unique, but slight, morphological covariation differences that occur over time in the midfacial skeleton from kyphosis and provides phenotypic clues that may be useful in diagnosing this condition in skeletal material.

No funding information to disclose.

ABSTRACTS

Differential energy gain from saturated and polyunsaturated fats

KATIA CHADAIDEH and RACHEL N. CARMODY
Human Evolutionary Biology, Harvard University

Dietary fats are almost fully absorbed in the small intestine, thus saturated and polyunsaturated fats are typically treated equally in calculations of dietary energy value. However, ingestion of different fat types alters the quantity and chemical profile of bile acid production, which may alter fat absorption in the small intestine and microbial metabolism in the colon. To test the hypothesis that different dietary fats have differential consequences for energy gain, we fed mice matched diets containing primarily saturated (milk) or polyunsaturated (flaxseed) fats, measuring changes in host and gut microbial phenotypes. Six-week-old male C57BL/6J mice were reared for four weeks on standard chow or one of four custom semi-purified chows spanning low-fat and high-fat intakes (n=6 per treatment): 15% saturated fat, 15% polyunsaturated fat, 45% saturated fat, or 45% polyunsaturated fat (w/w). In high-fat conditions, mice fed saturated fat exhibited greater increases in adiposity compared to mice fed polyunsaturated fat (p=0.031, t-test). Consuming saturated versus polyunsaturated fat also impacted gut microbial community structure (p=0.002, ANOSIM). In both the low-fat and high-fat conditions, the saturated fat diet was associated with increased relative abundance of Firmicutes (log₁₀LDA=4.16; LEfSe), a phylum associated with enhanced energy gain; in contrast, the polyunsaturated diet was associated with increased abundance of *Akkermansia muciniphila*, a bacterium associated with leanness via enhanced gut barrier integrity (log₁₀LDA=3.79; LEfSe). Together, our data suggest different caloric potentials for saturated and polyunsaturated fats, a finding that challenges conventional models of caloric value and our expectations about hominin diets in the past and present.

This study was supported by the Milton Fund, Dean's Competitive Fund for Promising Scholarship, and the Harvard Department of Human Evolutionary Biology.

Age-related variation in ingestive behavior patterns in *Sapajus* spp

JANINE CHALK-WILAYTO¹, MYRA F. LAIRD², KRISTIN A. WRIGHT³, ANNE O. RIVERA⁴, BARTH W. WRIGHT⁵, PATRÍCIA IZAR⁶, DOROTHY FRAGASZY⁷, CALLUM F. ROSS², DAVID S. STRAIT⁸, ADAM VAN CASTEREN⁸, ELISABETTA VISALBERGHI⁹, ROBERT S. SCOTT¹⁰ and MARIANA D. FOGAÇA¹¹

¹Department of Biomedical Sciences, Mercer University Medical School, ²Organismal Biology and Anatomy, University of Chicago, ³Department of Biomedical Sciences, University of Missouri-Kansas City, ⁴Department of Anthropology, Northwestern University, ⁵Department of Anatomy, Kansas City University of Medicine & Biosciences, ⁶Department of Experimental Psychology, University of São Paulo, ⁷Department

of Psychology, University of Georgia, ⁸Department of Anthropology, Washington University in St. Louis, ⁹Istituto di Scienze e Tecnologie della Cognizione, Consiglio Nazionale delle Ricerche, ¹⁰Department of Anthropology, Rutgers, The State University of New Jersey, ¹¹Neotropical Primates Research Group

Recent ecological, experimental, and comparative studies have highlighted the importance of ingestive behavior in shaping craniodental form in primate taxa. However, much of this research has focused on adult ingestive behaviors. Here, we compare ingestive behavioral patterns across age classes in *Sapajus libidinosus* from Fazenda Boa Vista, Brazil and *Sapajus nigritus* from Parque Estadual Carlos Botelho, Brazil. Using a subset of the data, we also examined the influence of food mechanical properties (FMPs) on ingestive pattern variation. Feeding behavior data were collected from two groups of *S. libidinosus* (n=517 feeding bouts) and two groups of *S. nigritus* (n=41 feeding bouts). Discarded food items were tested for toughness and elastic modulus using a Lucas portable mechanical tester. For each feeding bout, ingestive behavior patterns were analyzed as triplet sequences. Unique triplet sequence frequencies were compared across age classes. Food mechanical properties were categorized as high or low toughness and as high or low elastic modulus; the effect of FMPs on sequence frequency across age classes was determined. Younger individuals utilized more unique behavioral sequences than adults regardless of food toughness or elastic modulus and despite adults eating a greater range of food types. For all age classes, foods with high FMPs elicited fewer unique ingestive behavior sequences compared to foods with low FMPs. Collectively, these results suggest that juveniles and adults employ different ingestive behavior strategies, but FMPs alone do not appear to influence age-related variation in ingestive behavior frequencies. Instead, FMPs limit ingestive behavioral flexibility comparably across age classes.

Funding was provided by the Leakey Foundation, National Science Foundation (NSF-BCS-1440541, NSF-BCS-1440542, NSF-BCS-1440545, NSF-BCS-1627206), Northwestern University Weinberg College of Arts & Sciences Undergraduate Research Grant, and FAPESP #2008/55684-3, #10/51565-0.

The dynamic evolution of the xenobiotic-metabolizing cytochrome P450 enzymes (CYP1-3) among primates

MORGAN E. CHANEY^{1,2}, MELIA G. ROMINE¹, HELEN PIONTKIVSKA^{2,3} and ANTHONY J. TOSI^{1,2}

¹Department of Anthropology, Kent State University, ²School of Biomedical Sciences, Kent State University, ³Department of Biological Sciences, Kent State University

The enzymes in the three gene families CYP1-3 are biomedically relevant because of their role in metabolizing various xenobiotics, including

nearly all active compounds in pharmaceuticals. Because pharmaceuticals often mimic natural substances (e.g., plant secondary metabolites), researchers have persuasively argued that P450s may be relevant to the adaptation of species or populations to their specific diets. Therefore, we mined 24 primate genomes for 15 subfamilies of homologs within the CYP1-3 gene families to (1) infer rates of gene duplication and degeneration by mapping the phylogenetic relationships of these groups; and (2) test the hypothesis that dietary adaptation of primate species was accompanied by positive selection on the protein-coding DNA of these genes. Our results showed that some gene trees contained duplicated internal subtrees (e.g., CYP2C, CYP2D, CYP3A), implying that some taxa have retained gene duplicates where others have not. However, most of the gene trees showed an expected topology and a 1:1 correspondence between species and genes (e.g., CYP1B, CYP2E, CYP2J). Our hypothesis of positive selection acting on P450 genes was supported for some subfamilies (e.g., CYP2C, CYP2D), where codons with elevated dN/dS ratios were clustered within substrate-recognition regions of the translated P450 protein. Taken together, our findings indicate a pattern of adaptive importance for these P450 subfamilies that agrees well with their pharmaceutical importance. These results further suggest that some primate lineages have relied on enzymatic adaptation to their diets more than others.

Funded by the Kent State University College of Arts & Sciences

Evolving the primate retina: using time to generate high visual acuity

CHRISTINE J. CHARVET and DESELYN J. TINDAL-BURGESS

Psychology, Delaware State University

Primates surpass many other mammals in their visual abilities, having evolved an unusually high density of photoreceptors within their central retina called a fovea. Little is known about the developmental programs that might contribute to the emergence of a fovea in primates. To that end, we gathered a total of 386 developmental milestones gathered across 19 mammalian species (6 rodent, 3 carnivore, 1 ungulate, 6 marsupial species), including primates (i.e., marmosets: *Callithrix jacchus*, rhesus macaques: *Macaca mulatta*, humans: *Homo sapiens*). This is the largest cross-species dataset of developmental transformations to date. Developmental milestones capture temporal changes in synaptogenesis, gene and protein expression, axon formation, as well as neuronal production across the retina and the rest of the brain. We use these data to identify developmental processes giving rise to the high density of photoreceptors in the central retina (i.e., fovea) of primates. We found that the timing of synaptogenesis, and tract

ABSTRACTS

formation are conserved across the studied species. However, photoreceptor neurogenesis is selectively and significantly extended in the retina of primates compared with the timing of many other developmental transformations. These findings demonstrate that extending the duration of photoreceptor production accounts, at least, in part for the emergence of the fovea. Thus, modifying the timing of developmental programs serves to give rise to high visual acuity in primates.

This work was supported by an NIGMS grant (5P20GM103653)

Terrestrial tree hugging in a primarily arboreal lemur: a risky but effective thermoregulatory strategy

CHLOE CHEN-KRAUS¹, NJARATIANA A. RAHARINORO², RICHARD R. LAWLER³ and ALISON F. RICHARD¹

¹Department of Anthropology, Yale University, ²Department of Zoology and Animal Biodiversity, University of Antananarivo, ³Department of Sociology and Anthropology, James Madison University

Regulating body temperature can be a significant energetic stressor for primates, especially those facing highly variable and extreme climatic conditions such as are characteristic of lemur habitats across Madagascar. At Bezà Mahafaly Special Reserve, we observed Verreaux's sifakas (*Propithecus verreauxi*), a highly arboreal lemur, resting terrestrially, holding the trunk of a tree against their thinly-furred ventrums ("terrestrial tree hugging") during the mid-day heat of the late dry season. It is perplexing, however, that sifakas should choose to rest terrestrially, as they are more vulnerable to predation on the ground. We hypothesized that terrestrial tree hugging is a very effective means of dissipating heat. To investigate the benefits of this behavior, we studied six sifaka groups and collected data on the temperature of the air, ground, and at various heights on the trunk of the tree used during tree hugging bouts. We observed tree hugging most often when ambient temperatures were $\geq 36^{\circ}\text{C}$ (the average body temperature of sifakas). During tree hugging bouts, the temperature at the base of the tree was considerably cooler than the air (paired t-test, $t(62)=9.1$, $p<0.001$) and locations farther up the tree trunk (paired t-test, $t(62)=3.1$, $p=0.003$). We witnessed animals in all focal groups but one—the group who faces exceptionally frequent dog and livestock disturbances—engaging in this behavior. We therefore propose that terrestrial tree hugging is a highly efficient form of behavioral thermoregulation for sifakas during times of heat stress, but is risky and likely only occurs when and where predation threats are low.

This research was part of our larger study of sifaka behavior funded by National Science Foundation (NSF BCS-1745371) and the Yale University MacMillan Center.

When is object manipulation an expression of psychological disturbance caused by environmental stressors? A macaque-human comparison

SYDNEY CHERTOFF^{1,2}, KELSEY HARKNESS¹, I NENGAI WANDIA⁴, AFRA FOROUD^{1,2,3} and JEAN-BAPTISTE LECA¹

¹Department of Psychology, University of Lethbridge, ²Institute of Child and Youth Studies, University of Lethbridge, ³Department of Neuroscience, University of Lethbridge, ⁴Primate Research Center, Udayana University

Typically, behaviors are outward expressions of underlying attentional, motivational, and emotional processes. However, the correlational or possibly causal relationships between environmental stressors, attentional states, motivational/emotional mechanisms, and object manipulation as a potential motor outlet, remain poorly understood. The present research aims to explore the psychological underpinnings of repetitive object-oriented and self-directed behavioral sequences by free-ranging, urban-dwelling, and provisioned Balinese long-tailed macaques (*Macaca fascicularis*) that fit the loosely defined parameters of object manipulation, some of which being reminiscent of fidgeting in humans. The Eshkol-Wachman Movement Notation system and the Observer XT12 video scoring software were used to characterize the structure of object manipulation sequences performed by the macaques. Preliminary results (eight notations from one subject) indicate that object manipulation with food is limited to specific movement patterns whereas non-edible objects are manipulated in less functionally constrained, thus more varied, ways. Further, when manipulating non-edible objects, there was more asymmetry between left- and right-hand movements in the focused attentional state than in the unfocused one. Our study is the first to examine the performance of object-oriented actions from the perspective of fidgeting-like behaviors in non-human animals. Comparable data will be collected in children at the Lethbridge Montessori School, Canada, to conduct a cross-species comparison. This approach may provide an evolutionary-based view of the complex relationships between environmental stressors, attention, motivation, and object manipulation.

I would like to acknowledge the Natural Sciences and Engineering Research Council of Canada (NSERC) and the University of Lethbridge Research fund for their generosity and support.

Mortuary based variation in early stress experiences at CA-CCO-138

COLLEEN M. CHEVERKO
Anthropology and Heritage Studies, University of California, Merced

This study incorporates a mortuary approach to understand variations in stress experience in precontact central California. Specifically, this study investigates how relative wealth and social roles, inferred using mortuary associations, might covary with stress experiences throughout an individual's lifespan, including during their developmental periods. Linear enamel hypoplasia, femoral length, and vertebral neural canal diameters were measured in 74 individuals from the Hotchkiss Mound, a Late Period site from the Sacramento-San Joaquin Delta region. These developmental stress markers were compared to the presence of charmstones and quartz crystals as ritualistic artifacts, shell beads and ornaments as indicators of wealth, and projectile points and stone and bone tools as potential evidence of craft specialization. They were also compared by type of burial orientation and age-at-death. Using sex-specific z-scores, both femoral length and vertebral neural canal diameters vary according to mortuary indicators of wealth, but no differences in these developmental stress markers were observed between mortuary indicators of ritual or craft specialization, burial orientation, or age-at-death. The same associations were not observed using linear enamel hypoplasia; however, high degrees of dental wear greatly reduced the sample size available for dental analyses. These results suggest that there are complex associations between lived experiences of wealth, activity, and stress throughout the lifespan in precontact central California. They help us understand how mortuary associations can be used to explain variation in stress experience at the site and establish the need for additional studies that incorporate mortuary context in the future.

This study was funded by the Ohio State University Office of Energy and the Environment, a Coca Cola Critical Difference for Women Grant, and the Larsen Travel Award.

The use of bout's during activity decreases women's core temperature more than men's

HAYLEY K. CHEYNEY KANE¹ and CARA WALL-SCHEFFLER^{1,2}

¹Biology, Seattle Pacific University, ²Anthropology, University of Washington

Recent studies have recognized the importance of water transport for the subsistence strategies of many human populations. We are interested in how thermoregulatory strategies during water transport might compare with over-ground transport. For example, when people practice "bout" walking—walking in short bursts interspersed with periods of rest—they reset hypothalamic regulation of pace and potentially are able to walk further. Here we test whether bout-locomotion might also aid people in minimizing the heat gain during canoeing. We monitored eight people (4 men; 4 women) independently

ABSTRACTS

paddling continuously across a lake (avg ambient temp=23.9°C; avg humidity=61.7%). We measured participants' blood perfusion, heart rate (HR), core body temperature, and paddling speed during a trial, which consisted of periods of paddling (6 or 12 minutes) regularly interspersed with periods of rest (also 6 or 12 minutes). A single repeated-measures ANOVA was done for each dependent variable, with sex as a factor. People's paddling speed and HR did not change whether they had a long rest (LRE) or short rest (SRE) prior to paddling ($p=0.368$; $p=0.489$), nor was there a significant sex effect on speed or HR ($p=0.368$; $p=0.560$); however, females' core temperature decreased during long rows (LRO) when the LROs were preceded by a LRE, whereas their core temperature increased when the LRO was preceded by a SRE ($p=0.064$). This is potentially due to blood perfusion to the biceps during LROs being dependent upon the length of the preceding rest ($p<0.001$). Thus, bout-paddling might be a strategy for maintaining thermoregulation among women.

As the World Churns: Changing Activities and Identities in a Historic Dutch Dairy Farming Community

CELISE CHILCOTE¹, SABRINA C. AGARWAL¹, ANDREA WATERS-RIST² and MENNO HOOGLAND³

¹Anthropology, University of California Berkeley, ²Anthropology, Western University, ³Anthropology, Leiden University

The interpretation of patterns in types and associated strain levels of activities, and the application of biological characteristics of individuals make it possible to frame biological and cultural data within a social narrative. This study examines social identity in the historic dairy farming community of Middenbeemster, NL, through the examination of skeletal markers of bone growth and maintenance and activity-related stress. It was hypothesized that the high demand for Dutch dairy products during the occupation of Middenbeemster would be reflected in the manifestation and intensity of skeletal markers of activity, suggesting sex and age-related patterns of activity and workload. A total of 87 adults (M=46, F=41) were analyzed for: appendicular osteoarthritis, non-metric traits, and enthesal changes. Additionally, humeral and femoral diaphyseal cross-sectional geometry were examined in 108 adults (M=57, F= 51). Musculoskeletal development analyses provided strong support for a sex-based division of labor with several changes in activity patterns over the lifecourse for both sexes. Males exhibited changes in types of activities likely reflecting an age-associated change in duties of daily farm life from an apprentice-like position to more strenuous and variable activities. Results for younger women suggest they were involved not only in the caretaking of the home, but were also important

contributors to the dairy production process. A review of historical literature provides support for the inferred sex and age-based divisions of labor, however, the conclusions reached suggest a far more active role for women in the economic success of the dairy farms than was historically recorded.

High-Altitude Epigenetics

AINASH CHILDEBAYEVA^{1,2}, DANA C. DOLINOY^{2,3}, JACLYN M. GOODRICH², MARIA RIVERA-CHIRA⁴, FABIOLA LEON-VELARDE⁴, MELISA KIYAMU⁴, TOM D. BRUTSAERT⁵ and ABIGAIL W. BIGHAM¹

¹Anthropology, University of Michigan, ²Environmental Health Sciences, University of Michigan, ³Nutrition, University of Michigan, ⁴Departamento de Ciencias Biológicas y Fisiológicas, Universidad Peruana Cayetano Heredia, ⁵Exercise Science, Syracuse University

High-altitude adapted individuals show distinct circulatory, respiratory, and hematological adaptations to chronic hypoxia. Emerging genetic data support an evolutionary origin and a genetic basis for these observed physiological adaptations to high altitude. However, the epigenetic contribution to adaptation to hypobaric hypoxia has not been well characterized. We performed gene-specific and genome-wide analyses of DNA methylation in whole-blood samples from $n=600$ and $n=87$ individuals of high-altitude Quechua ancestry recruited in Peru, respectively. We found significantly higher LINE-1 repetitive element DNA methylation in individuals born at high altitude. We also found 161 significant differentially methylated regions between individuals born at high vs low altitude. Out of these, 17 are associated with oxygen-related pathways and seven are associated with pulmonary hypertension. Moreover, we found two DNA methylation sites near genes *SIX3* (upstream of *EPAS1*) and *MAP3K4* that mediated the relationship between high altitude and hemoglobin levels. This finding is particularly interesting given that the high-altitude Quechua are known to have increased hemoglobin levels compared to low-altitude Quechua. Our results illustrate that high altitude has a profound effect on the epigenome, and contribute to our understanding of the ways in which the human organism responds and adapts to the environment.

This project was funded by National Science Foundation grants 1132310 and 1613415, the Leakey Foundation, the Wenner-Gren Foundation, and the Department of Anthropology at the University of Michigan

Transcriptional signatures of the aging nonhuman primate brain

KENNETH L. CHIOU^{1,2}, ALEX R. DECASIEN^{3,4}, MICHAEL J. MONTAGUE⁵, CHET C. SHERWOOD⁶,

MICHAEL L. PLATT^{5,7,8}, JAMES P. HIGHAM^{3,4} and NOAH SNYDER-MACKLER^{1,2,9}

¹Department of Psychology, University of Washington, ²Nathan Shock Center of Excellence in the Basic Biology of Aging, University of Washington, ³Department of Anthropology, New York University, ⁴New York Consortium in Evolutionary Primatology, ⁵Department of Neuroscience, University of Pennsylvania, ⁶Department of Anthropology, The George Washington University, ⁷Department of Psychology, University of Pennsylvania, ⁸Department of Marketing, University of Pennsylvania, ⁹Center for Studies in Demography & Ecology, University of Washington

The primate brain is capable of rapidly and reliably processing complex stimuli. These abilities decline with age, which in humans sometimes manifests in neurodegenerative diseases such as Alzheimer's. Yet little is understood about heterogeneity of the aging process across brain regions and cells. To address this gap, we characterized gene expression in brains from a cross-sectional sample of a model population: the rhesus macaques of Cayo Santiago. We sequenced transcriptomes from 160 samples across 8 brain regions involved in various cognitive and sensorimotor functions. As expected, transcriptomes were highly region-specific, with age strongly influencing the transcriptional landscape of all tested regions. Interestingly, the number and identity of age-associated genes differed across regions. The superior temporal sulcus was most strongly affected, with 1,132 genes altered by age. Apart from differences in the number of age-associated genes, regions also varied in the direction and magnitude of changes in gene expression. Further, the magnitude of age-associated effects were distributed unevenly across regions, suggesting that the molecular consequences of aging are largely region-specific. We are now sequencing single-cell transcriptomes to better understand cell-type heterogeneity in aging. We are also testing the impact of social and environmental factors on age-related transcriptional changes. Together, our work underscores the importance of primate models for understanding the intersections of environment and evolution with regard to the aging phenotype.

This work is supported by the National Institutes of Health (NIA R00-AG051764, NIMH R01-MH108627, NIA T32-AG000057) and the National Science Foundation (BCS 1752393).

Dietary fiber and nutritional quality of the foods of Bornean orangutans (*Pongo pygmaeus wurmbii*) in Gunung Palung National Park, West Kalimantan, Indonesia

ISHRAT CHOWDHURY¹, MADELINE E. EOR¹, TRI W. SUSANTO², ERIN E. KANE¹, NANCY-LOU CONKLIN³ and CHERYL D. KNOTT¹

¹Anthropology, Boston University, ²Biology, National University of Indonesia, ³Anthropology, Harvard University

ABSTRACTS

Wild Bornean orangutans experience fluctuations in the availability of their preferred food, fruit. During periods of low fruit availability, orangutans rely on fallback foods which are expected to be higher in fiber and generally lower in free simple sugars. However, it is not clear whether there is a consistent relationship between fiber content and the content of other nutrients. Here, we examine acid detergent fiber (ADF) content of 101 plant foods consumed by orangutans in Gunung Palung National Park, West Kalimantan, Indonesia, and the correlation between ADF and other important plant macronutrients. Samples were collected during full-day behavioral follows between 1994-2001. Samples were analyzed in triplicate through a reflux apparatus, which quantified ADF proportion by weight. An ANOVA revealed significant differences between ADF concentrations of different plant parts ($F(5)=20.89$, $p < 0.001$). Post-hoc analyses ($\alpha=0.005$) determined that bark had a significantly higher ADF concentration than pulp and seeds ($p<0.001$), leaves had a significantly higher ADF concentration than seeds ($p<0.001$), and whole fruit had a significantly higher ADF concentration than pulp or seeds ($p<0.001$). We found a negative correlation between free simple sugar concentration and ADF ($R = -0.63$, $p<0.001$). However, there was no significant correlation between ADF and protein ($R=-0.14$, $p=0.17$) or lipid ($R = 0.134$, $p=0.19$) content. Our findings corroborate work showing that bark and leaves are particularly high in ADF. However, they underscore the fact that determining dietary quality is complex, and that food items that are high in fiber may still be good sources of non-carbohydrate energy.

National Science Foundation (BCS-1638823, BCS-0936199, 1540360, 9414388); National Geographic Society; US Fish and Wildlife (F15AP00812, F12AP00369, 98210-8-G661); Leakey Foundation; Disney Wildlife Conservation Fund; Wenner-Gren Foundation; Nacey-Maggioncalda Foundation; Conservation, Food and Health

Hormones from noninvasively collected samples to assess physiological responses to social, environmental and anthropogenic stressors in nonhuman primates

SHAHRINA CHOWDHURY^{1,3,6}, JANINE L. BROWN⁵ and LARISSA SWEDELL^{2,3,4,6}

¹Anthropology and Archaeology, Brooklyn College, CUNY, ²Anthropology, Queens College, CUNY, ³Primateology, New York Consortium in Evolutionary Primatology, ⁴Anthropology, Graduate Center, CUNY, ⁵Center for Species Survival, Smithsonian Conservation Biology Institute, ⁶Primateology, Filoha Hamadryas Project

Noninvasive techniques are increasingly employed to study correlates of behavior in wild animals. Recent improvements in protein assay methods enable us to extract hormone metabolites from fecal, urine, hair, and saliva samples

collected from wild nonhuman primates. The quantification of hormones relating to stress physiology, reproduction, and energetics enables us to answer a variety of questions in behavioral ecology and evolutionary biology, including about sociality, life history, demography, and conservation. We focus here on the use of noninvasively collected samples from wild nonhuman primates to quantify glucocorticoid (GC) hormones as a measure of physiological stress. Individual responses to both acute and chronic stressors can provide useful information about the effects of social and ecological factors on health, well-being, reproduction and survival, over both the short and long term. Using data from a study of baboons in South Africa, we provide examples of the ways in which GCs can be used to measure individual responses to three types of stressors: 1) social: the impact of social instability; 2) environmental: the effect of seasonality, and 3) anthropogenic: responses to conflict with humans. Finally, we discuss some limitations of these methods with regard to their value in interpretation and application. Despite the often-discussed negative nature of the effects of higher GC concentrations on fitness, the physiological stress response is also adaptive, and care must be taken to avoid interpreting elevated hormone levels as necessarily being indicative of maladaptation.

Funded by National Science Foundation BCS-0824590, LSB Leakey Foundation, Smithsonian Conservation Biology Institute and New York Consortium in Evolutionary Primatology

Exploring the Effect of Socioeconomic Factors on Body Size and Health in the United States from 2000-2018

ELAINE Y. CHU¹ and BRIANA T. NEW²

¹Department of Anthropology, University of Nevada, Reno, ²SNA International for Defense POW/MIA Accounting Agency

It has been previously demonstrated that body size is patterned by the complex interactions between socioeconomic status, social race, and ethnicity. Waist-to-height ratio (WtHR) is considered a more accurate indicator for body size related health risks than previous used methods, such as BMI. Because it does not carry sex, age, or size biases due to standardization of height differences, WtHR allows for comparisons among population groups. The purpose of this research is to investigate the intersectional effects of socioeconomic factors on anthropometric proxies for body size and health in the United States to provide insight into the multifactorial embodiment of health. Data was pulled from NHANES at six-year intervals from 2000-2018, allowing for the analysis of temporal trends. The proxies utilized for body size and social inequality in this analysis include WtHR, social race and ethnicity (SRE), and family-to-poverty income ratio (PFIR).

ANOVA and Tukey's HSD were used to explore the relationships both within and among years. Results of this study indicate that there are statistically significant relationships ($p < 0.05$) among mean WtHRs, PFIR, and SRE categories across years. General trends observed include an overall increase in mean WtHR over time, higher WtHRs for lower PFIR categories, which predominately include non-American White individuals, and higher WtHRs for SRE groups regardless of PFIR category. By examining relationships between proxies for anthropometric body size and social inequality, this research highlights the ways in which human biological variation manifests social inequality.

The Aftermath and Effects of Zika Virus on Human Growth and Development

AISHA A. CHUGHTAI

Anthropology, University of Pennsylvania

Zika virus (ZIKV) is a mosquito-borne flavivirus that took Brazil and, subsequently, the Americas by storm in 2015. Although ZIKV was first identified in 1952 with cases reported in Asia and Africa thereafter, it was during the 2015 pandemic that Zika became a public health emergency. In 2016, although over 900 patients were suspected of high-risk exposure and tested for Zika in Philadelphia, the Philadelphia Department of Public Health (PDPH) only reported a total of 46 "confirmed or probable" cases of Zika virus; in 2017, 11 cases were identified as confirmed or probable, and, thus far, there have been no confirmed cases in 2018. I intend to report and analyze the implications of the full statistical findings of reported, suspected, probable, and confirmed cases of Zika virus in Philadelphia County from 2015 to the present, focusing specifically on explanations for discrepancies between data reporting and outcome to show that an inadequacy of testing measures, protocol, and knowledge of the proliferation of ZIKV led to decreased surveillance and monitoring of congenital and physical birth defects. Further, I will address the current surveillance measures that have been implemented by the Maternal, Child, and Family Health division of the PDPH to retrospectively monitor congenital and physical birth defects in Philadelphia. Although ZIKV cases have decreased in 2018, it is essential to continue a conversation around Zika virus to better understand the potential for a re-emergence of this infectious disease and the on-going impact this will have on human growth and development.

Identifying dietary differences in howler monkey (*Alouatta* spp.) molars

TESSA CICAK

Anthropology, University of Minnesota

ABSTRACTS

Howler monkeys (*Alouatta* spp.) are highly selective foragers but diverse consumers. Whereas many species are primarily folivores, observational data show that they also consume significant amounts of fruit when seasonally available. The Brazilian *Alouatta belzebul discolor* has the highest frugivory rate among howlers, with fruit comprising up to 60% of its annual diet. Because there is a continuum of dietary behaviors, howlers represent a good model for investigating the effect of subtle dietary differences on tooth morphology. Dental topographic analysis (DTA) was used to assess whether *A. belzebul discolor* differs in its molar shape from more folivorous species, *A. palliata* and *A. seniculus*. Using surface and micro-CT scan data of m1-m3, DTA variables were extracted with Molar software. Four variables (Dirichlet normal energy, relief index, slope, and orientation patch count rotated) were calculated for each tooth position, and discriminant functions with cross-validation were used to assess differences. Results using all specimens (n=20) and a subset of variables, correctly classified 6/6 *A. belzebul discolor*, *A. palliata* and *A. seniculus* both had a majority of the specimens correctly classified, and misclassifications were placed into the other species rather than *A. b. discolor*. A subsequent analysis of only *A. palliata* and *A. seniculus*, was able to better distinguish these two species. Despite the modest sample size, DTA performed well at separating congeneric species with subtle dietary differences. These initial results show promise in detecting potentially ephemeral dietary behaviors and can be applied to further understand primate dietary niche strategies.

NSF-DDIG #0726134 University of Minnesota Thesis Research Travel Grant

Anatomic and geometric morphometric assessment of the Herto 16/5 endocranium (Middle Awash, Ethiopia)

LAURA E. CIRILLO¹, DOROTHY DECHANT², REBECCA S. JABBOUR³ and GARY D. RICHARDS⁴
¹Anthropology, University of Nevada, Reno, ²The Institute of Dental History and Craniofacial Study, A.A. Dugoni School of Dentistry, University of the Pacific, ³Biology, Saint Mary's College of California, ⁴Biomedical Sciences, A.A. Dugoni School of Dentistry, University of the Pacific

Early anatomically modern humans from the Herto-Bouri locality are dated from 160-154,000 years ago. Recovered remains include crania from two adults and a 6-7 year old juvenile. In the context of Middle Pleistocene hominins, the juvenile Herto 16/5 cranium is the oldest known and most complete modern human subadult. Here we present a preliminary description of the endocranial morphology and a shape assessment.

Morphological and shape analyses were conducted on an endocast from a new virtual reconstruction of Herto 16/5. Modern human

crania (n=38) aged 5.8-7.9 years were used for comparisons. Developmental ages derive solely from tooth calcification patterns. Procrustes-aligned shape variables were employed in a Principal Components Analysis (PCA).

Compared to recent juveniles, the Herto endocast is generally flatter with a lower height. The frontal lobe is broad with wide separation of the hemispheres. The inferior frontal gyrus is expanded. This contributes to a strong waisting of the endocast at the junction of the precentral and lunate sulci. The medial aspects of the occipital lobes appear to be rotated postero-inferiorly. The middle meningeal vasculature pattern is simple but modern. Venous drainage is left-dominated but consistent with the modern sample.

Thirty-three 3D endocranial landmarks were reduced through PCA to the 16 landmarks that captured the most significant variation in the sample. Variation explained by PC1-4 is 15.9%, 13.9%, 12.0%, and 10.4%, respectively. The endocranial anatomy of Herto 16/5 shows some specific differences relative to recent humans, but the shape analysis places it within the modern human range of variation.

The perils and promise of the WEIRD: contextualizing results from WEIRD and non-WEIRD populations

KATHRYN B.H. CLANCY
Anthropology, University of Illinois, Urbana-Champaign, Beckman Institute of Advanced Science & Technology, University of Illinois, Urbana-Champaign

WEIRD populations, or those that are Western, Educated, Industrialized, Rich, and Democratic, are sampled in the majority of human subjects research. Criticizing the overuse of WEIRD populations allows us to overlook or even justify our own problematic history of WEIRD anthropologists studying the non-WEIRD. What would better serve the scholarly endeavor is a more nuanced argument against essentializing human behavior and physiology, a core philosophical difference between psychology and anthropology. Leveraging datasets from our lab spanning the clinical, the convenient, the rural, and the responsive from the United States, Canada, and Poland for investigating gender, physiology, and behavior, I will make three empirically-grounded arguments. First, contextual information about WEIRD and non-WEIRD samples raises the value of the results gleaned from these populations. Engagement with participants in structured participatory action research, qualitative work, and gathering full histories of our participants' lives helps achieve this context. Second, the use of the scientific method, experimental design, and *a priori* hypotheses can limit emergent nuance from our data because it presupposes the objectivity of the often-WEIRD scientist as

well as the primacy of their research opinion. Anthropologists should include more grounded theory approaches to afford more space for the lived experiences of participants. Finally, WEIRD anthropologists overvaluing non-WEIRD samples can create a cultural norm that studying traditional populations is more rigorous. Prioritizing this type of rigor minimizes efforts to decolonize science, and risks ignoring contextual factors like race, gender, culture, and power that may cause harm to both scientific and participant pool communities.

This work supported by NSF Clancy #1317140 and the Illinois Leadership Center Faculty Fellows Program.

Aging Methods and Population Structures: Does Transition Analysis Call for a Re-examination of Bioarchaeological Data?

MELISSA A. CLARK, ALLYSON SIMON and MARK HUBBE

Anthropology, The Ohio State University

Age estimation of adult skeletal remains is notoriously difficult because the degenerative change of adult skeletons is far more variable across individuals, populations, and anatomical regions than the developmental changes that occur during growth. Additionally, age mimicry makes it difficult to discern between the true population age structure and the age structure produced as an artifact of the reference sample. Transition analysis is an age estimation method that was developed to improve the accuracy of age estimation, especially in older adults, by applying a stricter statistical framework based on multiple osteological age markers. However, despite the advantages offered by transition analysis, many bioarchaeologists continue to rely on age estimates produced using traditional aging methods. The continued and often unquestioned use of traditional methods can be problematic because these age structures are used to draw conclusions about life in the past. This study evaluates the effect of aging methods on age-at-death structure in a sample from the Late Archaic and Prehistoric periods in Northeast Ohio. Transition analysis was performed on 43 skeletons whose ages had been estimated in the 1990s using traditional methods. The maximum likelihood age estimates produced using transition analysis were then compared to the original age estimates. Our results show that the two aging methods produced vastly different age-at-death distributions, and subsequently, significantly different survival curves. This study shows that bioarchaeologists should be wary of taking pre-existing data at face value and should consider re-evaluating the validity of work that relies heavily on traditional aging methods.

ABSTRACTS

The Effects of the Missouri and Mississippi Rivers in the Epidemiological Spread of the 1918 Influenza Epidemic

SONIA A. CLARK and CAROLYN M. ORBANN

Health Sciences, University of Missouri

Few pandemics have notoriety akin to that of the 1918 Influenza pandemic; killing upwards of 50-100 million people worldwide, it was especially nefarious. Yet, despite intense interest in the global pandemic, most of the research on the pandemic has focused on urban areas. In Missouri, there is no formal model to understand how the flu spread outside of the two metropolitan areas, Kansas City and St. Louis. Here, we present results of an investigation into the hypothesis that human activity along the Mississippi and Missouri Rivers aided in the proliferation of the 1918-1920 Influenza epidemic. To test this, we collected data from death records for individuals dying of influenza or related diseases (like pneumonias) between January 1918-December 1920 in 15 Missouri counties. The data does not convey a unidirectional geographic pattern of spread along either the Missouri or Mississippi Rivers, likely due to the complex railroad network and other transportation routes present then. Most of these rural Missouri counties experienced a very small first pandemic wave in spring 1918, a large second wave in the fall of 1918, and a generally small third wave in the spring of 1919. The "echo" wave in the spring of 1920 was, unexpectedly, highly variable, and in some counties larger than any preceding epidemic wave. In conclusion, the data does not support our initial hypothesis that rivers were the primary method of transportation of influenza. Future research focusing on the role of railroads and overland transportation may reveal clearer geographic patterns of spread.

Funding for this project was provided through the University of Missouri's Ronald E. McNair Post-baccalaureate Achievement program.

Decontaminating Dental Calculus for Ancient Starch Research

SIOBHAN CLARKE, MARIA SOTO, JAMIE INWOOD and JULIO MERCADER

Anthropology & Archaeology, University of Calgary

Starch contamination of archaeological material, occurring through entombing soils, excavation equipment and techniques, and laboratory processing, is a known obstacle within archaeology. Thus, the need to establish authenticity is motivating researchers to improve upon classic protocols. The objective for this study was to use controlled laboratory conditions to determine if contaminant starch can be reliably removed from artificially created calculus, while preserving the integrity of both the calculus matrix and non-contaminant starch.

Our methodology consisted of five sequential steps: i) testing and understanding the decontamination efficiency of various concentrations of EDTA, hydrochloric acid, sodium hydroxide, calcium chloride, and alpha-amylase over time, ii) preparation of artificial calculus by co-precipitating ammonium phosphate, calcium chloride, and potato starch, iii) contamination of the synthetic calculus with corn starch and glycine, iv) decontamination, and v) decalcification.

This research is the first attempt at creating synthetic calculus to systematically test decontamination protocols for ancient starch research. Our results show that a treatment of 2% w/v solution of sodium hydroxide for 24 hours will fully disrupt contaminant corn starch that are adsorbed on the surface of the artificial calculus, while preserving entrapped potato granules and the leaving the matrix itself fully intact. Future avenues of investigation include determining the physical or chemical mechanisms that protect completely encased starch granules from gelatinization, and the application to archaeological dental calculus.

This research was fully sponsored by the Canadian Social Sciences and Humanities Research Council under its Partnership Grant Program no. 895-2016-1017

Shifts in biology and mental health among Hispanic immigrant mothers and children in Nashville, TN before and after the 2016 presidential election

ELIZABETH S. CLAUSING and AMY L. NON

Anthropology, University of California, San Diego

This study is an investigation of how immigration-related stress may impact the biology and health of Hispanic immigrant mothers and children, considering recent increases in divisive rhetoric and policies towards U.S. immigrants. This project involves comparison of biological samples and interview data in Nashville, TN from two time points spanning the recent presidential election. Structured interviews were conducted with 82 immigrant mothers and their children (aged 5-13) between 2015 and 2016 and again in 2018. Biological samples and data were collected (saliva, BMI, hair, and blood pressure) from children and mothers for genetic, epigenetic, and hormonal analyses to determine the biological consequences of exposure to immigrant-related stress. Using mixed-methods, we analyze perceived stressors, mental health, and buffering factors from mothers and children in relation to hair cortisol and epigenetics. Mothers report high levels of depressive symptoms (24.3%), anxiety symptoms (35.1%), and moderate perceived stress (86.5%) as well as significantly decreased levels of optimism over time (mean difference = -3.4; p-value < 0.001) in the mothers. At baseline, we see significant negative associations between optimism ($\beta = -0.08$; p-value = 0.03) and duration

in U.S. ($\beta = -0.07$; p-value = 0.02) with hair cortisol, and we expect similar results at follow up. We also expect lower levels of DNA methylation at two stress-related genes (glucocorticoid receptor and serotonin transporter) with greater levels of stress over time. Dramatic changes in stress over time can have traumatic biological consequences, especially for these already vulnerable families.

Funding Citation: Funds provided by the Chancellors Research in Excellence Scholars at UCSD (Application # 4-G021) and Foundation for Child Development (VU-14).

A natural history of the femoral neck

ALEXANDER G. CLAXTON

Anthropology, Boston University

The modern human femoral neck differs from that of our closest living relatives both externally and internally. These differences are in part thought to be indicative of the relatively stereotyped character of hip arthrokinematics in normal human locomotion, whether through evolutionary or bone functional adaptation. It will be helpful to put the human proximal femur into a larger evolutionary and developmental context to better understand how the human condition conforms to larger patterns in proximal femoral morphology and locomotion. A femoral neck evolved independently in at least two tetrapod lineages (archosaurs and mammals), roughly corresponding with a shift to a more parasagittal hind limb posture. However, the extremely prominent femoral neck present in multituberculates, who are often reconstructed as semi-sprawling, demonstrates that it is not inherently connected to hip parasagittalism. The two primary proximal femoral morphotypes in modern mammals, *coxa recta* and *rotunda*, roughly correspond to the range of motion at the hip. These morphotypes are congruent with the patterns of epiphyseal ossification ("coalesced" and "separate"). It has been assumed that those mammals with the "coalesced/*recta*" condition possess the primitive mammalian state and that those with "separate/*rotunda*" are derived. Observations from the mammalian fossil record and ontogeny call this assumption into question. In addition, there are cases within modern taxa that indicate an apparent reversal to "coalesced/*recta*" from the "separate/*rotunda*" condition and vice versa. Modern humans, though "separate/*rotunda*," have some features in common with "coalesced/*recta*," including thin superior femoral neck cortex. Care should be taken when interpreting femoral neck traits.

The Wild Primate Microbiome Partially Protects Against Obesity

JONATHAN B. CLAYTON^{1,2,3}, DIMITRIOS SIDIROPOULOS¹, GABRIEL AL-GHALITH¹, TONYA WARD¹, ROBIN SHIELDS-CUTLER¹, ABIGAIL

ABSTRACTS

JOHNSON¹, PAJAU VANGAY¹, RAN BLEKHMANN^{1,3}, PURNA KASHYAP⁴, AMANDA RAMER-TAIT⁵ and DAN KNIGHTS^{1,3}

¹University of Minnesota, Minneapolis, MN, USA, ²GreenViet Biodiversity Conservation Center, Danang, Vietnam, ³Primate Microbiome Project, Minneapolis, MN, USA, ⁴Mayo Clinic, Rochester, MN, USA, ⁵University of Nebraska, Lincoln, NE, USA

The gastrointestinal tract hosts trillions of bacteria that together form the gut microbiome. Metabolic diseases such as obesity and diabetes are correlated with shifts in microbiome composition and have been on the rise in Westernized countries. At the same time, Westernized diets low in dietary fiber have been shown to cause loss of gut microbial diversity. However, a mechanistic link between microbiome composition, loss of dietary fiber, and obesity is still lacking. We used nonhuman primates (NHPs) to study the effects of lifestyle disruption on gut microbiome composition. Captive NHPs are typically exposed to low-fiber diets and tend to have human-associated microbiota. In order to explore interactions between the gut microbiota and dietary fiber, we transplanted captive and wild primate gut microbiota into germ-free mice and then exposed them to either a high- or low-fiber diet. We found that the group receiving captive primate microbiota became obese, regardless of diet, and had higher levels of circulating inflammatory cytokines, while mice receiving a high-fiber diet and wild primate microbiota remained healthy. Using 16s rRNA gene sequencing we identified key bacterial taxa in each group, specifically a high abundance of Bacteroidetes in captive-donor mice and a higher abundance of Firmicutes in the wild-donor mice. These results suggest that wild NHP microbiota could serve as a reservoir for potentially protective therapeutic microbes effective in cross-species transplants.

Funding sources included Margot Marsh Biodiversity Foundation; Mohamed bin Zayed SCF; PharmacolNeuroImmunology Fellowship (NIH T32 DA007097-32) awarded to JBC; and the UMN Undergraduate Research Opportunities Program grant awarded to DS.

Geospatial distributions of trace metals found in 17th and 18th Century New York African Burial Ground grave soil samples using XRF technology

CARTER CLINTON¹, CANDICE DUNCAN², HASAN JACKSON³ and FATIMAH JACKSON¹

¹Biology, Howard University, ²Environmental Science and Technology, University of Maryland, ³Geographical Information Systems, NASA

The W. Montague Cobb Research laboratory at Howard University currently houses a collection of New York African Burial Ground (NYABG) soil samples. It consists of 92 samples derived from 59- cadaver associated burials interred during the 17th and 18th centuries in lower Manhattan. In this study, we undertake trace metal and geospatial

analyses to explore the range of factors that influence the lifestyles and the environmental factors of this historic NYABG population. X-ray fluorescence (XRF), a non-destructive, semi-quantitative technology allows us to identify between 15 and 19 elements per sample. Due to limitations of control data or standard reference material we confidently report findings for calcium, strontium, arsenic, zinc, and copper. Combinations of these elements further our understanding of West African cultural practices, diets, and local 18th century pottery factories. Our data show elevated levels of strontium (>7x) in burial samples potentially indicating a heavy vegetative diet of individuals. The observed decrease in copper concentrations as depth increases ($R^2=0.703$) suggests the source is a post burial contaminant. We also see prominent trendlines in copper, arsenic and zinc concentrations which can be discerned using our geospatial data. With geographical information systems (GIS) we determine the importance of increased concentrations in cluster burials and increasing/decreasing trends across the burial ground site. Typically, XRF is used in archaeological research, making this work the first of its kind to use the technology to support human existence in burial soil. We aim to introduce the effective use of XRF in bioanthropological studies.

This study was funded by the Sigma Xi Grant-in-Aid of Research and Nation Geographic's Explorer Grant.

Association of MAOA and HTTLPR genetic variants, trauma, resilience, and psychosocial outcomes in Syrian refugee youth

CHRISTOPHER J. CLUKAY^{1,2}, RANA DAJANI³, DIMA HAMADMAD⁴, KRISTIN HADFIELD⁵, CATHERINE PANTER-BRICK⁶ and CONNIE J. MULLIGAN^{1,2}

¹Anthropology, University of Florida, ²Genetics Institute, University of Florida, ³Biology and Biotechnology, Hashemite University, ⁴Taghyeer Foundation, Taghyeer Foundation, ⁵School of Biological and Chemical Sciences, Queen Mary University of London, ⁶Anthropology, Yale University

Genetic influences on responses to psychosocial stress and trauma is a topic of great import. For refugee populations, the impact of stressful adversity on their health and development is particularly important to understand. The MAOA gene and HTTLPR region of the serotonin transporter gene (HTT), in association with childhood adversity, have been previously linked to aggressive behavior and depression, respectively. However, few studies have examined the combined effect of genetic variants and protective factors, such as resilience, on response to trauma exposure.

We tested Syrian refugees for associations between trauma exposure, resilience, genetic variants, and six measures of psychosocial stress and mental health. Data were collected from a cohort of 399 Syrian adolescents (ages 12

-18), forcibly displaced to Jordan as a result of the ongoing war. Buccal swabs, sociodemographic data, and mental health measures were collected over three time points (baseline, ~10 weeks, ~52 weeks). Levels of resilience that captured individual, interpersonal, and social resources were measured for a subset of the sample ($n=320$). Using multilevel modeling, MAOA exhibited a direct effect on scores on the Perceived Stress Scale (PSS) ($p=8.6 \times 10^{-4}$) in males only. However, when resilience was added to the model, the associations of MAOA and trauma with PSS were attenuated, suggesting the importance of resilience above other factors. No associations with any of the six psychosocial measures were found with HTTLPR. This work highlights the value of longitudinal research that integrates genetic and self-reported data on psychosocial health and resilience.

Funded by University of Florida, Elrha's Research for Health in Humanitarian Crises (R2HC) Programme (Wellcome Trust and UK Government), National Science Foundation Graduate Research Fellowship (DGE-1315138 and DGE-1842473).

Assessing hominin hips using ilium cross-sectional shape

ZACHARY COFRAN¹, CAROLINE VANSICKLE², DANIEL GARCÍA-MARTÍNEZ³, CHRISTOPHER S. WALKER⁴ and BREANNA PIERCY¹

¹Anthropology Department, Vassar College, ²Department of Anatomy, A.T. Still University, ³PACEA, Université de Bordeaux, ⁴Department of Molecular Biomedical Sciences, North Carolina State University

The ilium has undergone drastic change through human evolution due to the adoption of obligate bipedal walking. Fossil hominin hips are often poorly preserved, missing most or much of the iliac crest. This study tests whether a two-dimensional cross-section of the iliac blade, which can be obtained from many fossil ilia, can serve as a proxy for iliac crest shape in living and fossil hominins.

We quantify iliac crest and cross-section shape in an ontogenetic series of humans and *Australopithecus africanus* (MLD 7 and Sts 14), using geometric morphometric techniques. The cross-section is defined by 20 sliding semilandmarks connecting the anterior- and posterior inferior iliac spines, perpendicular to the long axis of the iliac blade. The crest is defined by 11 semilandmarks between the anterior- and posterior superior iliac spines. We examine covariation between crest and cross-section shapes using two-block partial least squares (PLS) analysis.

Error analysis shows that the proposed cross-section can be reliably reproduced. Iliac crest and cross-section are significantly correlated in PLS dimension 1 (RV coefficient = 0.71, explaining 67% of covariation). Juveniles are characterized by higher PLS scores, associated

ABSTRACTS

with more elliptical cross-sections and relatively straighter crests. Adults are characterized by slightly narrower cross-sections and more sigmoid crests, due in part to development of the cristal tubercle. *Australopithecus africanus* PLS scores fall at a "hyper-juvenile" extreme of the human PLS trajectory. Results show that iliac cross-section shape may be useful for analyzing and even reconstructing fossil ilia.

The role of social interaction and nearest neighbor preferences in juvenile *Alouatta palliata* social development

ELIZABETH M.C. COGGESHALL^{1,3}, AMY L. SCHREIER^{1,2,3}, CARRIE MERRIGAN-JOHNSON^{3,4} and LAURA M. BOLT^{3,5}

¹Department of Anthropology, Central Washington University, ²Department of Biology, Regis University, ³Maderas Rainforest Conservancy, ⁴Department of Anthropology, University of Toronto at Mississauga, ⁵Department of Anthropology, University of Toronto

Primates' extended juvenile period allows essential time for socializing that may help develop social skills necessary for survival and reproduction in adulthood. While juveniles continue to rely on their mothers after weaning, they also explore independently and socialize with others to build relationships. In this study we examine juvenile *Alouatta palliata* social behavior and nearest neighbor preferences. We hypothesize that juveniles will (1) spend more time engaged in social behavior than adults and (2) will demonstrate a spatial preference for adult females compared to other age-sex classes because females are known to facilitate social development more than males or other juveniles. This study took place at the La Suerte Biological Research Station, Costa Rica from May-August 2018. We conducted scan sampling of focal juveniles, adult females, and adult males to collect data on activity and nearest neighbor distance and identity. As predicted, juveniles spent significantly more time in social behavior (3.4% of the time) than both adult females (0.5%) and adult males (0.1%). Juveniles were significantly more likely to be nearest neighbors with adult females (66.4% of the time) than with adult males (10.4%) or other juveniles (7.5%). In addition, juveniles were significantly closer to adult females (1.6m) than adult males (2.8m), but there was no difference between juveniles' proximity to adult females compared to other juveniles (1.5m). These results suggest that the juvenile period allows for increased social time and that juveniles rely on their mothers and other adult females for social opportunities, including social access to other juveniles.

Evolutionary origin of skeletal tissues: dissecting "homology" at the morphological, cellular, and molecular genetic levels

MARTY COHN, LESLIE SLOTA, DAVYS LOPEZ, GUANGJUN ZHANG and OSCAR TARAZONA
Dept. of Molecular Genetics & Microbiology; Dept of Biology; UF Genetics Institute, University of Florida

The use of shared morphological characters to infer phylogenetic relationships among primates and other organisms has long been plagued by the challenge of distinguishing homology from homoplasy. Comparative developmental studies have shown that homologous mechanisms (e.g., genetic circuits present in the LCA) can underlie the parallel evolution of non-homologous (homoplastic) structures. Cartilage, which forms most of the embryonic skeleton, is generally considered to be a vertebrate synapomorphy. However, classical zoological studies described enigmatic cartilage-like tissues in numerous invertebrates. Vertebrate cartilage consists mostly of type II collagen, encoded by the *Collagen2a1* gene. We showed previously that the *Collagen2a1* gene regulatory network was present in stem vertebrates and may have been critical for evolution of the vertebrate cartilaginous skeleton. We went on to investigate the structure and development of cartilage-like tissues in two protostomes, cuttlefish (a cephalopod mollusk) and horseshoe crab (an arthropod). We find that protostome and deuterostome (vertebrate) cartilage shares structural and biochemical properties, and that the molecular mechanisms of cartilage development are extensively conserved, from initial induction of chondrogenitor cells to synthesis of cartilage matrix. These findings suggest that the chondrogenic gene regulatory network evolved in the common ancestor of bilaterally symmetrical animals (Bilateria). Although cartilaginous tissues evolved in parallel in the major lineages of Bilateria, and, therefore, are not homologous at the structural/morphological level, our results reveal deep homology of the genetic program for cartilage development. We suggest that activation of this ancient core chondrogenic network underlies the parallel evolution of cartilage tissues in ecdysozoa, lophotrochozoa and deuterostomia.

Image processing techniques for extracting complex three-dimensional cortical pore networks from high-resolution micro-computed tomography (micro-CT) images of the human femoral neck and rib

MARY E. COLE¹, SAMUEL D. STOUT¹ and AMANDA M. AGNEW^{1,2}

¹Anthropology, The Ohio State University, ²Skeletal Biology Research Lab, The Ohio State University

Columns of new bone tissue retain central pores that extend the vascular network to nourish bone cells. Cortical porosity increases and converges during aging, causing bone loss and increased fracture risk. Micro-computed tomography provides a three-dimensional reconstruction of this complex, highly interconnected pore network, and can visualize how porosity changes due to varying mechanical and physiological stimuli over the lifespan. Most segmentation methods for microCT images separate bone and space by globally restricting the visible pixel brightness range. This approach excludes faintly outlined pores and trabecular margins, and cannot distinguish cortical pores and trabecular cavities within the ambiguous endocortical region. We developed custom macros for ImageJ (NIH) and CTan (Bruker) that overcome these image processing challenges. An age series of cadaveric human midshaft fourth ribs and distal femoral necks were imaged in a HeliScan Micro-CT at voxel size 6.41 μm for a 10 mm sample thickness. Slice histograms were normalized and restricted to a set pixel brightness range in ImageJ. A CTan macro imposed a Gaussian blur, an adaptive threshold mean of the minimum and maximum pixel brightness, and despeckling that extracted virtually all visible pores. After axial reslicing and femoral neck column merging in AvizoFire 8.1, a custom CTan macro automatically estimated the endosteal boundary to separate marrow-adjacent pores from trabecular cavities, generating a stack of isolated cortical pore spaces. Preliminary analysis of the rib of a healthy 34-year-old male indicates 16.3% cortical porosity by volume at the midshaft, with the largest cortical pore measuring 0.082 mm³.

Research was supported by the U.S. Department of Justice, Office of Justice Programs, National Institute of Justice under award number 2017-MU-CX-0009. The content is solely expressed by the authors.

Biomarkers of cardiac health across the lifespan in wild-born chimpanzees (*Pan troglodytes*)

MEGAN F. COLE¹ and ALEXANDRA G. ROSATI^{2,3}

¹Department of Anthropology, University of New Mexico, ²Department of Psychology, University of Michigan, ³Department of Anthropology, University of Michigan

Aging processes in chimpanzees (*Pan troglodytes*), our closest living relative, are crucial to contextualize the evolution of human health and longevity. Cardiovascular disease is a major source of mortality in humans, and therefore a key issue for comparative aging research. However, most work to date on cardiac health in chimpanzees has examined laboratory-housed populations. Importantly, risk factors for heart disease in humans, including obesity and elevated blood lipids, are lower in small-scale societies characterized by markedly higher physical activity

ABSTRACTS

level and better diet compared to Western populations, and this difference can be exacerbated during aging. Thus lifestyle may also be an important factor shaping cardiac health in other apes. Due to a more naturalistic diet, ranging space, and social context, wild-born chimpanzees living in African sanctuaries are a more evolutionarily-relevant population for understanding human health and aging. We measured body weight and blood lipids in semi-free-ranging chimpanzees (n=50) living at Ngamba Island Chimpanzee Sanctuary in Uganda during routine veterinary checks and compared them to data from US laboratory chimpanzees (n=471, from the Primate Aging Database). We found that chimpanzees at Ngamba exhibited lower body weight compared to lab-living chimpanzees (linear mixed models account for age and sex: n=9001 observations, $\chi^2=69.84$, $p<0.001$). Sanctuary chimpanzees also showed lower total cholesterol levels (n=2985 observations, $\chi^2=49.37$, $p<0.001$). These disparities increased with age: whereas sanctuary and lab-living chimpanzees had similar profiles as juveniles, they increasingly differed over the lifespan. Our findings support the hypothesis that lifestyle can shape health indices in chimpanzees, particularly during aging.

This study was funded by the National Institute on Aging of the National Institutes of Health (Award 1R01AG049395-01).

To be or not to be MZ or DZ: Diagnosing zygosity in South Australian white twins from nonmetric crown traits

STEPHANIE J. COLE, KRISTEN A. BROEHL, LAURA E. CIRILLO, SAVANNAH HAY, DORI KENNESSEY, ROSE L. PERASH, TATIANA VLEMINCQ-MENDIETA and G. RICHARD SCOTT

Anthropology, University of Nevada, Reno

The Turner-Scott Dental Anthropology System (ASUDAS) has been widely used in biodistance studies. When used in twin studies to investigate genetic and environmental influences on crown morphology, researchers find dental traits are largely under genetic control but note environmental and epigenetic influences play a role in trait expression. Here we use the Turner-Scott system to predict the zygosity of South Australian white twins based on trait-score consistency between twin pairs. Photos of 222 dental casts from 111 twin pairs were used to evaluate zygosity. Eight observers with various levels of experience were assigned a subset of 14 traits. To reduce scoring bias, individuals were assessed independently of their twin. After scoring was complete, trait scores were compared between twin pairs to make a zygosity estimate. A second estimate was obtained using overall gestalt, in which all information was considered. Trait and overall gestalt zygosity estimates were compared to the known zygosity of each twin pair to determine the accuracy of dental traits in estimating zygosity

relative to that obtained from overall gestalt. Accurate zygosity estimates from trait scores ranged from 51.3% to 74.6%, while zygosity estimates using overall gestalt ranged from 66.7% to 92.7%. With one exception, observers attained higher accuracy using overall gestalt. While trait scores are useful in zygosity diagnosis, additional information on tooth shape and eruption improves diagnostic accuracy. For both methods of zygosity estimation, error was commonly in the direction of diagnosing monozygotic twin pairs as dizygotic.

Research on South Australian white twins was funded in part by grants from the National Health and Medical Research Council of Australia, Australian Dental Research Foundation, and Wellcome Trust, UK.

Restructuring our idea of individual function and community participation: The ICF model in paleopathology

LARISSA COLLIER¹, LEAH LOWE¹ and CHIARA VILLA²

¹Physical Therapy, University of Central Arkansas,

²Section of Forensic Pathology, Department of Forensic Medicine, University of Copenhagen

The aim of this research is to demonstrate the feasibility of using the World Health Organization's International Classification of Functioning, Disability and Health (ICF) as a contemporary framework to explore and conceptualize the likely health, function, and disability of individuals in the past. Developmental dysplasia of the hip (DDH) is a joint disorder of the hip socket that can cause joint pain, joint dislocation, and arthritis over time. Two individuals from the Roman Iron Age cemetery of Simonsborg on the island of Zealand, Denmark display unilateral DDH and significant atrophy of the pelvis and lower limb bones on the affected side. Gross analysis and measurements are supplemented with CT scans to assess bone morphology and function.

Using the ICF and CT analysis, we can propose a descriptive profile of the individuals' function and disability which considers the interactions of DDH (the health condition) with the personal and environmental factors likely consistent with the Roman Iron Age. These interactions will be described through an analysis of body functions and structures, contextual assessment that explores these individuals' ability to engage in activities of daily life, and their potential quality of life determined by the individuals' potential level of participation in home and community. The ICF model and analysis of bone morphology and structure provides the framework to merge archaeological context with contemporary anatomical and functional knowledge and to help conceptualize the effect of disability on the daily life and community interactions in the past.

The effects of morphometric protocol on morphological integration statistics: a case study in scapulae

MARK A. CONAWAY, HYUNWOO JUNG and NOREEN VON CRAMON-TAUBADEL

Buffalo Human Evolutionary Morphology Lab, Anthropology, University at Buffalo

Research on integration in the postcranium of macaques has yielded different integration values among elements. However, the extent to which these results are due to differences in the morphometric quantification of shape is unclear. Here, we explore the effect of morphometric protocol on a single skeletal element: the scapula. Landmark data were collected on 3D scans of scapulae of 20 adult *Macaca fascicularis*, and *Gorilla gorilla*. Each scan was landmarked twice, first with anatomical (n = 13) and then sliding semilandmarks (n = 22, 4 curves). Both landmarking protocols characterized previously identified developmental modules of the hominoid scapula (the glenoid, coracoid, and blade-acromion). Five comparable datasets were created, each containing 78 traits. The first contained the 78 pairwise distances among 13 anatomical landmarks, and the other four datasets were randomly selected from 231 possible interlandmark distances when semilandmarks were included. The Integration Coefficient of Variation (ICV) and Magnitude of Integration (r^2) were calculated for each dataset. Distributions of these statistics were created via a resampling protocol and results were compared statistically via pairwise Mann-Whitney U tests with Bonferroni correction.

Within semilandmark datasets, values for both measures of integration were found to be statistically lower than those acquired solely from anatomical landmarks. Consistent with previous research, ICV values were most sensitive to average multivariate correlation amongst traits, rather than the number of traits. This suggests that the method of shape quantification can have a significant impact on the assessment of morphological integration, and should be considered carefully in future studies.

Dental Fracture Mechanics: What broken teeth can reveal about diet and feeding behavior

PAUL J. CONSTANTINO¹ and BRIAN R. LAWN²

¹Biology, Saint Michael's College, ²Materials Measurement Laboratory, National Institute of Standards and Technology

Dental Fracture Mechanics (DFM) is the application of fracture mechanics theory to the study of tooth evolution and adaptation. For the past decade, this approach has been used to study how teeth break, deduce the mechanisms that evolution has devised to protect teeth from fracture, and examine how these mechanisms

ABSTRACTS

vary among vertebrate species, both extant and extinct. It has been applied to the study of broad trends in mammalian dental evolution, as well as detailed studies of particular taxa such as sea otters. DFM also has implications for human dentistry. It has revealed how small cracks inside human teeth that arise during development may actually protect the teeth from catastrophic failure later in life, and it elucidated a mechanism whereby induced cracks in human teeth can actually “self-heal” to limit further damage. Here, we review the basic premise of DFM and draw attention to some of its diverse applications. As a specific case study, we present new data to highlight the role of DFM in extracting dietary information from tooth chipping in fossil hominins. For example, while tooth chipping shows that *Paranthropus boisei* could generate the highest bite forces (> 3000 N) of any fossil hominin examined thus far, it also reveals that *P. boisei* did not regularly use that force to consume hard objects (chipping frequency per tooth of 4.4%). These results support those derived using dental microwear texture analysis, and point to *P. boisei* as a consumer of softer, tougher vegetation.

First complete primate skull from La Venta, Colombia

SIQBHAN B. COOKE^{1,2}, LAUREN B. HALENAR-PRICE^{2,3}, LAURA STROIK⁴, ANDRES LINK⁵, GUSTAVO A. GIRALDO CORREA⁶, BRIAN SHEARER^{2,7,8}, RYAN P. KNIGGE⁹ and MELISSA TALLMAN^{2,4}

¹Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine, ²NYCEP Morphometrics Group, New York, NY, ³Department of Biology, Farmingdale State College, SUNY, ⁴Department of Biomedical Sciences, Grand Valley State University, ⁵Department of Biology, Universidad de Los Andes, ⁶Department of Geology, Universidad de Caldas, ⁷Department of Cell Biology, New York University School of Medicine, ⁸Department of Anthropology, The Graduate Center, CUNY, ⁹Department of Orthopaedic Surgery, University of Missouri, Columbia

We describe the first undistorted platyrrhine skull recovered from La Venta, a Middle Miocene Colombian paleontological site. The specimen was surface collected from ~13.3-13.7 Ma sediments and is a member of the pitheciid genus *Cebupithecia*. The cranium and mandible, which were cemented together with matrix, were μ Ct scanned and digitally cleaned. Three-dimensional landmarks were placed on major cranial and dental features and analyzed using three-dimensional geometric morphometric (3DGM) techniques.

Fossil primates from La Venta are mostly known from dental or mandibular remains and have similar morphology to extant genera. Dentally, the specimen has procumbent, narrow lower incisors and upper and lower molar cusps that are positioned at the edge of the occlusal surface

creating wide basins. Dental shearing crest development is moderate and similar to that of the frugivorous genus *Callicebus*; incisor morphology is consistent with sclerocarp foraging. In landmark analyses of molar shape, it falls close to *Cebupithecia sarmientoi*.

In terms of cranial shape, this fossil lies outside the range of extant variation and is relatively de-encephalized like other early platyrrhines; however, it is closest to the distribution of extant pitheciids. A wide interorbital distance, prognathic midface, and rounded palate are all similar to *Callicebus*. These characteristics indicate that while dental morphology was already derived by the Middle Miocene, a more primitive cranial shape was retained. Previously discovered postcranial remains from *Cebupithecia* are also generalized. Thus, we propose that a transition to sclerocarp foraging was the earliest “step” towards modern pitheciid morphology.

National Geographic Society/Waite Grant W387-15; GVSU Center for Scholarly and Creative Excellence

Animal models as a platform to probe the spatio-temporal coordination of cortical remodeling and its functional significance

DAVID ML. COOPER¹, KIM HARRISON¹, BEVERLY HIEBERT¹ and JANNA ANDRONOWSKI²

¹Anatomy, Physiology and Pharmacology, University of Saskatchewan, ²Biology, University of Akron

The complex heterogeneous microarchitecture of cortical bone was first described over 300 years ago and subsequent inquiry has revealed its dynamic nature. Changes progressively superimposed in the cortex over the lifespan, brought about by the process of remodeling, have presented analytical opportunities in Biological Anthropology including age estimation, assessment of functional adaptation, and the diagnosis of disease. While the dynamic nature of cortical bone microarchitecture has long been appreciated, our knowledge of how the remodeling process is locally regulated in space and time remains rudimentary. Key factors limiting our understanding include relatively little information regarding the 3D microarchitecture of cortical bone and a complete lack of dynamic longitudinal spatio-temporal (4D) information. Individual remodeling events have never been followed over time, or directly observed *in situ* and *in vivo*. To address this limitation we have undertaken a research program at the Canadian Light Source synchrotron aimed at combining animal models of elevated cortical bone remodeling with *in vivo* high resolution phase contrast micro-computed tomography imaging. Initial experiments focused on rats are now transitioning to those utilizing rabbits, since this larger model has cortical microarchitecture which more closely resembles that of humans. The proof-of-principle experiments presented here have established

that remodeling-related resorption events can be resolved and tracked over subsequent imaging sessions. This advance has set the stage for direct testing of hypotheses related to localized coordination of remodeling including the steering of the resorption events that initiate new osteon formation as well as stimuli related to osteon morphology and dimensions.

Dispersal decisions in monogamous owl monkeys (*Aotus azarae*): How ecological and social factors influence the timing of natal dispersal

MARGARET K. CORLEY and EDUARDO FERNANDEZ-DUQUE

Anthropology, Yale University

The timing of natal dispersal may be highly flexible and dependent upon a variety of ecological and social factors. Understanding proximate factors that influence when individuals leave their group can provide insight into ultimate explanations of dispersal patterns in a species. We investigated social and ecological factors associated with the age and timing of natal dispersal in socially monogamous owl monkeys (*Aotus azarae*) in the Argentinean Gran Chaco. Specifically, we constructed multivariate models to examine how proximate factors, namely adult replacements, births, group size, and environmental variables such as rainfall (as proxies of resource abundance) explained variation in the age and timing of dispersal for 129 individuals from 26 different social groups monitored 1997-2016. Timing was highly flexible (age range = 1.7-5.3 years), but all individuals left their natal group prior to reproducing. Experiencing an adult replacement, particularly the replacement of a same sex adult as a subadult, was associated with dispersal. Dispersals were concentrated in the spring and early summer, but individuals were more likely to depart outside of this preferred season if there had been a recent infant birth in their group and if there was less than average rainfall, and thus increased resource scarcity, during the fall/winter season. Our results suggest that inbreeding and competition avoidance may explain dispersal in different circumstances. Including individuals that disappeared produced somewhat different results from analyses limited to individuals with confirmed dispersals. Our findings suggest that researchers should be cautious when drawing inferences about dispersal from the disappearance of offspring alone.

Funding: NSF-BCS-0621020, 1503753, 1219368, 1232349, 1503753, and 1540255.

ABSTRACTS

Variation of Skeletal Growth and Development Patterns in Populations with Diverse Socio-Economic Backgrounds

LOUISE K. CORRON¹, KYRA E. STULL^{1,2} and YUERAN YANG³

¹Department of Anthropology, University of Nevada, Reno, ²Department of Anatomy, University of Pretoria, ³Department of Psychology, University of Nevada, Reno

Intrinsic (e.g. genetic) and/or extrinsic (e.g. disease, environment, quality of life) factors produce population differences in skeletal growth and/or developmental indicators, which are used to study subadults in biological anthropology. This comparative study on growth and development variability aims to evaluate the extent of these divergences and their expression in various populations.

Growth and development indicators from four modern samples of children aged birth to 15 years of known age and sex from Colombia (N=57), France (N=581), the United States (N=880), and South Africa (N=174) were compared. Indicators include measurements and epiphyseal fusion stages of the long bones and the pelvis. Each country is characterized by the Human Development Index (HDI) and the Gini coefficient, which capture country-level differences in socio-economic status (SES) and wealth equality levels, respectively. MANOVAs and hierarchical linear models (HLMs) were used on the indicators and country-specific parameters to account for variability at different levels and evaluate the impact of SES on each indicator.

Analyses suggested that the trends in metric variables are significantly different among the countries. HDI informs these differences more than the Gini coefficient. The differences in long bone growth primarily reflect differences in the environment, but only become significant after the age of 8 years. Epiphyseal fusion also demonstrates population differences; countries with higher HDI and lower Gini coefficients transition to upper fusion stages earlier.

These findings provide a broader understanding of the level of expression of growth and development variability in populations presenting with different genetic, environmental and socio-economic backgrounds.

This research was funded by two federal grants (NIJ 2015-DN-BX-K409 and NIJ 2017-DN-BX-K144)

Polygenic Adaptation to Amazonian Rainforest

CAINĂ M. COUTO-SILVA¹, KELLY NUNES¹, MARIA CÁTIRA BORTOLINI², FRANCISCO M. SALZANO² and TÁBITA HÜNEMEIER¹

¹Department of Genetics and Evolutionary Biology, University of São Paulo, ²Departamento de Genética, Universidade Federal do Rio Grande do Sul

Humans have entered America, the last continent to be peopled, ~15 thousand years ago, and in less than 2 thousand years, they quickly spread themselves into South America. American continent presents a wide variety of harsh environments so that different patterns of genetic adaptation would be required for successful subsistence of the first Americans. The Amazonian Rainforest is one of the main ecoregions of the Americas, and the native-Americans living there are yet poorly studied. Here we propose to study the genetics and demography of these people, focusing on the analysis of natural selection. We used ~600k SNP array data from 119 Brazilian native individuals to assess population substructure and to infer natural selection. Population Branch Statistics (PBS) has been applied – an Fst-based selection test – using both Siberians and East Asians from HGDP dataset as outgroup. SNPs with the highest PBS values and corresponding genes were reported. PBS results were further supported by iHS (Integrated Homozygosity Statistics), along with two cross-population tests to contrast extended homozygosity haplotype between populations (XP-EHH and Rsb). When considering all Statistics applied for detecting positive selection, we identified overlapping genes participating in immune response, muscle contraction, and cellular response to stress. Additionally, we assess polygenic adaptation by analyzing SNP networks under selection through Signet R Package and BlockBuster Software. The functions of the genes identified by linkage disequilibrium and Fst-based approaches together with preliminary results regarding polygenic adaptation suggest that the immune system had an essential role in Amazonian Rainforest adaptation.

This project has been supported by FAPESP, CAPES, and CNPq.

Scapular retroversion asymmetry and its correlates: New indicators of habitual upper limb activities

LIBBY W. COWGILL¹ and SCOTT D. MADDUX²

¹Anthropology, University of Missouri, Columbia, ²Center for Anatomical Sciences, University of North Texas

Variation in humeral torsion, or the orientation of the humeral head relative to the distal humeral articular axis, has been linked to functional causes in humans. Specifically, high levels of asymmetry has been detected in populations engaged in repetitive overhand throwing. In addition, studies of overhand pitchers have shown that the glenoid fossa of the scapula, which articulates with the humeral head, displays corresponding changes in angulation in order to maintain congruence with the humeral head. This analysis explores variation and asymmetry in glenoid retroversion, a feature previously only documented in the clinical literature.

Preliminary analysis was conducted on humeri and scapulae of two Holocene human populations (n=69) and a small sample of Late Pleistocene fossils (n=13). Asymmetry in glenoid retroversion ranges from 0 to 22 degrees, with 89% of individuals showing higher levels of retroversion on the right side. Asymmetry in humeral torsion and glenoid retroversion are positively correlated (r=0.444, p<0.001). In addition, although there is considerable overlap, glenoid asymmetry is generally higher in the fossil sample than in the Holocene groups. This research suggests that like humeral torsion, glenoid retroversion has a functional explanation. While previous studies have highlighted links between humeral torsion and habitual activities such as overhand throwing, additional research is needed to evaluate the shoulder girdle as an integrated system.

Ancient DNA reveals genetic effects on anthropometric phenotypes in Prehistoric Europe

SAMANTHA L. COX^{1,2}, CHRISTOPHER B. RUFF³ and IAIN MATHIESON¹

¹Department of Genetics, Perelman School of Medicine, University of Pennsylvania, ²Department of Physical Anthropology, Penn Museum, University of Pennsylvania, ³Center for Functional Anatomy and Evolution, John Hopkins University School of Medicine

A fundamental consideration in human evolution is the relationship between genetics, environment, and morphological plasticity in producing phenotypic change. Ancient DNA, combined with information about the genetic basis of anthropometric traits from genome-wide association studies (GWAS), allows us to separate these effects. We analyzed genome-wide data from 1155 individuals (45,000-1000BP), along with measurements from 2178 skeletons (34,000-100 BP) in Europe to investigate the relationship between genetic and phenotypic changes in anthropometric traits. Using GWAS summary statistics, we make genetic predictions of phenotype (height, sitting height, leg length, BMI, and bone mineral density) and compare them with observed data. In general, measured changes follow—but are more extreme than—those predicted by genetics. We show that the decrease in stature from the Early Upper Paleolithic to the Neolithic is predicted by genetics. Genetic sitting height remains constant, consistent with the observation that change in stature is driven mainly by changes in leg, not torso, length. Genetic heel bone mineral density decreases sharply between the Mesolithic and Neolithic, as does measured femoral cross-sectional diaphyseal shape—which we interpret as parallel responses to decreases in mobility. Geographically, there is an E-W cline of decreasing stature during the Mesolithic, consistent with genetic predictions. In the Early Upper Paleolithic there is a N-S

ABSTRACTS

cline that is not predicted by genetics and may reflect an environmental effect on development. Our results reveal a significant contribution of genetic change—driven by selection, admixture or drift—to phenotypic change, in addition to the consequences of morphological plasticity.

Funding was provided by the Alfred P Sloan Foundation and the Charles E Kaufman Fund of the Pittsburgh Foundation.

Geophagy in The Gambia: An exploration of the motivators for eating earth among men and women

JENNIFER DANZY CRAMER¹, MAWDO JALLOW², JOSHUA D. MILLER³ and SERA L. YOUNG⁴

¹Sociology, Anthropology, General Studies, American Public University System, ²Head of Research & Development Unit, Department of Parks & Wildlife Management- The Gambia, ³Department of Anthropology, Northwestern University, ⁴Department of Anthropology & Institute for Policy Research, Northwestern University

Geophagy, the purposive consumption of earth, is common in both human and animal populations worldwide. Despite its high prevalence among vulnerable populations (e.g. pregnant females), the causes and consequences of geophagy remain unclear. Indeed, the perceived motivations and norms that influence the expression of geophagy have been little characterized outside of East and Central Africa and the American south. Available evidence suggests three potential roles of geophagy as: a medicament, a micronutrient supplement, or a non-adaptive behavior. Therefore, our goal was to conduct the first study of geophagy in The Gambia, characterizing the behavior and exploring associated environmental and cultural factors in an area where both humans and baboons have been observed eating earth from the same sources. We conducted 35 semi-structured interviews with adults in 23 villages. Villages and participants were selected as part of a larger study examining the human-primate interface; additional sites were added through snowball sampling. Participants were 18 to 65 years old; 30 were women, 5 men. Most participants (83%) identified pregnancy as a motivating factor for consuming clay because it was perceived to help with indigestion, nausea, and vomiting. Some (8.5%) reported that consuming clay helps other health issues such as asthma, parasite infection, ulcers, and general indigestion. No respondents indicated nutritional value of geophagic earth. Stated reasons for geophagy were consistent with the medicament hypotheses. However, chemical and mineralogical analyses and biological assays are needed to rigorously test these hypotheses; these are planned for future mixed-species studies.

Field research funded by an American Public University System faculty research grant. Conference presentation funded by American Public University System.

The dietary niche of blue, red-tailed and hybrid monkeys (*Cercopithecus mitis*, *C. ascanius*, and *C. mitis* x *C. ascanius*) in Gombe National Park, Tanzania

SARAH H. CRAWFORD¹ and KATE M. DETWILER^{1,2}

¹Department of Anthropology, Florida Atlantic University, ²Department of Biological Sciences, Florida Atlantic University

Gombe National Park, Tanzania, is home to six diurnal primate species, which include *Pan troglodytes*, *Papio anubis*, *Piliocolobus tephrosceles*, and three guenon species (Tribe Cercopithecini). This research represents the first multi-year investigation of the dietary niche of Gombe's *Cercopithecus* population, contributing to our understanding of dietary overlap and distinctiveness among Gombe's sympatric primates. Our study group is a mixed species hybrid group, which consists of *C. ascanius* (n=29), *C. mitis* (n=8), and *C. ascanius* x *C. mitis* hybrids (n=10). We collected feeding data using *ad libitum* observations as well as instantaneous scan sampling at 30 minute intervals from July 2014 to March 2018. We defined feeding as an individual consuming a species-specific plant part or ingesting an invertebrate. In total, we collected 12,689 feeding records from 2,422 hours of observation. We analyzed feeding records to identify a total of 57 plant species in our group's diet. An overlap analysis showed 80% similarity between the plant species of each sympatric primates' diet with the top 20 plant species of our group. We also compared the frequency of diet items in our group with other *Cercopithecus* groups in East Africa, and found an unusually high percentage of invertebrate eating (54%) in our group. These findings suggest that invertebrates are an important food resource for the Gombe study group and insectivory may help facilitate coexistence among primate species where there is high dietary niche overlap.

Ancient proteomics analysis in the early contact period, St. Catherines Island, Georgia

FABIAN CRESPO¹, TIMOTHY CUMMINS², MICHAEL MERCHANT², JON KLEIN², LAUREN SPRINGS³, DEBORAH A. BOLNICK⁴, CLARK S. LARSEN⁵ and DAVID H. THOMAS⁶

¹Anthropology, University of Louisville, ²Medicine, University of Louisville, ³Anthropology, University of Texas at Austin, ⁴Anthropology, University of Connecticut, ⁵Anthropology, The Ohio State University, ⁶Anthropology, American Museum of Natural History

Between AD 1565 and 1680, native communities on St. Catherines Island experienced dramatic cultural, social, and biological transformations linked largely to circumstances of the arrival of Europeans, the later establishment of the Mission Santa Catalina de Guale, and eventually abandonment of the site. Previous bioarchaeological

analyses of the mission population identified dental and skeletal markers of physiological stress and disease. Molecular studies are needed to provide new insights on the formation of pathological phenotypes in bone. Ancient proteomics analysis offers a unique opportunity to document the biochemical foundations of chronic physiological stress and disease in past populations. The objective of this study was to conduct the first proteomics analysis of skeletal remains recovered from the early Fallen Tree cemetery, dating prior to the seventeenth-century mission. Protein extraction and high-resolution mass spectrometry was conducted on samples from 21 individuals interred at the Fallen Tree cemetery. Bioinformatics analysis was performed using gene ontology for protein identification and molecular pathways. Results show robust protein detection in all samples, with higher frequency of collagen proteins. Molecular pathway classification analysis reveals proteins associated with integrin signaling pathways, blood coagulation processes, and immune function. Mapping of the Fallen Tree bone protein profile documents a unique biochemical landscape, having important implications for health and quality of life in this early post-contact setting. In particular, these results allow biochemical and paleopathological correlations, especially associated with stress and chronic inflammatory responses during the contact period among one of the first native groups to interact with Europeans.

Funding: Funded by the St. Catherines Island Foundation, NSF Award 1518079.

Who Pays the Costs of Cohesion? Maintaining behavioral synchrony in baboon troops on the move

MARGARET C. CROFOOT^{1,2,3} and ROI HAREL¹

¹Department of Anthropology, University of California, Davis, ²Animal Behavior Graduate Group, University of California, Davis, ³Smithsonian Tropical Research Institute

When on the move, social animals must modulate their speed and coordinate their behavior to stay in contact with other members of their group. Due to differences in body size and locomotor capacity, some individuals are predicted to have to walk faster (or slower) than their preferred pace to stay together. Who pays these costs of maintaining group cohesion? Using GPS collars with integrated accelerometers, we continuously tracked nearly an entire troop of olive baboons (*Papio anubis*) in Laikipia, Kenya. We identified the footfalls of walking baboons from patterns of three-dimensional acceleration and defined each group member's 'characteristic walking profile' based on the distribution of step frequencies observed when they were walking alone. When walking as part of a group, smaller baboons increased their step frequency relative to their characteristic walking profile. Larger

ABSTRACTS

individuals also changed their locomotor behavior, decreasing their step frequency during group movement, but did so to a lesser degree. Further, after controlling for position within the group, smaller baboons had higher overall dynamic body acceleration (ODBA), a measure which has been shown to correlate with energy expenditure. Together, these results suggest that for baboons, collective movement imposes costs which are born disproportionately by smaller group members. They also highlight the importance of considering the role of movement capacity in shaping a species' movement ecology, and illustrate an approach for accomplishing this under socially and ecologically relevant field conditions.

Funding for this research was provided by National Science Foundation (IOS-1250895 and III-1514174) and David and Lucille Packard Foundation grants to MCC.

Behavioral markers of stress in separated captive female and male ring-tailed lemurs (*Lemur catta*)

CARMEN M. CROMER¹, LISA M. PACIULLI¹ and JENNIFER L. VERDOLIN²

¹Department of Biological Sciences, North Carolina State University, ²Department of Wildlife, Fisheries, and Conservation Biology, University of Arizona

In animals, stress is mediated by social and physiological factors. Although it is clear that subordinates are particularly vulnerable to stress, little is known about the relationship between stress and social rank in female-dominant species, such as lemurs. Therefore, in this study, the frequency of stress-related behaviors was examined in five male-female pairs of ring-tailed lemurs (*Lemur catta*) at the Duke Lemur Center in Durham, N.C. The lemurs were video-recorded while separated from their companions for 15 minutes. Previously established markers of anxiety (e.g., vocalizations, pacing, scratching) were coded, and the Mann-Whitney U test and Audacity software were used to analyze the data. The results showed that males scent-marked significantly more than females ($p < 0.009$). Although not significant, females scratched, paced, and emitted more "high-arousal" calls than males. Also, both sexes vocalized at similar rates, and mean levels of anxiety were higher in females. Thus, social dominance did not appear to reduce stress. A possible explanation is that female ring-tailed lemurs, like top-ranking male baboons (*Papio anubis*), are more susceptible to stress during periods of social instability. This would imply that the female ring-tailed lemurs experienced more stress when separated from their partner-males than vice versa. Limitations of the study include the small sample size and lack of control of potentially confounding variables such as age, gonadal status, and health. Future research should incorporate larger sample sizes and better control of confounding variables.

Geometric morphometric assessment of skull symmetry in 6-8.0 year old humans

JESSICA M. CRONIN¹, ANA M. SHAUGHNESSY², JANE VANNAHEUANG³, LAURA E. CIRILLO⁴, GARY D. RICHARDS⁵ and REBECCA S. JABBOUR⁶

¹Department of Integrative Biology, University of California, Berkeley, ²Department of Molecular and Cell Biology, University of California, Berkeley, ³Department of Public Health, University of California, Berkeley, ⁴Department of Anthropology, University of Nevada, Reno, ⁵Department of Biomedical Sciences, A.A. Dugoni School of Dentistry, University of the Pacific, ⁶Department of Biology, Saint Mary's College of California

Asymmetries of the skull are well-documented. However, little is known of the complex interplay between developmental rates and duration, functional components, and constraints that result in skull symmetry or asymmetry. Consequently, we are ill equipped to differentiate potentially problematic changes resulting from the current epidemic of asymmetric skulls (plagiocephaly) related to SIDS prevention. Here we provide a geometric morphometric assessment of normal children to establish the range of symmetry/asymmetry from which to address potentially problematic changes from the normal condition.

We compiled 38 normal skulls with developmental ages of 5.8-7.9 years. Ages are based solely on dental calcification patterns. With the mandible articulated on the cranium, we used a Microscribe to digitize 254 3D landmarks; 38 are employed herein. The sample was split into right/left halves. Analysis of Procrustes-aligned shape variables with Principal Components Analysis (PCA) was carried out in Morphologika 2.

Variation explained by PC1-4 is 18%, 13.2%, 9.9%, and 6.65%, respectively. PC1 relates to increased cranial base flexion and anteroposterior fronto-occipital expansion. PC2 relates to skull shortening and height increase. No individual is symmetrical on PC1-2 and only 16% of individuals approach coincidence of the right/left side plots. On PC1 13% and 24% of individuals show low to moderate right/left separation, respectively while 18% and 24% do so on PC2. Individuals with +PC1 and -PC2 scores show the lowest degree of right/left asymmetry on PC1-2. Delineating the range of symmetry in this sample provides a basis from which to identify causative factors underlying asymmetry.

Funding provided by Undergraduate Opportunity Fund Grants to Jessica Cronin, Ana Shaughnessy, and Jane Vannaheuang.

Fur regrowth varies among and within individual cheirogaleid lemurs

BROOKE E. CROWLEY¹ and ERIN E. EHMKE²

¹Departments of Geology and Anthropology, University of Cincinnati, ²Duke Lemur Center, Duke University

We monitored fur regrowth rates for captive mouse lemurs (*Microcebus murinus*) and dwarf lemurs (*Cheirogaleus medius*) exposed to relatively constant temperatures and natural variability in photoperiod between February 2017 to October 2018. Two males and two females were included from each species. A small patch of fur was shaved from each lemur's hip, thigh, or tail base on a bi-monthly basis (8x total) and regrowth was monitored on a bi-weekly basis. Fur regrowth varied considerably both within and among individuals. In many cases, regrowth was patchy or occurred in spurts (slow initially followed by rapid regrowth). Excluding one mouse lemur shave with an unusually long regrowth time (342-356 days), fur growth was, on average faster for mouse lemurs (7-14 to 215-229 days) than dwarf lemurs (27-40 to 313-327 days; Welch $t=6.06$, $df=53.59$, $p=0.017$). There were no differences in regrowth between dwarf lemur sexes ($p>0.05$); male mouse lemurs exhibited significantly slower regrowth than females ($t=2.81$, $df=26$, $p=0.0092$). Regrowth rates differed significantly among individual shaves for dwarf lemurs ($\chi^2=22.23$, $df=7$, $p=0.023$). Regrowth was considerably slower for shaves done in Fall 2017, a period during which individuals exhibited some torpor behavior. Regrowth was variable but statistically indistinguishable among shaves for mouse lemurs ($\chi^2=10.086$, $df=7$, $p=0.19$). However, one male showed trends similar to those observed by dwarf lemurs. These results indicate that cheirogaleid fur growth is affected by both metabolic differences among individuals and external factors. A constant growth rate cannot be assumed for these small-bodied primates.

Being Overweight is Associated with Lower Physical Activity in US Population but Not among Forager-Horticulturalists

DANIEL K. STUMMINGS¹, BENJAMIN C. TRUMBLE², JONATHAN STIEGLITZ³, HILLARD KAPLAN¹ and MICHAEL GURVEN⁴

¹Economic Sciences Institute, Chapman University, ²Center for Evolution and Medicine, Arizona State University, ³Anthropology, Institute for Advanced Study in Toulouse, ⁴Department of Anthropology, University of California-Santa Barbara

Inactivity is thought to be a major driver in the etiology of chronic diseases of aging, including cardiovascular disease (CVD), diabetes and obesity. Recent studies suggest that the Tsimane, forager-horticulturalists in Bolivia have the lowest levels of CVD. While recent studies suggest that extant subsistence-level populations exhibit high levels of physical activity, much of this evidence is undermined by small sample sizes, and subjective measures of activity. Here, we objectively measure physical activity among Tsimane adults ages 30-85 y ($n=539$, mean age 56, 49% male) using accelerometry (Actigraph GT3X), and test for association with obesity/overweight, a primary risk factor of cardiometabolic

ABSTRACTS

disease. Activity and its relationship with BMI are compared to a US population collected as part of National Health and Nutrition Examination Survey (n=3179, median age 54, 49% male). Age-standardized prevalence of obesity/overweight among Tsimane and U.S. was 11%/26% and 37%/35%, respectively. Tsimane spend fewer daily minutes sedentary ($\beta=-56.4$, $P<2e-16$), and more minutes in light ($\beta=26.9$, $P<1.5e-5$), and moderate activities ($\beta=29.4$, $P<2e-16$) than age- and sex-matched Americans; their estimated activity energy expenditure is greater than Americans at every age and sex. While we find strong associations between physical activity and being obese or overweight in the US population, overweight Tsimane show no differences in activity levels, whereas obese Tsimane show a marginal but weak tendency to be less active. Future research will combine individual-level physical activity with dietary intake data to disentangle their additive and interactive effects on an expanded set of risk factors of chronic disease.

Patterns of cranial morphological diversity among peoples of African descent

ANDREANA S. CUNNINGHAM and VALERIE BURKE DELEON

Department of Anthropology, University of Florida

The Trans-Atlantic slave trade instigated the widespread cultural and geographic rupture of African descent peoples. The skeletal diversity observed in African descendants is reflective of this history, and its study through geometric morphometrics provides a useful means of tracing migration-bound morphological relationships. This study utilized a 3D landmark geometric morphometric approach to assess morphological distribution within a dataset of pre-emancipation individuals buried in Cuba and post-emancipation individuals from the United States and South Africa. This study included 91 crania from individuals of documented African descent, including 66 individuals from the Smithsonian's Robert J. Terry Anatomical Skeletal Collection and over 25 individuals from the University of Pennsylvania's ORSA CT scan database. Variables were defined to distinguish individuals by geographic origin in the full sample and in each subsample.

Fixed landmark and sliding semilandmark data were collected from each individual, using a MicroScribe for physical crania and Amira software for CT scans. The data were tested with PCA, ANOVA, and permutation analyses. Geographic origin had significant effects on shape in both the full sample and the isolated Terry data. Within the Terry Collection subset, the full factorial ANOVA of geographic origin and sex on cranial shape was significant. Pre-emancipation individuals in the ORSA subsample were associated with higher PC1 scores in the PCA, but they shared considerable overlap with post-emancipation

Terry individuals. These results suggest that geographic distinction may occur alongside lasting morphological connections, providing a platform to further explore morphological distribution through expanded migration routes.

This material is based upon work supported by the National Science Foundation Graduate Research Fellowship under Grant No. DGE-1315138 and DGE-1842473.

Proximate and Ultimate Causes of Rising NCD Mortality in the Mississippi State Asylum (1855-1935), Jackson, MS

ASHLEY C. DAFOE¹, MOLLY K. ZUCKERMAN¹, NICHOLAS P. HERRMANN², AMBER M. PLEMONS³ and BRITTANY N. HIGGS⁴

¹Anthropology & Middle Eastern Cultures, Mississippi State University, ²Anthropology, Texas State University, San Marcos, ³Anthropology, Michigan State University, ⁴NA, Colonial Williamsburg

Epidemiologic transitions do not cause themselves. Rather, they have both proximate and ultimate causes, which can be context-specific. The second transition, which initiated in association with industrialization in many nations in the 19th century and, in a modified form, is ongoing in industrializing nations, comprised a shift from a high burden of mortality and morbidity from acute, epidemic infections to mortality largely from non-communicable diseases. This novel epidemiologic regime is often attributed to increases in longevity that accompanied industrialization and modernization. However, this explanation may overlook diverse proximate and ultimate causes of changing mortality. Here, we employ a case study comprising epidemiologic and demographic trends in the Mississippi State Asylum (MSA), which housed 35,000 patients between 1855 and 1935. Transcribed admission and discharge records representing (n=2,338) deaths amongst patients between 1855 and 1929 were coded into ICD-9 categories. These revealed dramatic increases in the proportion of mortality from cardiovascular disease (CVD) (1855-1872: <.1%; 1900-1905: .5%; 1926-1929: 24.6%) when compared to other causes of death. Here, we investigate likely proximate and ultimate causes of this trend, focusing on changing epidemiologic environments in the MSA, namely coincident increases in mortality from respiratory diseases and nutritional deficiencies, declines in gastrointestinal disease mortality, and proportionately very low infectious disease mortality associated with improved living conditions. We evaluate our findings within an ecological immunological framework focused on the role of early life-pathogen exposure in the development of chronic hyper-inflammatory responses, oriented towards uncovering both proximate and ultimate causes of the second transition in specific contexts.

Oral health in a rural population of the Brazilian Amazon: Implications for interpretation of dental caries in the past

PEDRO DA-GLORIA¹, BARBARA A. PIPERATA², CHRISTIAN HOFFMANN³, MARIA REGINA SIMIONATTO⁴, RODRIGO OLIVEIRA^{5,6} and FERNANDO N. NOGUEIRA⁷

¹Graduate Program in Anthropology, Federal University of Pará, ²Department of Anthropology, The Ohio State University, ³Department of Food Science and Experimental Nutrition, University of São Paulo, ⁴Department of Microbiology, University of São Paulo, ⁵Department of Genetics and Evolutionary Biology, University of São Paulo, ⁶Department of Stomatology, University of São Paulo, ⁷Department of Biomaterials and Oral Biology, University of São Paulo

Dental caries is a pathological condition caused by the fermentation of carbohydrates by oral bacteria. Traditional interpretation of past caries frequencies considers dietary habits as the main cause of this pathology, as exemplified by the association between increased caries prevalence with the transition to agriculture. Other authors suggest that human biology, such as hormones, immune function, pregnancy, and genetic background, should be also considered when interpreting the prevalence of caries in past populations. In this study, we aim to test the relative importance of diet and human biology in predicting caries rates in relatively isolated, rural Amazonian communities located along the Middle Solimões River, Brazil. This population still practices slash and burn agriculture, fishing, hunting, and collecting, with industrialized foods making only moderate contributions to their diet. In addition, the population has limited access to dental and medical services and a relatively high fertility rate. We collected data on saliva flux, dietary habits, oral pathologies, oral hygiene, and reproductive histories of 107 riverine people (39 men and 68 women; average age of 27 years). We ran a multiple linear regression using decayed, missing, and filled teeth as a dependent variable. Our model explained 20.7% of the variation and found age and stimulated saliva flux as the main predictors of caries prevalence. Although this is a preliminary model, we can highlight the importance of saliva flux as a protector against caries, emphasizing a multifactorial interpretation of caries disease.

Funded by FAPESP (process 2013/0069-0)

Priority of Access Model is a Good Fit Despite the Occurrence of Following, an Alternative Mating Strategy in Wild Crested Macaques (*Macaca nigra*)

LISA M. DANISH^{1,2}, ANDRE PASETHA³, MUHAMMAD AGIL⁴ and ANTJE ENGELHARDT⁵

¹Biology, Nazareth College, ²Sexual Selection, German Primate Center, ³Biology, Institut Pertanian Bogor, ⁴Veterinary Science, Institut Pertanian Bogor,

ABSTRACTS

⁵Natural Sciences and Psychology, Liverpool John Moores University

Alternative mating strategies have been shown to result in deviation from the Priority of Access (PoA) Model. One such strategy is following, in which males maintain proximity to consorting pairs for hours and even days. While this strategy is highly effective in olive baboons, it remains less studied in the macaques. We examined fit to the PoA Model and following in wild crested macaques (*Macaca nigra*), collecting behavioural data using scan sampling on two habituated groups from May 2015 to May 2016 in the Tangkoko Reserve in North Sulawesi. Generalized Linear Mixed Models were used to examine the influence of dominance rank, number of fertile females and following on consorting. The PoA Model was a good fit to the data for both groups. While following did influence whether a male was able to consort with a female ($z=3.51$, $p<0.001$), it did not influence of the length of time consorting males were able to consort ($t=1.32$, $p=0.19$) and only 23% of consort takeovers were carried out by followers. Dominance rank influenced both the likelihood of consorting ($z=6.44$, $p<0.001$) and time spent consorting ($t=3.20$, $p=0.003$), while the number of fertile females had no influence. Thus, unlike olive baboons, following does not result in deviation from the PoA Model. We suggest that following may be less effective in this species due to one of these factors and offer initial exploration: 1) costs of consorting; 2) female choice for high ranking males; and 3) lack of coalitions for fertile females in this species.

Fulbright FIRST Fellowship and Leibniz-DAAD Fellowship to LMD, DFG to AE

Metabolic syndrome in urban young adults from Merida, Mexico Authors:

SUDIP DATTA BANIK¹, ALEJANDRA ITZEL NUDEL ONTIVEROS² and ROSA MARÍA MÉNDEZ GONZÁLEZ¹

¹Human Ecology, CINVESTAV-IPN Unidad Merida, ²Nutrition, Universidad Modelo, Merida

Increasing prevalence of overweight, obesity, elevated body fat (BF), diabetes and metabolic syndrome (MetS) in Mexican populations are major public health concerns. **Objectives:** (1) To evaluate body mass index (BMI) based overweight and obesity, body fatness. (2) To estimate MetS prevalence using IDF, ATP III, and EGIR criteria. **Methods:** In this cross-sectional study, participants were 21 to 24-year-old University students (22 men, 20 women) from Merida, Mexico. Height (cm), body weight (kg), waist circumference (WC, cm), systolic and diastolic blood pressure (BP, mm Hg) were measured. BMI (kg/m^2) was calculated. BF was estimated using bioelectrical impedance analysis. Clinical biochemistry tests were done for fasting blood glucose (FBG, mg/dL), insulin (μmL), triglyceride (TG, mg/dL), and high-density lipoprotein (HDL-C,

mg/dL). **Results:** Mean values of age (23.4 years) and anthropometric characteristics were: height (men 172 cm, women 156 cm), BMI (men $26 \text{ kg}/\text{m}^2$, women $31 \text{ kg}/\text{m}^2$), WC (men 89 cm, women 92 cm), body fat (men 17%, women 29%). Frequencies of overweight (men 47%, women 39%) and obesity (men 12%, women 39%) were remarkable. Other MetS characteristics were: BP (systolic: men 124 mm Hg, women 112 mm Hg; diastolic: men 83 mm Hg, women 78 mmHg), FBG (men and women $94 \text{ mg}/\text{dL}$), insulin (men, $9 \mu\text{mL}$, women $26 \mu\text{mL}$), TG (men $105 \text{ mg}/\text{dL}$, women $166 \text{ mg}/\text{dL}$) HDL-C (men $47 \text{ mg}/\text{dL}$, women $43 \text{ mg}/\text{dL}$). MetS frequencies were: IDF (men 12%, women 15%), ATP III (men 24%, women 15%), EGIR (men 41%, women 8%). BMI, WC, BF showed significant ($p<0.05$) association with dyslipidemia and hyperinsulinemia.

No funding

Traumatic predictors of femicide: A forensic anthropological approach to domestic violence

MICKI J. DAVID and HEATHER WALSH-HANEY
Justice Studies, Florida Gulf Coast University

Blunt-force and gunshot trauma (BFT) tend to occur most frequently in interpersonal and domestic violence (DV) cases. Current literature often fails to recognize DV prevalence in forensic contexts. Historically, the role of forensic anthropologists (FAs) was minimized to evaluating the mechanism of BFT without opining whether observations were consistent with DV. Previous research highlights fracture production biomechanics while ignoring how those data may corroborate circumstantial evidence of DV. Recently, emphasis is placed on FAs understanding the social, cultural, and economic factors that contribute to DV being a social construct. The aim of this study is to differentiate between known DV and non-DV BFT. The objective of this research is to distinguish male and female differences in prevalence, distribution, and pattern of BFT from which DV may be inferred. The sample consists of 116 contemporary individuals (94 males; 22 females) with evidence of BFT. Relative to the sample size, results show male-female differences in BFT pattern and frequency. Females exhibited higher frequencies of perimortem BFT (36%) compared to males (14%); males exhibited higher rates of perimortem gunshot trauma (11%) than females (5%); and both males (55%) and females (32%) had relatively high frequencies of antemortem injuries. When medical records were evaluated for analysis, less information was available for females (24%) than males (76%), suggesting a discrepancy in which data identifying DV-related antemortem injuries are collected. In conclusion, sex differences in BFT frequency and pattern may indicate femicide or DV occurrence when the death is framed in contextual and social contexts.

The molecular consequences of migration in a regional Amazonian city

RANDY E. DAVID

Biological Anthropology, University of Kansas

Much of the research on the history of migration in the New World has underscored the continents' complex pattern of peopling, focusing on the Peruvian Andes and Valley of Mexico. Significantly less attention has been accorded to assessing population movements, particularly urbanization, in other key, regional, areas of the Americas, most notably western Amazonia. This is surprising given that urbanization has proven consequential in terms of natural resource exploitation, public health initiatives, economic opportunities, and regional development trajectories.

Nearly four-fifths of the population of Peru currently resides in urban areas, such as the historically important city of Yurimaguas, in the Lower Huallaga River Valley. Approximately 200 DNA buccal swab samples were collected from city residents. The mitochondrial control region and the non-recombining region of the Y chromosome were analyzed, respectively, via Sanger sequencing and a commercially available SNP kit. Tests were run to assess population equilibrium or demographic expansion. The resultant interpretation was that the population as a whole was in equilibrium, however when divided into its five most prevalent haplogroups, the population was found to be the result of an agglomeration of numerous expanding subpopulations. Haplogroup distributions were compared between the total sample and subdivisions of the sample by language type, living environment, and age, for both mtDNA and NRY DNA, revealing differential distribution patterns. Lastly, Φ_{ST} and exact differentiation tests were used to determine that there exists a statistically significant difference between the genetic composition of population subdivisions, based on specific, modern, quantitative migratory factors.

Anthropology and Experiential Learning on a Study Abroad in South Africa

LISA M. DAY¹, JERRI L. HARRYMAN¹, BRIGID JACOBY¹, JACOB JONES¹, CHRISTINA A. MCGRATH¹, KELSEY D. O'NEILL¹, SAMANTHA M. PHILBEN¹, MARIE VERGAMINI², LAUREN J. VOLKERS¹ and AMY L. RECTOR¹

¹Anthropology, School of World Studies, Virginia Commonwealth University, ²Integrative Life Sciences, Virginia Commonwealth University

Experiential learning is a key feature of a holistic anthropology curriculum. Though there are many experiential learning options, study abroad programs offer opportunities for students to put the knowledge learned in the classroom to work in the real world. Since

ABSTRACTS

2012, Virginia Commonwealth University has run "Paleoanthropology: History and Legacy of Evolution in South Africa," a faculty-led study abroad for more than 50 undergraduates.

Visits to museums and fossil sites were critical for learning about history and cultures of the country. Tours of fossil vaults at the Ditsong Natural History Museum and the University of Witwatersrand introduced students to the most important fossils for human evolutionary studies in South Africa. Fossil dig sites in the Cradle of Humankind, including Sterkfontein and Swartkrans, and the West Coast Fossil Park in the Western Cape provided behind the scenes access to actual paleoanthropological field work. To place these evolutionary studies within a contemporary context, students experienced the Apartheid Museum, Hector Pieterse Museum, and Voortrekker Monument.

Ecology of Kruger National Park, Golden Gate Highlands National Park, and Blyde River Canyon provided analogues for paleoenvironments of our earliest ancestors. Students were asked to think about each experience from an anthropological perspective, and nightly debriefs allowed them to talk about the day and the things they learned; these were critical to the learning experience and processing often difficult emotions. Teaching anthropology outside the classroom – far outside a classroom – gives students a unique opportunity to experience activities and engagement that typical classroom instruction cannot provide.

A tale of two stresses: Comparing the relationships between maximum incisor shearing strength and maximum incisor bending strength and anthropoid diet

ANDREW S. DEANE, LAUREN N. AUSTIN and JACOB W. MOFFITT

Anatomy and Cell Biology, Indiana University School of Medicine

Anthropoid incisors play a critical role in the pre-processing of food items prior to ingestion and are strongly influenced by dietary mechanical loading. Accordingly, anthropoid incisors are subject to a variety of stresses applied in multiple directions. Bending stress occurs when transverse loading is applied perpendicular to the long axis of the incisor crown and where one surface experiences compressive stress while the opposite surface experiences tensile stress. Shear stress, however, results from unaligned forces working to displace different components of the incisor crown in opposite directions and would result in displacement of the crown in a horizontal plane at the cemento-enamel junction (CEJ).

This study contrasts prior analyses of anthropoid incisor maximum bending strength with new analyses of anthropoid incisor maximum shearing strength. Incisors representing extant hominoids and platyrrhines (n=187) with known

diets were modeled as cantilevered beams and maximum shearing strength (CA) was calculated for the maxillary and mandibular central and lateral incisor crowns. Results indicate that incisal shearing strength tracks diet in both hominoids and platyrrhines similar to maximum bending strength, however the differences between soft- and hard-object frugivores, particularly among hominoids, are accentuated relative to similar analyses of maximum bending strength. This suggests that the relative difference between the shearing stresses generated by soft- and hard-object frugivory are likely greater than the differences in bending strength generated for each group. Similarly, hylobatids had lower than expected maximum shearing strength possibly reflecting the tendency for gibbons and siamangs to bypass their incisors altogether during ingestion.

Estimating extinct primate vomeronasal traits using maximum likelihood ancestral state reconstruction methods

REBECCA M. DECAMP and EVA C. GARRETT

Department of Anthropology, Boston University

Living primates vary in their olfactory abilities, which includes the capabilities of their vomeronasal system (VNS). The VNS is comprised of the vomeronasal organ (VNO), forming the vomeronasal groove (VNG) on the maxilla, and vomeronasal receptor (VR) genes that code for proteins on VNO receptors. The VNG length is significantly related to the number of intact V1R genes in primates. This relationship allows us to estimate V1R counts in the primate fossil record using VNG length through computed tomography. We sought to reaffirm previous findings using a multimodal approach, including a phylogenetic least-square regression to measure the relationship between VNG length and V1R gene count ($P < 0.0002$, $R^2 = 0.525$), as well as a maximum likelihood-based ancestral state estimation. Our dataset included 49 primate species (both fossil and extant). The results of our maximum likelihood model showed that the primate last common ancestor had an intact V1R gene count of 42.7 (95% CI = 15.6, 69.8), which is smaller than the reconstructed V1R gene count for the basal strepsirrhine fossil *Adapis* (52.4 with 95% CI = 13.7, 91.0), yet larger than the reconstructed V1R gene count for the basal haplorhine fossil species *Rooneyia viejaensis* (40.1, with 95% CI = 12.1, 68.1). We suggest based on these reconstructions that instead of retaining a larger V1R gene count as the ancestral state, strepsirrhines expanded their V1R gene repertoire from a more intermediary V1R gene count, while the haplorhine V1R gene repertoire decreased from that same intermediate ancestral V1R gene count.

The long, twisting road: searching for biomarkers of chronic psychosocial stress

JASON A. DECARO

Anthropology, University of Alabama

Several biomarkers are effective for monitoring context-specific responses to recent experience but lose validity when applied as markers of chronic stress. For instance, most of the variance in cortisol, blood pressure, and catecholamines reflects momentary not persistent regulatory states. Serial sampling can extend their utility from moments to days, and to the extent the sampling frame captures typical experience they may also reflect chronic stress. Yet, cost and participant burden can be high, and typical days elusive. Three additional alternatives are discussed. First, latent herpesvirus blood spot models have been developed in light of psychoneuroimmunology research suggesting anti-herpesvirus surveillance declines during chronic psychosocial stress. Unfortunately, mixed results in anthropological field studies have challenged the generalizability of these markers. Second, cortisol output over months can be estimated in hair. Yet hair sampling is challenging in some populations (e.g., if children's hair is routinely cut very short, or hair is heavily treated). Third, chronic stress may be inferred from long-term down-stream effects detectable in blood spots, like systemic inflammation. Such markers may be examined individually or combined into an allostatic load index, but they are sensitive to a variety of other stressors, including pathogenic environments. There remains no perfect chronic stress marker for all populations or study designs, and in practice the boundary between "psychosocial" and other forms of stress is blurry. Nevertheless, sufficient options are now available that valid chronic stress markers typically can be incorporated singly or in combination, contingent on careful attention to the limitations of each.

Quest for consilience: Using dental morphology, craniometrics, and stable isotopes to classify an undocumented skull collection

DOROTHY DECHANT¹ and LAURA E. CIRILLO²

¹Institute of Dental History and Craniofacial Study, Arthur A. Dugoni School of Dentistry, University of the Pacific, ²Department of Anthropology, University of Nevada, Reno

The Atkinson Library of Applied Anatomy at the University of the Pacific Dugoni School of Dentistry consists of over 1400 international crania. Similar to collections amassed around the 1930-40s, little identity information is known. This study applies both non-invasive and minimally invasive techniques to 130 adult skulls collected from Mexico City to explore the sex, ancestry, provenance and socioeconomic status of an unknown sample through multiple lines of evidence.

ABSTRACTS

Cranial macromorphoscopic traits and craniometrics were used to estimate sex. Ancestry was estimated through 28 cranial measurements, by discriminant function analysis using Fordisc's forensic database, and 12 dental morphology traits, using rASUDAS. Provenance confirmation and diet information were provided by stable isotope analysis of bone collagen carbon and nitrogen isotopes, and bone bioapatite carbon and oxygen isotopes derived from a subset of half (65) the skulls. The isotope results allowed the assessment of socioeconomic status and aided in a final cluster analysis.

Sex and ancestry estimations differed in outcome. Sex estimation from craniometrics and morphological data was consistent, with discordance in <1% of the sample. Ancestry estimation, however, resulted in substantially different clustering based on the cranial compared to the dental data; 46% of the sample showed discordant classification between the two methods, predominantly due to dental classification of Western Eurasian being categorized as Asian or Black in Fordisc.

This study explores how to reconcile such seemingly conflicting data, and investigates the utility of multiple lines of evidence for re-establishing biographical information lost from skeletal samples.

Trabecular ontogeny of African ape third metacarpals

KIM P. DECKERS¹, CHRISTOPHER J. DUNMORE¹, MATTHEW M. SKINNER^{1,2} and TRACY L. KIVELL^{1,2}

¹Skeletal Biology Research Centre, School of Anthropology and Conservation, University of Kent, ²Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology

Little is currently known about how trabecular bone develops and responds to biomechanical loading during ontogeny in primates. Information on bone modelling and remodelling in African apes throughout ontogeny will inform studies that infer functional differences from variation in adult trabecular bone. Using microCT data and a 'whole-epiphysis' method, we describe ontogenetic changes in trabecular bone morphology of the third metacarpal (Mc3) of *Gorilla gorilla* (n=4) and *Pan troglodytes* (n=4), spanning four dental age categories.

In both *Gorilla* and *Pan*, bone volume fraction (BV/TV) was high throughout the head and base of the Mc3, and surrounding the epiphyseal plate, throughout ontogeny. *Gorilla* specimens under 3 years of age demonstrate a palmar concentration of trabeculae in the Mc3 head. The trabecular bone remodels to a more adult-like pattern by age 6, where high BV/TV is concentrated in the disto-dorsal region of the head and surrounding the epiphyseal plate. *Pan* individuals under 4 years of age show high BV/TV throughout the head and base, with no localised concentrations within the

head. Between 4-7 years, remodelling maintains a higher palmar concentration of BV/TV in the Mc3 head, but by 8 years of age BV/TV distribution in the head resembles the adult condition, with highest BV/TV concentrated disto-dorsally. In both species, changes in high BV/TV concentrations are consistent with ontogenetic changes in locomotor behaviours, and the strongest remodelling patterns occurred at ages when an adult-like frequency of knuckle-walking locomotion occurs, indicating that changes in African ape locomotion likely influence trabecular bone modelling throughout ontogeny.

Radiocarbon Evidence Pertaining to the Origin and Spread of Treponemal Disease

MICHAEL DEE

Centre for Isotope Research, University of Groningen

The chronology of the origin and spread of treponemal disease has long been a source of conjecture. Claims of treponemal infection have been reported at more than 50 sites around the world thought to predate the Modern era. While the pathology in least 20 of these cases is widely accepted, the associated dating evidence is often called into question. In this study, the chronological evidence pertaining to these cases is reanalyzed with emphasis on the use of radiocarbon dating. The two principal causes of spurious radiocarbon dates are diet-derived reservoir effects and flawed sample selection. Radiocarbon dates from human tissues can be offset to older ages if the individual consumed significant quantities of marine or freshwater fish in his or her life. Corrections can be made for such reservoir effects if supporting data are available, especially carbon and nitrogen stable isotope ratios. However, some reservoir corrections have been applied without sufficient rigor, resulting in calendar date ranges that are either incorrect or misleading. This reanalysis includes both a critique of past reservoir corrections and suggestions for best practices in future research. Moreover, due to the complications associated with dietary effects, it is often preferable to avoid the direct dating of human tissue. Selecting samples from plant-based artifacts is recommended, so long as the contemporaneity with the human remains can be assured. Radiocarbon results from several such studies are also reviewed. Ultimately, a robust case is presented for considerable time depth to treponemal disease at various locations around the world.

Using DNA to determine the species and geographic origins of elephant ivory discovered in a 16th century Portuguese shipwreck

ALIDA DE FLAMINGH¹, ASHLEY COUTU^{2,3}, SHADRECK CHIRIKURE², JUDITH SEALY², RIPAN S. MALHI^{1,4} and ALFRED L. ROCA^{1,5}

¹Program in Ecology, Evolution and Conservation Biology, University of Illinois at Urbana-Champaign, ²Department of Archaeology, University of Cape Town, ³Department of Archaeology, Newcastle University, ⁴Department of Anthropology, University of Illinois at Urbana-Champaign, ⁵Department of Animal Sciences, University of Illinois at Urbana-Champaign

Shipwreck cargo provides a snapshot into the past, and may prove invaluable for uncovering human and animal histories otherwise unknown. Diamond mine dredging of the Namibian seabed led to the discovery of the *Bom Jesus* shipwreck. Excavation of the shipwreck revealed a rich cargo, including Portuguese coins suggesting that the ship sank between 1525 and the 1530s. The cargo also contained more than 100 unworked elephant tusks. The geographic origin of this ivory was unknown. We used ancient DNA methods to show that the tusks were from African forest elephants (*Loxodonta cyclotis*) from West Africa. The ancient ivory samples matched nuclear DNA typical of forest elephants but not savanna elephants, while the mitochondrial DNA was characteristic of elephants from West Africa but not Central Africa. The diversity of mitochondrial DNA established that the elephants were from at least 17 different herds. This study shows that ancient DNA techniques can be employed to determine the provenance of shipwreck cargo, to compare the genetic characteristics of ancient and modern wildlife populations, and to corroborate historical accounts of maritime trade routes.

Temperature alters chest redness in male geladas

PATRICIA M. DELACEY¹, THORE J. BERGMAN^{1,2} and JACINTA C. BEEHNER^{1,3}

¹Psychology, University of Michigan, ²Ecology and Evolutionary Biology, University of Michigan, ³Anthropology, University of Michigan

Across a variety of taxa, sexual selection has produced badges of status that communicate the strength of the signaler to nearby rivals. Skin pigmentation is one such badge of status where the intensity of color has been shown to be associated with competitive ability. However, there must be a cost associated with the badge to prevent poor-quality males from signaling high quality. Here, we examine the putative costs associated with a badge of status in a wild population of geladas (*Theropithecus gelada*) in Ethiopia. Male geladas have a patch of skin on their chest that is known to be redder in males of higher status. We examined whether decreasing temperature

ABSTRACTS

(internal or external) causes a decrease in redness. We used digital photos, calibrated with a color standard, to measure redness (ratio of red to green) in male chest patches. We found that external measures of temperature such as time of day, time of year, mean maximum temperature, and altitude had no effect on variation in chest color. By contrast, we found that internal measures of temperature did have an effect on chest color. Specifically, redder chests were associated with (1) higher chest skin temperatures ($R^2=0.63$, $p<0.001$); (2) receipt of a hot pack to the chest during the annual darting ($F_{2,42}=5.58$, $p=0.007$, $r=0.46$); and (3) recent displays compared to baseline activity levels ($t(7)=2.0913$, $p=0.075$). These data suggest that cold temperatures may constrain chest redness in this cold, high altitude environment.

Polynesian ancestry in South America? A genomic insight from Mocha Island, Chile

CONSTANZA DE LA FUENTE¹, ROBERTO CAMPBELL², FRANCISCA SANTANA^{3,4}, MAURICIO MORAGA⁵ and ESKE WILLERSLEV¹

¹Center for GeoGenetics, University of Copenhagen, ²Programa de Antropología, Instituto de Sociología, Pontificia Universidad Católica de Chile, ³Laboratory for Archaeology and the History of Art, University of Oxford, ⁴Instituto de Ciencias Naturales Alexander Von Humboldt, University of Antofagasta, ⁵Programa de Genética Humana, Facultad de Medicina, Universidad de Chile

A contentious and recurrent debate within the population history of the Americas concerns the contact between Polynesia and South America. From a genomic perspective, the presence of a Native American component has been studied on Easter Island, however the reverse has not been formally tested on individuals within South America. Evidence of contact between the Chilean coast and Polynesia has been suggested based on material cultural similarities and domesticated species. In addition, human remains from Mocha Island (Southern Chile) have been argued to hold Polynesian traits based on morphological analyses. We analyzed 12 samples (10 individuals) from this island, including the individuals specifically ascribed to have Polynesian affinities.

We successfully obtained low coverage whole genomes from three individuals. All the individuals belong to Native American mitochondrial lineages well represented in the region. In addition, we estimated the genomic affinities of these individuals with other population worldwide distributed. In a Principal Component Analysis, individuals from Mocha Island cluster together with other Native American populations. A more detailed characterization was performed using the outgroup-f3 statistic, showing additional support for their South American proximity, with the highest affinity to individuals from Southern Chile. Furthermore, the individual morphologically

proposed as Polynesian falls within the expected Native American diversity. Consequently, our results find no support for possible admixture between local population and Polynesian voyagers.

NSF BCS-0956229, FONDECYT 3130515, FONDECYT 11150397, Lunbeck Foundation, Danish National Science Foundation

Incisor microwear textures in four genera of Sumatran primates

LUCAS K. DELEZENE¹, SARA A. JEFFRESS¹, MARK F. TEAFORD² and PETER S. UNGAR¹

¹Anthropology, University of Arkansas, ²Basic Science, Touro University

On Sumatra, *Pongo*, *Macaca*, *Presbytis*, and *Hylobates* differ in the manner and extent to which they use their anterior teeth in food acquisition and processing, and these feeding behaviors are related to their niche partitioning. To investigate the relationship between diet, tooth use, and dental wear, microwear textures were analyzed for the central incisors of four genera of sympatric Sumatran primate for which field observations of anterior tooth use are available. Using a white light confocal microscope, ten ISO-25178 texture attributes that reflect microwear feature size (Sz, Sv, S5v, Sda, Sdv, Vwv), anisotropy (Str), surface roughness (Sa), surface complexity (Sdr), and feature density (Ssk) were recorded. Microwear was recorded from the center of the incisal edge of the labial surface of high-resolution epoxy casts of maxillary central incisors of adult wild-collected Sumatran specimens of *Pongo abelii* ($n = 31$), *Hylobates lar/agilis* ($n = 36$), *Presbytis melalophos/thomasi* ($n = 39$), and *Macaca fascicularis* ($n = 20$). In line with previous feature-based studies, there is strong overlap among the four genera in microwear attributes. *Pongo* has smaller features (Sda, Sdv, and Sz) than either *Hylobates* or *Presbytis*, while *Hylobates* exhibits the largest features. *Presbytis* exhibits less surface roughness (Sa) than that of *Macaca*, while also having the least complex surfaces (Sdr). No observable differences among taxa were found for anisotropy. These findings align with reported field observations of tooth use and illustrate the potential for using microwear texture analysis to infer patterns of anterior tooth use in extinct primates.

Funding provided by the Leakey Foundation.

Current and future applications of minimally-invasive biomarkers in the detection and treatment of various types of cancers

ALICIA M. DELOUIZE¹, FARNOUSH A. ABAR², GEETA EICK¹ and JOSH SNODGRASS¹

¹Anthropology, University of Oregon, ²Samaritan Hematology and Oncology Consultants, Samaritan Health Services

Currently, cancer screening, staging, and therapy mostly rely on invasive procedures, such as imaging (which carries a .05% to 1.8% increased risk of developing a cancer), biopsies, venous blood tests, and invasive physical exams. We ran analyses on a global sample from the Study for AGEing and adult health (SAGE), and found that 80.6% of women over 50 years old have never received a mammogram and 59.7% have never received a pelvic exam in nationally representative samples from India, Mexico, China, Russia, Ghana, and South Africa. The benefits of developing and utilizing biomarkers from sample types that are considered minimally-invasive across disciplines (such as urine, feces, saliva, scent, and blood micro-samples) include improved screening capabilities, better monitoring of treatment and disease, and an improved quality of life for patients. There are currently three FDA approved minimally invasive sample biomarkers for different cancers and numerous in development, including DNA, RNA, metabolic, proteomic, bacterial, and cellular biomarkers. Successful development and widespread adoption of minimally invasive screening and tracking options for different cancers can both improve and save lives worldwide.

NIH NIA YA1323-08-CN-0020; NIH R01-AG034479; WHO; Ministry of Health in Mexico; Shanghai CDC in China; NDH in South Africa; University of Ghana Medical School; USAID; University of Oregon Bray Fellowship.

To Correct for Size or Not: Examining the Problem Using the Pelvis

HILLARY DELPRETE

History and Anthropology, Monmouth University

Examining sexual dimorphism in the pelvis is complicated, and this complexity is compounded by the relationship between size and pelvic measures; bigger individuals have comparatively bigger pelvises. Some researchers choose to adjust for size when examining pelvic dimorphisms, whereas others do not. Unfortunately, this choice has an effect on the outcome of the analysis. This study examines 23 pelvic measures of 119 individuals from the Hamann-Todd Collection to examine how data adjustment affects which measures appear dimorphic. Three independent sample t-tests were run on this data; for the first analysis the data was unadjusted, for the second analysis it was adjusted for body size by dividing each measure by the femoral head diameter raised to the 1.7125 power for each individual, and in the third analysis it was adjusted for pelvic size by dividing each measure by the geometric mean for each individual. In each case, the measures that appeared to be sexually dimorphic differed. Using the unadjusted data, three of the 23 measures were not dimorphic: anterior space of the midplane, sacral breadth, and anterior space of the outlet. Using the data adjusted for pelvic size, five different measures were not

ABSTRACTS

dimorphic: anterior space of the inlet, transverse diameter of the inlet, interacetabular distance, length of the superior pubic ramus, and circumference of the inlet. According to the t-test for the data adjusted for body size, all pelvic measures were dimorphic. These conflicting results demonstrate the problematic nature of data correction and further emphasize the difficulty in comparing studies.

no funding to declare

Exploring pathways to skeletal phenotypes: Biomarkers of inflammation, skeletal health, and oral health in NHANES 2003-2004

SOPHIA C. DENT, STEPH M. BERGER and JACOB S. GRIFFIN

Anthropology, University of North Carolina at Chapel Hill

Skeletal phenotypes represent complex interactions between physiology and environmental influences that serve as sensitive indicators of context at individual and population levels. Periodontal disease (PD) is an inflammatory disease of dental tissues and an important phenotype of interest in modern clinical and bioarchaeological research due to its impact on systemic health. Although bioarchaeologists have used PD to examine the impacts of various cultural processes on past populations, additional research is needed to verify common assumptions about the physiological mechanisms by which specific social factors influence skeletal phenotypes. This study examined the pathway connecting biocultural factors, inflammation, and the expression of PD with a sample (n=5051) from the US National Health and Nutrition Examination Survey (NHANES, 2003-2004). Generalized linear regression models found: statistically significant, positive associations (p < 0.01; denoted with *) between PD diagnosis and BMI [0.054*(0.005)], CRP [0.142*(0.034)], parathyroid hormone [0.003*(0.001)], and total cholesterol [0.006*(0.001)]; and negative correlations between PD diagnosis and BAP [-0.023*(0.002)] and social support [-0.542*(0.177)]. Mediation analysis found that CRP mediated the relationship between biocultural factors and PD diagnosis and demonstrates that PD is a marker of systemic inflammation and reduced bone mineralization. This model supports the use of the PD phenotype to make inferences about biocultural factors in past populations. We argue that future studies should utilize modern datasets to explore pathways that contribute to skeletal phenotypes and bridge the gap between modern and past population research.

Infanticide or expected child mortality? The curious abundance of babies in the Iron Age necropolis of Kopila hillfort, Korčula, Croatia

LARESA L. DERN¹, DAVORKA RADOVČIĆ², EMILY R. ORLIKOFF¹ and MICHELLE M. GLANTZ¹

¹Anthropology, Colorado State University,

²Anthropology, Croatian Natural History Museum

Most archaeological sites yield few sub-adult remains and when recovered they are often too poorly preserved for analysis. A lack of children in the archaeological record has limited our perspective on variation in human growth and development and the history of children in the past. In this context, the abundant collection of remains excavated from a Late Iron Age, Illyrian necropolis on the island of Korčula, Croatia is a remarkable resource and the high representation of children is somewhat curious. Often, large deposits of infants from Classical Antiquity and the Iron Age Mediterranean are controversially interpreted as the byproduct of infanticide. This study estimates age at death for 1177 isolated teeth from three tombs via assessment of dental development using Moorrees' and Iruita's systems, as well as Liversidge's tooth length regression formulas. The resulting relative age profiles are employed to test the null hypothesis that these assemblages are the result of typical mortality rates rather than widespread infanticide. Additionally, this study begins investigation into the growth and development patterns of the Kopila sample. The unique size and quality of this sample allow for a refined reconstruction of age at death. Overall, the wide age distribution and formalized deposition suggest that these assemblages are the result of a normal demographic pattern rather than widespread infanticide. These results do not preclude the possibility that some of the individuals included in the deposit were victims of infanticide. Future research will expand on these results with analysis of dental non-metric traits and post-cranial remains.

Impacts of grit on dental microwear formation: a time series approach

LARISA R.G. DESANTIS¹, MARK F. TEAFORD² and MARIANA DUTRA FOGAÇA³

¹Department of Earth & Environmental Sciences, Vanderbilt University, ²Department of Basic Sciences, Touro University, ³Conservation and Biodiversity, Federal University of Maranhão

Decades of research have used dental microwear as a tool for inferring diet, with a more recent debate focused on distinguishing between the contributions of food and/or grit on dental microwear formation. While experimental and museum-based studies have demonstrated that diet is the overarching signal recorded via dental microwear, it is challenging to examine dental microwear formation over long periods of time—especially in humans. Here, we examined

a series of tooth facets taken from the same human individual over a period of approximately 8 months. Tooth impressions were acquired prior to and after the consumption of a diet that included corn muffins, where the corn was prepared with a sandstone grinding surface and then with a granite grinding surface. The same facets were re-examined after each treatment and analyzed via dental microwear texture analysis (DMTA). Complexity values vary < 1 between each time step, while anisotropy values vary by < 0.001. There is greater variability between different facets than there is between treatments. DMTA attributes do not consistently increase or decrease over time with either of the grit-treatments, suggesting that grit does not dramatically erase or rewrite dental microwear. Instead, dental microwear attributes are remarkably conserved with identifiable features clear throughout ~8 months during the study. These data suggest that dental microwear in modern humans represents a most recent, but potentially longer term diet-record than previously thought and that grit may have less of an effect on dental microwear textures than expected.

Funding was provided by Vanderbilt University.

Joint proportions in early hominins

ANJALI M. PRABHAT¹, CATHERINE K. MILLER² and JEREMY M. DESILVA^{1,2}

¹Anthropology, Dartmouth College, ²Ecology, Evolution, Ecosystems, and Society, Dartmouth College

In general, human evolution has been characterized by an increase in lower limb joint size and a decrease in upper limb joints as a result of bipedalism and reduction of arboreality. However, the pace at which this transition occurred and the ancestral condition from which it evolved still remain unknown. Previous work has shown that *Australopithecus afarensis* exhibited human-like proportions, while *A. africanus* retained ape-like limb joint sizes. Here, we re-examine these proportions and include additional hominin taxa. Measurements were taken at the elbow (humeral biepicondylar breadth, radial head diameter, ulna trochlear width), femur (head diameter and subtrochanteric width), and ankle joints (tibia, talus) on African great apes (N = 26), humans (N = 24), and fossil hominins. Data were expressed as a geometric mean that represented each specimen's relative upper limb to lower limb ratio. *A. afarensis*, *Homo erectus*, and *H. naledi* resembled humans, whereas *A. africanus*, *A. sediba*, *Paranthropus robustus*, and *P. boisei* all fell near or within the ape range for upper limb to lower limb ratios. These results demonstrate that in spite of being committed bipeds, the South African australopithecids and *Paranthropus* may have exhibited a greater degree of arboreal behavior than *A. afarensis*, despite being chronologically younger. Our findings create a phylogenetic dilemma in

ABSTRACTS

which either the human-like body proportions of *A. afarensis* are homoplastic or the ape-like upper limbs of both South African australopiths and *Paranthropus* are secondarily derived.

Life history insights from dried blood spot-based measurement of bone turnover markers

MAUREEN J. DEVLIN¹, GEETA N. EICK² and J. JOSH SNODGRASS²

¹Anthropology, University of Michigan, ²Global Health Biomarker Laboratory, Department of Anthropology, University of Oregon

Bone is a dynamic organ whose continual turnover is influenced by life history stage, including growth, reproduction, and aging; energy availability; activity level; climate; disease; and other factors. Bone turnover data are essential to anthropologists but challenging to measure in field settings. The present study reviews and synthesizes information on the viability of measuring bone formation and resorption markers in dried blood spots (DBS), a field friendly, cost-effective, minimally invasive collection technique. Markers of bone formation include osteocalcin (bone matrix protein), P1NP (propeptide of type 1 collagen), and alkaline phosphatase (osteoblast enzyme). Markers of bone resorption include Ctx (collagen breakdown product) and TRAcP5b (tartrate-resistant acid phosphatase 5b, osteoclast enzyme). Considerations include clinical relevance, stability in dried blood, assay availability and cost. Results show that osteocalcin (formation) and TRAcP5b (resorption) have the strongest potential for DBS measurement. Osteocalcin is synthesized by osteoblasts and is the predominant non-collagenous protein in bone matrix. TRAcP5b is an enzyme produced in proportion to osteoclast number. Both markers are clinically validated, stable in dried blood, and measurable using existing assays. We conclude that DBS measures of osteocalcin and TRAcP5b have the potential to address anthropological questions about bone gain and loss across life history (e.g. at puberty and menopause) and in response to environmental factors. For example, relative osteocalcin and TRAcP5b levels could be used in combination with imaging (e.g., calcaneal ultrasound) to assess pubertal bone mass acquisition. Future studies must delineate population variation in these markers in DBS samples at different life history stages.

Support: NSF BCS-1638786

Assessing the existence of the male-female health-survival paradox in past populations

SHARON N. DEWITTE

Anthropology, University of South Carolina

In many modern populations, women live longer than men, but experience higher burdens of disease and disability and poorer self-rated health. This male-female health-survival paradox has received increasing attention as demographic transitions produce higher proportions of elderly people in living populations. However, this trend has been understudied in past populations. The ability to estimate age in skeletal samples, even for the oldest individuals, via the method of transition analysis, provides the opportunity to examine patterns of skeletal pathologies with advanced age in the past. This study examines sex-differences in trends of periodontal disease (PD) across the medieval period in London using a sample (n = 986) from several cemeteries. PD has previously been shown, in this context, to be associated with elevated risks of mortality and with periosteal new bone formation, suggesting that it reflects underlying immune responses or frailty more generally. Previous research has also revealed improvements in survivorship following the 14th-century Black Death in London. For this study, the results of binary logistic regression, and hierarchical log-linear analysis reveal: 1) an increased risk of PD with age, 2) increased survivorship after the Black Death, and 3) declines in PD after the Black Death that are of greater magnitude for females compared to males. These results do not reveal the existence of a male-female health-survival paradox in the medieval period, at least with respect to PD. However, they do corroborate existing evidence of substantial improvements in health in general in the aftermath of the Black Death.

Funding was provided by NSF (BCS-1261682; BCS-1539502), the Wenner-Gren Foundation (#7142, #8247), and the American Association of Physical Anthropologists.

Modelling ontogenetic changes in masticatory performance within *Macaca fascicularis* and their impact upon dietary and social ecology: a multibody dynamics study

EDWIN DICKINSON¹, LAURA C. FITTON² and KORNELIUS KUPCZIK¹

¹Max Planck Weizmann Center, Max Planck Institute for Evolutionary Anthropology, ²Center for Anatomical and Human Sciences, Hull York Medical School

Many Cercopithecine primates demonstrate developmental shifts in dietary and/or social ecology. In *Macaca fascicularis*, the size and mechanical resistance of frequently ingested foods increases during development, as does the frequency of canine-baring social displays. However, it is unclear how these behavioral shifts may relate to ontogenetic changes in masticatory anatomy in this species. To this end, we applied multibody dynamics techniques to investigate the effects of developmental changes in muscle

size, muscle architecture, and craniofacial form upon masticatory performance within *M. fascicularis*, and to explore how these anatomical changes may contribute to shifts in the dietary/social ecology of this species. Across a series of models (infant, juvenile, adult female and adult male), maximum bite force and gape were measured at different stages of jaw closure at several locations along the dental row.

With increasing age, individuals displayed an improved ability to consume larger food-stuffs and produce higher bite forces, mirroring reported dietary shifts within this species. The adult male model also demonstrated a significantly improved anterior gape capacity, reflecting the increased importance of canine-baring jaw postures within these individuals. Changes in muscle size contributed most significantly to increases in bite force, while craniofacial form imparted a more significant effect upon gape potential than muscle architectural changes.

These findings demonstrate the close relationship between masticatory form and dietary/social ecology during ontogeny, in which anatomical changes during development enable older individuals to consume larger and more mechanically challenging foods, and enhance the role of the masticatory apparatus within social display behaviors.

Financial support was provided by the Max Planck Society.

Analysis of an American Heroine?: The Skeletal Remains from the Gravesite of "Captain" Molly Corbin

ELIZABETH A. DIGANGI

Anthropology, Binghamton University

Margaret (Molly) Corbin is known for her bravery during the American Revolutionary War when in November 1776 she took over her husband's cannon after he was killed in action. She was seriously wounded and taken prisoner by the British; and later became the first woman to receive a pension from the American government due to her service and subsequent disability. The historical record indicates that she sustained grapeshot wounds to her shoulder and breast, rendering one arm permanently unusable. Following her death several decades later, she was buried in a small cemetery on the estate of financier J.P. Morgan in Highland Falls, NY. In the 1920s, the Daughters of the American Revolution discovered her unmarked gravesite and petitioned the US Military Academy in West Point to lay her to rest there. In 2016, this gravesite was accidentally disturbed during construction activities. The skeletal remains were subsequently exhumed and subjected to forensic anthropological analysis. While the remains were significantly fragmented, it was nevertheless possible to estimate several biological parameters, including age-at-death,

ABSTRACTS

sex, antemortem trauma, and pathology. Given the fragmentary nature of the skeleton, thorough osteological knowledge was essential, as even fragments contributed to the osteobiography. The resulting picture was that of a middle-aged man lacking shoulder injuries but with several other antemortem traumatic and pathological conditions. In all likelihood he was alive during the colonial period or later, and his remains were mistaken for Molly Corbin's in the 1920s. He was reburied at West Point, and Margaret Corbin's gravesite remains unknown.

Nutrient goals of wild Bornean orangutans at Gunung Palung National Park: a case for nutrient balancing

ANDREA L. DIGIORGIO^{1,2} and CHERYL D. KNOTT^{1,2}
¹Anthropology, Boston University, ²Gunung Palung Orangutan Project

Bornean orangutans (*Pongo pygmaeus wurmbii*) have historically been characterized as frugivores and energy maximizers under an optimal foraging paradigm. While orangutans do consume more fruit and energy when fruit is available, the Geometric Framework of Nutrition (GF) suggests that energy maximization is not the only goal of foraging. Instead, GF suggests that in addition to energy goals, animals also balance nutrient intake. To test this theory, we investigated which nutrient balances were most tightly defended using feeding and nutritional data from 51 full-day follows of wild Bornean orangutans collected in Gunung Palung National Park in West Kalimantan, Indonesia. We predicted that, like other frugivorous primates, orangutans would most strongly maintain a non-protein to protein energy ratio (NPE:PE). Using linear regressions on all nutrient combinations, we find that an NPE:PE ratio of 10.12:1 was the most strongly defended nutrient ratio (Adjusted $R^2 = 0.86$, $p < 2e-16$). To investigate the influences of this foraging goal, we tested whether this ratio was different between sexes ($t = 1.65$, $p = 0.11$), fruit availability z-scores ($F = 5.27$, $p = 0.026$), and animals (ANOVA, $F = 1.78$, $p = 0.09$). We discuss the impact of each of these variables on orangutan foraging and nutrient balance, and the mismatch between available and consumed NPE:PE. Our data suggest that, in addition to energy, maintaining a nutrient balance and a range of protein intake are important foraging goals of orangutans.

DiGiorgio: NSF GRFP Grant No. DGE-1247312, Boston University; DiGiorgio and Knott: NSF BCS-1540360; Knott: US Fish and Wildlife Service, LSB Leakey Foundation, National Geographic Society, Disney Conservation Fund

Relationship among molecular markers, blood biochemistry, and anthropometry in Amazonian Native American populations

ISABELA G. DINIZ^{1,2}, HILTON P. SILVA¹ and JOÃO F. GUERREIRO²
¹PPGA, UFPA, ²PPGBM, UFPA

The epidemiological and nutritional transition among Native Americans is developing fast in Latin America, which partly explain the emergence of chronic noncommunicable diseases, specially obesity. Nevertheless, obesity is a multifactorial disease and presents very complex inheritance patterns where the cumulative contribution of diverse genes results in a greater or smaller individual susceptibility to certain environmental factors. In this sense, we sought to investigate the relation of Body Mass Index (BMI), cholesterol, glucose and triglycerides with three single nucleotide polymorphisms - SNPs (ABCA1 rs9282541; ADRB3 rs4994; and PPARG rs1801282) known in the literature as associated with obesity in populations around the world. A total of 590 adult individuals (51.86% female, mean age 39.44), living in 11 indigenous villages in the State of Pará participated in the study. The overall mean BMI and blood biochemistry among these populations were within normal limits. However, when groups were considered separately, the highest overweight frequency (BMI ≥ 25) found was 72.7% in one given population. We found association of BMI with the SNPs of the ABCA1 and ADRB3 genes. In addition, marginal association was found with the SNP of the PPARG gene ($p = 0.06$). All polymorphisms were tested for relative risk (odds ratio). The mutant alleles of the ADRB3 and PPARG genes had an odds ratio of 1.37 and 1.47, respectively. In contrast, the mutant allele of ABCA1 presented a lower relative risk than the wild-type allele (0.48) suggesting a protection against obesity to the carriers of this Native American peoples' exclusive variant.

UFPA, CNPq and CAPES.

Skeletal trauma as an indicator of past living conditions in Medieval Cambridge

JENNA M. DITTMAR¹, PIERS D. MITCHELL², CRAIG CESSFORD^{2,3}, SARAH INSKIP¹, BENJAMIN NEIL³, ISABELLA K. SEALEY⁴ and JOHN ROBB²

¹McDonald Institute for Archaeological Research, University of Cambridge, ²Department of Archaeology, University of Cambridge, ³Cambridge Archaeological Unit, Department of Archaeology, University of Cambridge, ⁴School of Clinical Medicine, University of Cambridge

The aim of this research is to explore the past living conditions experienced by the inhabitants of Medieval Cambridge through the analysis of skeletal trauma and the assessment of fracture risk. The skeletal remains of 326 individuals from Medieval Cambridge that were buried in the semi-rural parish cemetery of All Saints by the Castle

($n=79$), the Augustinian Friary ($n=38$), and the hospital of St. John the Evangelist ($n=209$) were assessed. Individuals with evidence of skeletal trauma were further analyzed using radiography, to class fracture type. One or more fractures were identified on 25.1% ($n=82/326$) of individuals examined. At each of these sites, fractures were more commonly found on males than females. Fractures were most commonly found on the individuals buried in the parish cemetery (36.7%, $n=29/79$), followed by those in the hospital cemetery (22.48%, $n=47/209$). Within the Augustinian Friary, fracture prevalence was much lower (15.7%, $n=6/38$). The individuals buried in the parish and hospital burial grounds represent a cross section of Medieval society that likely engaged in physical labor at some point in their lives. The higher prevalence rate of skeletal trauma found in these two cemeteries may be associated with the living conditions and reflect the occupational hazards experienced by poor laborers. Comparatively, the friars and wealthy patrons buried within the friary were less likely to experience fractures as the friars were principally engaged in preaching and other spiritual activities, and the patrons of the friary would have been relatively wealthy and unlikely to be involved in manual labor.

Funded by the Wellcome Trust Biomedical Humanities Collaborative Grant programme

Variation in the human calcaneus: investigating the relationship between skeletal phenotype and behavior

LILY J. DOERSHUK¹, NICHOLAS B. STEPHENS¹, JAAP P.P. SAERS², TEA JASHASHVILI^{3,4}, KRISTIAN J. CARLSON^{5,6}, ADAM D. GORDON⁷, JAY T. STOCK^{2,8} and TIMOTHY M. RYAN¹

¹Department of Anthropology, Penn State University, ²Department of Archaeology, Cambridge University, ³Department of Radiology, Molecular Imaging Center, University of Southern California Keck School of Medicine, ⁴Department of Geology and Paleontology, Georgian National Museum, ⁵Department of Integrative and Anatomical Sciences, University of Southern California Keck School of Medicine, ⁶Evolutionary Studies Institute, University of Witwatersrand, ⁷Department of Anthropology, University at Albany, SUNY, ⁸Department of Anthropology, Western University

Humans exhibit high levels of inter- and intra-population variation in trabecular bone structure. Consistent with a *bone functional adaptation* framework, this pattern has been associated with variation in behavior, in which human groups with high levels of activity/mobility (inferred from subsistence behavior) tend to have a more robust skeletal phenotype. However, most previous research has investigated this phenomenon by comparing bone structure between populations that are genetically, environmentally, and behaviorally distinct. We aim to control for these potentially confounding factors by comparing

ABSTRACTS

two groups from Central/Southern Illinois that are behaviorally distinct, but relatively genetically and environmentally similar. The Black Earth represent Middle Archaic hunter-gatherers and Norris Farms represents Oneota agriculturalists. High-resolution (~0.05 mm) microCT scans of the calcaneus from Black Earth (n= 14) and Norris Farms (n = 17) individuals were analyzed using a whole-element approach. Six trabecular bone microarchitectural variables were measured across the entire calcaneus using Medtool 4.2, including bone volume fraction (BV/TV), trabecular thickness (Tb.Th), trabecular separation (Tb.Sp), trabecular number (Tb.N), degree of anisotropy (DA), and bone surface density (BS/BV). Between group comparisons show that the Black Earth and Norris Farms differ significantly in Tb.Th, DA, and BS/BV. No significant differences were detected in BV/TV, Tb.Sp, or Tb.N. The Black Earth have thicker and less highly oriented trabecular bone structure, as well as lower bone surface density than the Norris Farms. The relationship between skeletal phenotype and human behavior is complex; future studies may benefit from deeper investigation of variation present within and between human groups.

NSF BCS-1719187, NSF BCS-1719140, RCUK/BBSRC grant BB/R01292X/1, NSF GRFP Grant No. DGE1255832.

The application of histomorphometry to puberty in the archaeological record

JESSICA AM. DOLDING-SMITH, ROSIE PITFIELD, CHRIS DETER and PATRICK MAHONEY

Human Osteology Lab, Skeletal Biology Research Centre, School of Anthropology & Conservation, University of Kent

Adolescence is marked by the onset of puberty whereby hormonal changes cause the body to mature into its reproductive capacity, adult body size, and behavioural maturity. Specific bony secondary sexual characteristics develop during the six stages of puberty: initiation, acceleration, peak height velocity, deceleration, maturity, and completion. Macroscopic skeletal indicators of puberty provide one way to estimate the stage of puberty attained at the time of death.

This study determines if underlying microscopic changes in bone growth are linked to the macroscopic skeletal stages of puberty. Age-at-death was reconstructed from dental formation for 40 juvenile skeletons from Blackgate, Newcastle (n=17), Fishergate Barbican, York (n=13), and St Gregory's Priory, Canterbury (n=10). Pubertal stage was estimated from the hamate hook, distal hand phalanges, distal radius, proximal ulna, iliac crest, cervical vertebrae, and mandibular canine root. Microscopic features of bone remodelling were measured from previously produced histological thin-sections of the anterior humerus mid-shaft (n=40) using CellSens analysis software. Secondary osteon density, size, and shape parameters were measured.

Analyses revealed a curvilinear relationship between puberty stage and bone remodelling. Osteon population density increases during the acceleration phase of puberty and then tapers off throughout subsequent puberty stages. This indicates that pubertal stage relates to bone remodelling, with the fastest remodelling being associated with the most rapid puberty stage. This is the first study to explore the possible link between puberty and microstructural bone growth.

This research was funded by the University of Kent Vice Chancellor's Research Scholarship and the Dora Harvey Memorial Research Scholarship.

Where the Wild Things Are...and How They Get There: Bonobo, chimpanzee and human use of visual spatial information navigating in virtual reality

FRANCINE L. DOLINS, CHARLES MENZEL, KARLINE JANMAAT, KEN SCHWELLER, MATTHIAS ALLRITZ and JOSEF CALL

Behavioral Sciences, University of Michigan

What kinds of spatial information do human and nonhumans attend to in their environment? How does this knowledge form the basis of intelligent spatial behaviors? We studied 5 bonobos (1 adolescent, 4 adults), 6 adult chimpanzees and 24 humans (children, adults in US, Congo), and compared their performance on virtual touch-screen navigation-foraging tasks (VR). Fruits (apples, bananas, grapes) were located in a simulated outdoor environment. Individual ordered preferences for these fruits were determined prior to testing. In Experiment 1, subjects were required to navigate to touch the fruits to receive rewards. These were auditory ("ding"), visual (piece of fruit glowed, then disappeared), and food for the nonhuman apes (they were given pieces of fruit corresponding to the virtual fruit; humans were given corresponding plastic fruits). Our goal was to compare these species' spatial strategies in localizing the fruits, and to determine whether their visits to fruit locations were in order of individual preference. In Experiment 2, we evaluated their ability to project spatial knowledge gained in virtual environments to solve spatial problems in the real world in a one-to-one correspondence (equivalence). Bonobos outperformed the chimpanzees, while children and adult humans from Congo and US differed from each other but were similar to bonobo patterns of performance. These results are discussed with attention to performance of young bonobos and human children and previous results using VR to test human, bonobo and chimpanzee navigation and spatial strategies. This cross-species, cross-cultural approach lends insight into the emergence of apes' complex cognitive abilities.

Funded by the Templeton World Charity Foundation and the University of Michigan-Dearborn.

Exploring *In Vivo* Linear Microcrack Prevalence By Sex and Age as a Variable of Skeletal Fragility

VICTORIA M DOMINGUEZ^{1,2} and AMANDA M AGNEW²

¹Department of Anthropology, Lehman College-CUNY, ²Skeletal Biology Research Laboratory, The Ohio State University

Experimental research has established that excessive loading generates skeletal microdamage, which reduces bone's fracture resistance. However, bone biologists take for granted that microdamage develops in the skeleton in response to the body's habitual loading, accumulating and repairing due to wear-and-tear. Some scholars suggest that as age increases, a mismatch arises between pace of damage accumulation and repair, so that older individuals have more microdamage and thus an increased susceptibility to fracture. Unfortunately, current understanding of *in vivo* rates of microdamage is limited. Thus, this study takes a preliminary look at *in vivo* linear microcrack prevalence in the ribs based on age and sex.

The sample consisted of the left or right 6th rib of 30 individuals (15 female, 15 male) ranging in age from 40–99 years (mean=70, sd=17). Ribs were assumed to undergo similar loading across individuals due to respiration. Samples were stained *en bloc* prior to slide preparation in order to distinguish *in vivo* from processing microdamage. Sections were assessed for linear microcracks (crack number, crack length), as well as area variables (cortical area, porosity) used to calculate microcrack areal densities for analysis (crack density, crack surface density). Independent samples *t*-tests indicated no sex differences in any variables examined. Linear regression demonstrated a statistically significant, but weak, relationship between crack density and age ($R^2=0.106$, $p=0.04$). Observed trends suggest further research is warranted, particularly looking at *in vivo* microdamage across skeletal elements and how interaction with other features of skeletal microstructure might play a role in variability.

Impediments to human bipedalism in tropical rainforests

NATHANIEL J. DOMINY¹ and VIVEK V. VENKATARAMAN²

¹Anthropology, Dartmouth College, ²Human Evolutionary Biology, Harvard

Recent advances in light detection and ranging (LiDAR) technologies have upset prevailing views on the structural uniformity of tropical rainforests. Internal structures (often conceptualized as strata or layers) are variably complex, and this complexity is known to affect environmental and biotic interactions. Habitat complexity will also affect the movement ecology of primates, but comparative studies of habitat complexities are

ABSTRACTS

few. Given that vegetation in the understory is expected to have large effects on the terrestrial movements of primates, including humans, we used ground-based LiDAR (LD90-3100HS first-return laser rangefinder operating at 890 nm and 1 kHz; Riegl, Horn, Austria) to compare the density of vegetation in the understories of 14 lowland rainforests spanning the tropics. We differentiated between rainforests occupied by foragers and horticulturalists because Diamond (1991; *Nature* 354:111-112) argued that foraging under denser conditions should favor smaller statures to economize the energetic costs of hip, knee, and ankle flexion. Thus, variation in the prevalence of understory vegetation may have contributed to the independent origins of the human pygmy phenotype. To test this hypothesis, we calculated vegetation area density in a cubic meter 1 m above the ground. We found that seven forager-occupied forests have denser understory conditions (mean: $0.39 \pm 0.27 \text{ m}^2 \text{ m}^{-3}$) than those of non-foragers ($n = 7$; mean: $0.12 \pm 0.07 \text{ m}^2 \text{ m}^{-3}$; Wilcoxon $Z = 2.81, P < 0.01$). This finding supports the hypothesis that dense understory vegetation is an impediment to efficient bipedalism and a potential selective pressure on human body size.

This research was supported by the David and Lucile Packard Foundation (Fellowship in Science and Engineering no. 2007-31754).

Día de Salud: A model for community-based outreach to improve health care access for low-income families

ALLISON C. DONA^{1,2}, GEETA EICK^{1,2}, ASHLEY HUYNH¹ and J. JOSH SNODGRASS^{1,2}

¹Anthropology, University of Oregon, ²Global Health Biomarker Lab, University of Oregon

The Oregon-based nonprofit organization Huerto de la Familia ("The Family Garden") and the Global Health Biomarker Laboratory at the University of Oregon come together each year to host Día de Salud, a free health fair for underserved Spanish-speaking individuals in Eugene, Oregon. Día de Salud aims to provide general health information through anthropometric measurements, functional measures (including spirometry), blood pressure, and finger-prick biomarkers (including blood glucose, lipids, hemoglobin, and hemoglobin A1c) as well as consultations with volunteer medical and dental professionals from the community. Each year, 20-25 undergraduate volunteers from the University of Oregon, most with at least some level of Spanish language skills, assist at the event through conducting intake interviews, collecting anthropometric measurements, obtaining capillary blood from finger prick, and providing child care for participant families. Since its creation in 2010, Día de Salud has served between 60 to 80 people every year. This poster describes Día de Salud, including its successes and challenges, in order to outline a model for community-based outreach to improve health

care access for low-income families. Although not a substitute for comprehensive primary health care, Día de Salud combines community outreach and anthropology to provide health care services to underserved populations.

Investigating patterns of growth disturbances in a Neolithic sample from Liguria (northwestern Italy, 4800-4400 BCE) from the analysis of enamel defects and diet

IRENE DORI^{1,2}, ELIZA ORELLANA GONZÁLEZ¹, GWENAËLLE GOUDE³, ALESSANDRA VARALLI⁴, JACOPO MOGGI-CECCHI² and VITALE S. SPARACELLO¹

¹UMR 5199 PACEA, University of Bordeaux, ²Department of Biology, Lab. of Anthropology, University of Florence, ³CNRS, Minist Culture, LAMPEA, Aix-en-Provence, Aix Marseille Univ., ⁴Department of Archaeology, Durham University

The demographic expansion associated with the Neolithic Transition appears to have been a consequence of increased female fertility, due to a reduced interbirth interval, which increased reproductive fitness despite high infant mortality. This implies a more rapid weaning process, which can expose the weanling to nutritional stress and infectious risks.

We explored these micro-evolutionary adaptations and life-history parameters in a chrono-culturally homogeneous Neolithic skeletal sample (Square Mouth Pottery, 4800-4400 cal BCE) from the Finalese area (Liguria, northwestern Italy; $n=12$). We jointly analyzed patterns in enamel growth disturbances (linear enamel hypoplasia, LEH) to explore early childhood stress, and diachronic dietary changes via isotopic ($\delta^{13}\text{C}$, $\delta^{15}\text{N}$) incremental dentine analysis ($n=2$). Based on evidence of a highly infectious local environment, we expected that the investment in immune defense with the cessation of breastfeeding would come as a cost to growth, resulting in a well-defined signal of developmental stress. Results indicate a statistically significant increase in enamel defects around 2.5-3 years, followed by a rapid decline. Isotopic data suggest the introduction of weaning foods by the first year, but also a rather long time for the reaching of the adult levels of $\delta^{15}\text{N}$. This suggests that maternal milk may have been supplemented well into the second year, as proposed for other Neolithic sites, and as observed ethnographically in areas with high pathogen load and limited nutritional resources. This may have been a strategy to maximize children immunity, although it may have been an unsuccessful strategy, given that all the individuals died before reaching adulthood.

ID: Marie Skłodowska-Curie grant agreement No. 752626; VSS: Programme, IdEx (University of Bordeaux) ANR-10-IDEX-03-02.

Impact of subsistence, latitude, and terrain on lower limb bone robusticity in a globally distributed skeletal sample

TABITHA DORSHORST and BRIGITTE HOLT
Department of Anthropology, University of Massachusetts

While well documented, the relationship between the mechanical influences of long-distance mobility and lower limb robusticity is complicated by the impacts of topography and body proportions. Femoral rigidity and shape indices have been shown to correlate with terrain and effective temperature. Furthermore, studies conflict as to whether the femur or the tibia reflect variability in activity patterns more clearly and consistently. We investigate the competing influences of mobility, terrain, and latitude in a large globally distributed, human skeletal sample spanning 28,000BP-1990AD. Relative strength (section modulus) and Ix/Iy shape index of midshaft femur and tibia are compared among three groups of varying mobility: Hunter-gatherer ($N=468$), Agricultural ($N=2421$), and Industrial/Mechanized ($N=306$). Local terrain is quantified as flat, hilly, or mountainous. Latitude is used to explore possibly confounding effects of climate on cross-sectional properties. Partial correlation analysis shows significant positive correlations between mobility and relative strength and shape index for males and females. Higher latitude groups exhibit significantly increased relative strength, but lower Ix/Iy ratios. The decrease in Ix/Iy results from significantly higher medio-lateral bending rigidity, reflecting wider pelvis. With latitude and mobility held constant, terrain also significantly correlates with relative femoral and tibial relative strength for both sexes, but interestingly not with shape. Tibial properties exhibit stronger relationships with mobility and terrain, but femoral shape correlates more strongly with latitude than tibial shape. Our data confirm the strong impact of terrestrial mobility on lower limb structure, and the need to account for the confounding effects of body breadth and topography.

In search of the Denisovans: biomolecular ways for the identification of new human fossils in the Eurasian archaeological record

KATERINA DOUKA^{1,2}, SAMANTHA BROWN¹, TOM HIGHAM², ANATOLY DEREVIANKO³ and MICHAEL SHUNKOV³

¹Department of Archaeology, Max Planck Institute for the Science of Human History, ²School of Archaeology, University of Oxford, ³Siberian Branch, Russian Academy of Sciences

Since the publication of genome sequences from Denisovans and Neanderthals, research into the evolutionary significance of processes such as large scale human migrations and interbreeding, has flourished. Yet the lack of well provenanced,

ABSTRACTS

reliably dated and genetically analyzed human remains from Late Pleistocene Asia, and especially the lack of Denisovans outside the unique eponymous locus, is noticeable.

In this talk, we will introduce an interdisciplinary project ("FINDER") that applies a combination of analytical techniques to identify, characterize and analyse new hominin remains from several sites in Eurasia with the aim of finding new Denisovan fossils. At the heart of the project lies an analytical technique called collagen peptide mass fingerprinting, or ZooMS. ZooMS is a fast and cheap technique that utilises the internal variation of bone collagen peptides to taxonomically classify a bone. The method has immense potential in identifying hominin bone remains from highly fragmentary bone assemblages. Here we apply this method to bones from several sites in North and SE Asia aiming to find new Denisovans and expand their geographic distribution further in space and time.

This project has received funding from the European Research Council (ERC) under the European Union's Horizon 2020 research and innovation programme under grant agreements ERC-2016-StG-715069-FINDER (to KD) and ERC-2012-AdG-324139-PalaeoChron (to TH).

Gorilla hindlimb muscle fiber phenotypes

DANIEL J. DOYLE¹, MEGAN HOLMES^{1,2}, DANIEL SCHMITT¹, ANGEL ZEININGER¹ and CHRISTINE E. WALL^{1,3}

¹Evolutionary Anthropology, Duke University, ²Physician's Assistant Program, Duke University School of Medicine, ³Duke Lemur Center, Duke University

Muscle fiber type may have undergone selection based on locomotor patterns in hominoids. O'Neill and colleagues recently proposed that humans have a slow, fatigue resistant, energy efficient (MHC-I) phenotype that differs from the fast (MHC-II) phenotype of chimpanzees (*Ptroglodytes*) and may have evolved concurrently with increased daily travel distance in early hominin bipeds. Large-bodied gorilla (*G.g.gorilla*) with a short daily travel distance allows us to test the relationship among hindlimb muscle fiber type, mass, and locomotion. If fiber phenotype reflects daily travel distance, the MHC-I phenotype should be human>chimpanzee>gorilla with chimpanzee and gorilla having >50% MHC-II. If body mass is a better predictor, the MHC-I phenotype should be gorilla>human>chimpanzee with gorilla and human having slower phenotypes.

Immunohistochemistry was performed on fresh frozen gorilla (n=1 adult female, 1 silverback) muscle from vastus lateralis, gastrocnemius, and biceps femoris to distinguish MHC-I, MHC-II and hybrid fibers. Proportion and percent cross-sectional area of muscle section (%CSA) were calculated for each fiber type and compared to published data for chimpanzees and humans.

For each muscle, fiber type proportion and %CSA for MHC-I is human>gorilla>chimpanzee. Overall, gorilla shows a fast phenotype and is very similar to chimpanzee. This supports the idea that humans are unusual in having a slow locomotor muscle phenotype. It also suggests that, contrary to the slow phenotype predicted by large body mass, gorilla has a fast fiber phenotype that is consistent with the dynamic force capabilities suggested by O'Neill and colleagues for chimpanzee.

Supported by NSF BCS-1517561 and BCS-1719743.

Markers of subtle activity variation? Enthesis bilateral asymmetry in humans

MICHELLE S.M. DRAPEAU¹ and OLIVIA A. DE CARVALHO²

¹Dept. of Anthropology, Université de Montréal, ²Departamento de Arqueologia, Campus de Laranjeiras, Universidade Federal de Sergipe (LABIARQ/DARQ/UFS), Brazil

Enthesis morphology is known to be determined by a number of factors, such as age and body size, while also being determined by muscle activity. As a consequence, activity-related changes are difficult to tease apart from these confounding factors. In order to control for the non-activity related influences that affect entheses morphology, we compare the right and left side of individuals. This is particularly interesting in humans because of the asymmetrical use of the upper limbs, individuals generally favor one upper limb over the other. More specifically, we tested whether limb preference, as measured from the asymmetry in cross-sectional geometry correlates with the asymmetry in entheses morphology.

Our sample consists of 14 Sadlermiut Inuit individuals (females=6, males=8) for which we visually assessed bilateral entheses morphology of upper and lower limb muscles and collected bilateral cross-sectional CT scans from the femur and humerus. Because of the non-continuous nature of entheses morphology scoring, non-parametric tests are used in all statistical analyses.

Our cross-sectional analyses show that, as expected, the Sadlermiut upper limbs are significantly asymmetric while the lower limbs are not. In the lower limb, there is no correlation between asymmetry of cross-sectional geometry and of entheses morphology, likely because the low level of lower limb asymmetry. However, in the upper limb, asymmetry of the cross-sectional geometry is positively correlated with some entheses markers, although not all. The correlation between upper-limb 'robusticity' and entheses development suggests that relatively subtle activity differences are enough to induce entheses changes.

This research was funded by the CNPq, Brazil (to OAdeC) and by the FQRSC, Canada (to MSMD).

Dental microwear texture analysis as a tool for discerning intra-population dietary patterns: Evidence from the Croatian Copper Age site of Potočani

JESSICA L. DROKE¹, JAMES C.M. AHERN^{1,2}, IVOR JANKOVIĆ^{1,2}, MARIO NOVAK², JACQUELINE BALEN³, HRVOJE POTREBICA⁴ and CHRISTOPHER W. SCHMIDT⁵

¹Anthropology, University of Wyoming, ²Anthropology, Institute for Anthropological Research - Zagreb, ³Archaeology, Faculty of Humanities and Social Sciences, University of Zagreb, ⁴Prehistoric Archaeology, Archaeological Museum in Zagreb, ⁵Anthropology, University of Indianapolis

Dental microwear texture analysis (DMTA) is a dietary reconstruction method typically used for interspecies comparisons. More recently, DMTA has been employed as a tool for discerning differences in human subsistence patterns, but its utility in detecting intra-population dietary variation has been little explored. This study utilized dental remains of 37 individuals from the Croatian Copper Age site of Potočani (cca 4100 BCE) to investigate dietary patterning according to age and sex within the population. Standard DMTA procedures were followed to observe phase II wear facets on the occlusal molar surfaces. The three texture variables, calculated using scale-sensitive fractal analysis software (Sfrax® and Toothfrax®), included complexity (Asfc), anisotropy (ePlsar), and textural fill volume (Tfv). As a whole, results indicate relatively high anisotropy values for the individuals from Potočani ($\bar{x}=0.0031$) signifying considerable consumption of fibrous, homogenous foods and consistent with the farming of domesticates. Complexity values for the population are also elevated ($\bar{x}=2.313$) suggesting a hard or gritty diet consistent with the exploitation of wild or seasonally available foods such as nuts or berries. Overall, DMTA signatures from Potočani indicate a diet rich in farmed domesticates along with substantial supplementation of wild resources. Further investigation into sex-based variation in diet indicate that adult males consumed a harder more heterogeneous diet than adult females who ate a softer more fibrous diet, while age-based analyses indicate that sub-adults show a moderately hard and fibrous diet. These analyses indicate that DMTA is an effective tool for discerning fine-scale dietary patterns within bioarchaeological populations.

Funding was provided by the Center for Global Studies, University of Wyoming to JLD and by the National Science Foundation (BCS 0922930) to CWS.

ABSTRACTS

A probable case of cranial osteopenia in aboriginal societies from northern Argentina

HILTON DRUBE^{1,2}, SUSANA MARTÍNEZ², ELINA SILVERA², SUSANA SALCEDA^{3,4} and GUILLERMO LAMENZA^{3,4}

¹Facultad de Ciencias Médicas, Universidad Nacional de Santiago del Estero, ²Facultad de Ciencias Exactas y Naturales, Universidad Nacional de Catamarca, ³Facultad de Ciencias Naturales y Museo, Universidad Nacional de La Plata, ⁴CONICET, Consejo Nacional de Investigaciones Científicas y Técnicas

Osteopenia is a pathological condition that involves a decrease in bone mineral density and consequently a disproportionate loss of bone mass. Such decrease in bone mineral density is the cause of symmetrical biparietal thinning or resorption in the human skull and its precise etiology is considered to be uncertain. This paper aims to present a case of cranial osteopenia which has caused the presence of biparietal thinning in an adult individual from an archaeological site in northern Argentina dated at the time of contact in the area. Age and sex examination and anthropometrical measurements were performed using standard techniques. Macroscopic evaluation was complemented with X-ray images. The affected skull belongs to a male individual of +50 years. Resorption affects symmetrically both parietals. Thinning in both bones extends from the upper temporal line up to 21 mm of the sagittal suture, covering a depressed surface located between the lateral eminence and the coronal suture. The affected areas form two significant concavities, appreciable in the superior and the lateral norms of the cranium. Both depressions on the skull exhibit diameters of 60 and 40 mm. Diploe and the outer and inner tables are of equal thickness. Cranial osteopenia, including bilateral resorption of parietal bones, is not a common finding in ancient skeletal material. The importance of the present study is to add a particular archaeological case in northern Argentina, and consequently in the southern cone of South America, to the geographic distribution of this rare condition in past populations of the world.

Funding support provided by FHCSys-UNSE, FCM-UNSE, FACEN-UNCa and FCNyM-UNLP.

Key questions and future directions: Integrating biomarkers to understand (trans) gender experience and health disparities

L. ZACHARY DUBOIS¹, ROBERT-PAUL JUSTER², JAMES GIBB³, TIAN WALKER¹ and SALLY I. POWERS⁴

¹Anthropology, University of Oregon, ²Psychiatry and Addiction, University of Montreal, ³Anthropology, University of Toronto, ⁴Psychological and Brain Sciences, University of Massachusetts Amherst

Transgender and gender diverse (TGD) people have become increasingly visible and access to transition-related care is rising, particularly for youth. Political backlash and entrenchment in a gender binary, however, continue to marginalize TGD people, increasing risk for stress-related health disparities. Nonetheless, research use of biomarkers among TGD people remains limited. The 2016 National Institute of Health recognition of sexual and gender minority people as a health disparities population increases available funding for much-needed research. In this review, we identify future directions in this emerging area and show that the use of minimally-invasive biomarker sampling enables essential health data to be collected from a population often excluded from research. Among sexual minorities (e.g. gay men) biomarkers have been successfully employed to understand health risks due to structural inequities, stigma, and minority stress. To date, however, only two studies have assessed TGD health by integrating biomarkers to understand pathways linking stigma and stress to: 1) health among transmasculine people and 2) health among HIV+ transgender women of color. We identify key areas for future research, discuss research challenges and possible solutions, and specify theoretical approaches useful in this endeavor. Future areas should integrate intersectional, life-history, and developmental approaches to investigate areas including: developmental trajectories and long-term effects of minority stress, the role of social support and close relationships in resilience, interactions among exogenously-administered sex-hormones and stress physiology, and aging. Biological anthropologists are well positioned to lead community-based biomarker research to address the needs of this marginalized and hard-to-reach population.

Implementing Nutritional Geometry to identify dietary constraints and strategies in the red-bellied lemur (*Eulemur rubriventer*)

AMANDA DU BOUR¹, JEAN-LUC RAHARISON^{2,3}, BRUNO RAMORASATA^{2,3}, JESSICA ROTHMAN⁴ and MITCHELL T. IRWIN^{1,2}

¹Department of Anthropology, Northern Illinois University, ²SADABE, Madagascar, Antananarivo, ³Department of Animal Biology, University of Antananarivo, ⁴Department of Anthropology, Hunter College

Nutritional Geometry is a modeling tool that considers how the mixture of nutrients influences health and disease rather than focusing on any one nutrient in particular. We explored the nutritional ecology and dietary strategies of the red-bellied lemur (*Eulemur rubriventer*); particularly considering the balance of macronutrients and whether protein is the nutritional driver for foraging choices (protein leverage). We recorded the plant parts and insects in a single female's

diet in the Ankadivory region, near Tsinjoarivo, Madagascar. Daytime follows were conducted for 30 days during the lean season; for six of these days plus six days in the abundant season, food intake during the 24-hour cycle was recorded. Diet items were analyzed for their compositions of protein, fat, nonstructural carbohydrates, and fiber; we quantified intakes of available protein and non-protein energy (carbohydrates and fat). The hypothesis that protein is the limiting macronutrient in *E. rubriventer* diets and drives foraging choices (i.e. was constant across seasons) was not supported. The study subject exceeded her recommended protein requirement (3.15-4.9 g of protein/day) in the lean season (5.07 g of protein/day) and the abundant season (8.76 g of protein/day); the protein: non-protein energy ratio varied three-fold across seasons. Finally, the 24-hour diet information revealed day-night differences, implying that, for cathemeral animals such as *E. rubriventer*, only looking at daytime diet consumption can lead to inaccurate diet profiles. This project provides information crucial for a more comprehensive understanding of food selection by *E. rubriventer*, and is important for both captive management and habitat protection.

Greenville Zoo Conservation Fund from the Greenville Zoo, Founders Grant from Northern Illinois University.

Geometric morphometric analyses of carpals and tarsals demonstrate differences in wild and captive baboon populations

MADELYNNE M. DUDAS

Department of Anthropology, University of Texas at Austin

Morphological studies favor wild specimens over captive specimens because captive environments often have different physical demands that developmentally impact skeletal anatomy. While these differences have been quantified in long bones and crania, little is known about the effect of rearing environment in carpals and tarsals. Quantifying the extent to which a captive environment impacts carpal and tarsal morphology helps clarify their range of phenotypic plasticity. In this study, three-dimensional geometric morphometric (3D GM) analyses of *Papio cynocephalus* carpals and tarsals from a wild and captive sample were performed to identify any significant shape differences between the two groups (n = 60) when size is controlled for. Digitized landmarks on the talus, medial cuneiform, capitate, scaphoid, tibia and radius were collected for each individual. It was predicted that shape differences would be associated with a lesser range of motion in the captive specimens due to the invariable hard surfaces of their enclosures and a broader range of motion in the wild specimens due to their substrate variability and grasping uses. The results indicate that there are statistically significant differences in shape

ABSTRACTS

between captive and wild samples, particularly in the capitate ($p < 0.001$). To address specific predictions about shape differences that were not met, other confounding factors (diet, genetics, disease, and maturation rate) were considered. Although there are shape differences revealed in this study, it is useful to perform these types of analyses to determine if aspects of the captive skeleton warrant inclusion in comparative studies in order to increase sample sizes.

The paleontological record of the *Australopithecus anamensis* site of Allia Bay, East Turkana

LAURENCE DUMOUCHEL

Center for the Advanced Study of Human Paleobiology, The George Washington University

Between 1995 and 1997, a team from the National Museums of Kenya led by Dr. Meave G. Leakey recovered 31 *Australopithecus anamensis* fossil remains from the Lonyumun Member of the Koobi Fora Formation at Allia Bay, locality 261-1. Detailed description and analyses of these hominin fossils were produced, in addition to primate remains from the same locality and carbon and oxygen isotope values from a subset of the fauna. Here, we identify and analyze the remaining vertebrate fossils, over 1,500 specimens.

The faunal composition of the macromammals from the Allia Bay assemblage ($n = 1,711$) differs significantly from that of the pencontemporaneous site of Kanapoi, West Turkana ($n = 1,950$) at the family-level ($p < 0.001$) despite substantial overlap in their faunal lists. Noteworthy differences include a larger proportion of carnivorous mammal fossils at Kanapoi, and a larger proportion of Hippopotamidae fossil remains at Allia Bay. Hominins are also proportionally less abundant at Allia Bay than at Kanapoi. In addition, our stable isotope analyses reveal that the distribution of carbon isotopic compositions of each taxon is generally more ^{13}C depleted at Allia Bay ($n = 114$) relative to the same taxon at Kanapoi ($n = 78$). This trend is particularly strong in tragelaphin and aepycerotin $\delta^{13}\text{C}$ values, suggesting important differences in use of C3 and C4 vegetation between these sites.

Our analyses allowed to broaden the range of known habitats for *Australopithecus anamensis* and demonstrate that these hominins were able to thrive in more mesic environments, like those found at Allia Bay.

Funded by the Leakey Foundation, Sigma Xi Grants-in-Aid of Research, Explorers Club Washington Group inc, Evolving Earth Foundation, Cosmos Club Foundation and the Lewis N. Cotlow Fund.

Reconstructing host immune status in acquired syphilis: a bioarchaeological and immunological approach

MEGAN E. DUNCANSON¹, MOLLY K. ZUCKERMAN², SHARON DEWITTE³ and FABIAN CRESPO¹

¹Anthropology, University of Louisville,

²Anthropology and Middle Eastern Cultures, Mississippi State University, ³Anthropology and Biology, University of South Carolina

Most immune responses against acquired syphilis's causal bacterium, *Treponema pallidum*, are determined by the host, not the pathogen; therefore, reconstructing each host's inflammatory response or phenotype (IP) is crucial to interpreting the disease's clinical manifestations, including skeletal lesions. Our study integrates experimental protocols with osteological analysis to explore the potential immunological interplay between systemic inflammatory responses against *T. pallidum* and other pathogens, such as *Porphyromonas gingivalis*, which is causal to periodontitis (PD), a commonly found local inflammatory reaction. We assessed established data on the presence/absence of PD in individuals with lesions suggestive or specific to syphilis ($n = 33$) and those without these lesions ($n = 111$) from post-Medieval St. Thomas Hospital and Lower St. Bride's cemeteries, London, UK. For the *in vitro* protocols, we exposed human peripheral blood mononuclear cells (PBMCs) to the immunomodulatory *T. pallidum* antigen Tp47 on day one; on day two, we exposed the same culture to *P. gingivalis*. The consequent expression of pro-inflammatory cytokines (TNF α , IFN γ , IL-1) was measured by ELISA. The osteological analysis revealed a higher frequency of PD in the pathological sample ($p = .04$; $p < .1$) than the control, especially in those with gummata (35%), representing a hyper-inflammatory response. The experimental results show that early exposure to Tp47 induces shifts in the expression of TNF α ; IFN γ ; IL-1 by the PBMCs. Together, these results suggest that an inflammatory interplay may be at work between *T. pallidum* and *P. gingivalis*, supporting the hypothesis that osteological lesions, specifically PD, could be used to reconstruct IP during syphilis infection.

Arboreal primate gait kinematics: Do wild data validate laboratory inferences?

NOAH T. DUNHAM¹, ALLISON MCNAMARA², BRIGITTE DEMES³, LAURA E. JOHNSON⁴, LIZA SHAPIRO² and JESSE W. YOUNG¹

¹Anatomy and Neurobiology, Northeast Ohio Medical University, ²Anthropology, University of Texas at Austin, ³Anatomical Sciences, Stony Brook University, ⁴Pathology and Anatomical Sciences, University of Missouri

Laboratory investigations have provided important insight into the functional underpinnings of primate locomotor performance; however, it is unclear to what extent gait patterns in the

laboratory reflect those of primates moving in natural settings. We filmed quadrupedal locomotor activity in eight platyrrhine species at the Tiputini Biodiversity Station, Ecuador, and three additional platyrrhine species at La Suerte Biological Field Station, Costa Rica, and also quantified the diameter and orientation of locomotor substrates using remote sensors ($N = 1,233$ strides). We compared overall arboreal quadrupedal gait kinematic patterns in free-ranging individuals to those of laboratory platyrrhine congeners. As expected, gait kinematics of free-ranging individuals were more variable than laboratory counterparts. Within the free-ranging dataset, *Ateles* and *Alouatta* increased limb phase on inclines ($p = 0.04$; $p = 0.002$, respectively), *Lagothrix* increased duty factors on inclines ($p = 0.002$), *Cebus* increased duty factors on declines ($p = 0.02$), and both *Saimiri* and *Saguinus* displayed an inverse relationship between limb phase and substrate diameter ($p = 0.05$; $p = 0.03$, respectively). This study confirms the preference for diagonal sequence gaits in free-ranging primates (i.e., 87.9% of all recorded symmetrical strides) and that in both settings primates tend to adjust gait patterns to promote security through longer contact times on non-horizontal substrates and increased limb phase on inclined substrates. We show that laboratory and field investigations of primate locomotion yield consistent patterns but that field studies can capture additional aspects of gait variability and flexibility in response to the increased substrate complexity of natural environments.

Research supported by the National Science Foundation Grants BCS-1640552 and BCS-1640453.

First metacarpal trabecular morphology: Implications for thumb use in great apes and *Australopithecus*

CHRISTOPHER J. DUNMORE¹, TRACY L. KIVELL^{1,3,4}, NICHOLAS B. STEPHENS^{2,3}, AMELINE BARDO¹, JEAN-JACQUES HUBLIN³ and MATTHEW M. SKINNER^{1,3,4}

¹Skeletal Biology Research Centre, School of Anthropology and Conservation, University of Kent, ²Department of Anthropology, Pennsylvania State University, ³Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology, ⁴Evolutionary Studies Institute, University of the Witwatersrand

Fossil hominin thumb morphology is often compared to that of extant hominids, for which we have observed manual behaviors, to infer the locomotor and manipulative capabilities of extinct hominins. Preserved internal trabecular morphology can provide evidence for fossil hominin thumb use since it remodels in response to loading experienced during life. Here we use micro-CT data to analyze trabecular architecture of the first metacarpal in extant great apes ($n = 41$), early and recent *Homo sapiens* ($n = 13$), *Australopithecus africanus* (StW 418),

ABSTRACTS

Australopithecus sediba (MH2), *Paranthropus/early Homo* (SK 84 and SKX 5020) and *Homo neanderthalensis* (n=3). We apply a geometric morphometric approach to the subarticular regions of 'whole-epiphysis' trabecular models, to test for significant differences in relative trabecular bone volume fraction and degree of anisotropy between species. Results indicate that *H. sapiens* have significantly different first metacarpal trabecular architecture from that of other extant hominids, consistent with abduction of the thumb during forceful pad-to-pad precision grips. Great ape trabecular architecture is generally consistent with a habitually adducted thumb, used in pad-to-side and non-precision grips. Though, Neanderthal and MH2 trabecular morphology generally appears more similar to recent humans than extant apes, StW 418 demonstrates a more mosaic morphology, while SK 84 and SKX 5020 diverge further from the human pattern. These findings offer further insight into the manual behaviours of fossil hominins, as well as the adaptive shift from locomotor to manipulative hand use that occurred in our evolutionary history.

This research was supported by European Research Council Starting Grant #336301, The Fyssen Foundation, and the Max Planck Society.

Preliminary results from a recently discovered Holocene burial site in Northern Laos, Tam Pa Ping

TYLER E. DUNN^{1,2}, ALEXANDRA J. ZACHWIEJA², LAURA L. SHACKELFORD³, NGUYEN THI MAI HUONG³, PHILIPPE DURINGER⁴, JEAN-LUC PONCHE⁴, CAROLINE AICHHOLZEL⁴, QUENTIN BOESCH⁴, ELISE PATOLE-EDOUMBA⁵, ANNE-MARIE BACON⁶, DAOVEE SIHANAM⁷, PHONEPHANH SICHANTHONGTIP⁷, THONGSA SAYAVONGKHAMDY⁷ and FABRICE DEMETER⁸

¹Department of Medical Education, Creighton University School of Medicine, ²Anthropology Department, University of Illinois at Urbana-Champaign, ³Institute of Archaeology, Vietnam Academy of Social Sciences, ⁴Ecole et Observatoire des Sciences de la Terre, Universite de Strasbourg, ⁵Museum Histoire Naturelle de la Rochelle, ⁶French National Center for Scientific Research, ⁷Ministry of Information and Culture of Laos, ⁸Musee de l'Homme, Paris.

Since 2003, archaeological research has been resumed in the Annamite Mountains of Huà Pan Province, northern Laos, with ongoing excavations at two modern human fossil-bearing sites, Tam Hang and Tam Pa Ling. These sites date to the terminal and Late Pleistocene. In December 2016, another cave site was discovered while conducting a geologic survey of the region, Tam Pa Ping. This new site is located on the Pa Hang Mountain within 100 m of these previously identified sites. Tam Pa Ping contained a single burial dating to 2996 +/- 47 years BP with associated grave goods. Osteological analysis suggests

this individual is an adult male, approximately 30 years old, with perimortem trauma to the thorax. There is evidence of cultural continuity in both burial practice and antemortem body modification between this individual and those buried at Tam Hang. There are stylistic similarities in the grave goods at Tam Pa Ping and Tam Hang, and both sites show intentional use of a cave as a primary burial location. Similarly, individuals from both sites show evidence that their anterior maxillary incisors were removed before death as indicated by antemortem alveolar resorption. This individual has an average measured $\delta^{13}C_{app}$ of -7.13‰, an indication of more C4 than C3 vegetation consumption. This find suggests that this area was occupied, either continuously or sporadically, through several glacial events from the earliest securely dated evidence of modern human occupation in Southeast Asia to the current period and contributes to the limited skeletal samples in the region

Quantifying growth pulses across the first year of life in rural Gambian infants

JAMES DYKES¹, JASON A. CUMMINGS², DANIEL J. NAUMENKO^{1,3}, G. KESLER O'CONNOR⁴, ZOFIA STANLEY⁴, NABEEL AFFARA⁵, DAVID B. DUNGER⁶, KEN K. ONG^{6,7}, ANDREW M. PRENTICE⁸, SOPHIE E. MOORE^{8,9} and ROBIN M. BERNSTEIN^{1,3}

¹Institute of Behavioral Science, University of Colorado Boulder, ²Department of Computer Science, University of Colorado Boulder, ³Department of Anthropology, University of Colorado Boulder, ⁴Department of Applied Mathematics, University of Colorado Boulder, ⁵Department of Pathology, University of Cambridge, ⁶Department of Paediatrics, University of Cambridge School of Clinical Medicine, ⁷MRC Epidemiology Unit, University of Cambridge School of Clinical Medicine, ⁸MRC Unit The Gambia, London School of Hygiene and Tropical Medicine, ⁹Department of Women and Children's Health, King's College London

Growth pulses, or so-called 'mini growth spurts' are short term growth events, and have been previously modeled using an approach that characterizes the presence or absence of a Gompertz event in a series of four consecutive measurements. Here, we present a modified Gompertz detection method applied to detailed longitudinal growth data from infants in rural Gambia enrolled in the HERO-G (Hormonal and Epigenetic Regulators of Growth) study. Weight and crown-heel length were measured every other day between day 9 and day 365 of postnatal life. Growth data were considered in chunks of four consecutive data points (or ~one week), and only those with no missing data or outliers were considered for fitting (N=69 (F=36, M=33)). We used a self-starting function that obtains starting values for non-linear least squares regression (SSGompertz from the growthmodels package in R), then attempts a Gompertz fit within each chunk. If successful, the algorithm starts again

on the next data point after the successfully fit event. If an event is not detected, the algorithm re-starts on the second data point of the chunk that resulted in failed detection, thus scanning every possible set of four consecutive points. Applying this method to our growth data reveals significant variation in the number and pattern of detected Gompertz events among individual infants. Specifically, greater total numbers of Gompertz events and longer consecutive runs of Gompertz events within the first 100-150 days of postnatal life are associated with positive growth outcomes at one year.

Funded by the Bill and Melinda Gates Foundation (OPP1066932)

Evaluating the Significance of Hominin Femoral Variation

LESLEY H. EASON
Anthropology, University of Arkansas

Delineating species in the hominin fossil record relies on reference to the pattern and magnitude of variation among extant primates. Fossils are generally attributed to the same species when the magnitude of morphometric variation of a fossil sample is subsumed by that of extant reference species. With few exceptions, recent research has recognized that the magnitude of cranial and post-cranial variation among hominin samples is exceeded by that of extant reference species. Furthermore, there is no system-wide pattern of variation across reference samples with regard to phylogeny, geographic range, body size, habitat or diet (Harmon and Plavcan, 2011; Eason, 2015; Plavcan, 2017; Eason, 2018).

Using univariate, bivariate, and multivariate techniques, this study expands on previous research by comparing the pattern and magnitude of morphometric variation of the proximal and distal femur across thirty-three anthropoid species. Traditional linear data and 3D geometric morphometric data are compared for 335 specimens comprising platyrrhines, colobines, cercopithecines, hylobatids, and great apes from 25 extant taxa. Morphometric variables for 54 *Australopithecus* and *Homo* fossils are compared to extant reference taxa. As with previous studies, results reveal no system-wide pattern of morphometric variation with regard to phylogeny, geographic range, body size, habitat, or diet. More importantly, the entire magnitude of morphometric variation among hominin fossils is subsumed by that of single-sex subsamples of extant reference species. These results demonstrate that morphometric variation of the femur is not useful for delineating hominin taxa, thus interspecific behavioral differences among hominins are difficult to interpret with reference to such variation.

ABSTRACTS

Fluctuating sea levels in Australomelanesia and some shifting hypotheses about human population of Flores, Indonesia

ROBERT B. ECKHARDT¹, SAKDAPONG CHAVANAVES¹, KENNETH J. HSÜ³ and MACIEJ HENNEBERG⁴

¹Laboratory for the Comparative Study of Morphology, Mechanics, and Molecules, Department of Kinesiology, Pennsylvania State University, ²Laboratory for the Comparative Study of Morphology, Mechanics, and Molecules, Department of Kinesiology, Pennsylvania State University, ³Department of Geosciences, University of Chinese Academy of Sciences, Beijing, China, ⁴Anthropology and Comparative Anatomy, University of Adelaide

Since discovery of human bones in Liang Bua Cave, Flores (Brown et al., 2004; Morwood, et al., 2004) supporters of "Homo floresiensis" have maintained validity of initial key attributes (endocranial volume as small as 380 ml, stature of 1.06 m, absent external chin) despite subsequent corrections: endocranial volume of 430 ml (Jacob, et al., 2007), stature >1.25 m (Eckhardt et al., 2014), absence of external chin and presence of retromolar sulcus in undoubted *Homo sapiens* (Eckhardt, et al., 2015). Hypothetical taxon supporters argue that island isolation was an essential explanatory element for defining phenotypic features (Baab & McNulty, 2009), with Flores having been reached only once. The collateral view of steady body size diminution on Flores since supposed single colonization has been falsified (Brumm, et al., 2016); if anything, body size has increased through time on the island, though recent genetic data (Tucci, et al., 2018) cast serious doubt on single population continuity and evidence for a new species. Our hypothesis (Jacob, et al., 2007) remains that numerous sea level fluctuations over time make it likely that the island was colonized by humans multiple times, with only the archetypical LB1 specimen (62/100 total sample bones, including the only known skull) being a developmentally abnormal individual. Here to the already long list of LB1 abnormalities we document that in dimensions of M¹ interdental width (28 mm), palatal skeletal coronal width (51 mm) and palatal coronal height (14.5 mm), LB1 falls within the Down syndrome range and outside that of normal patients.

Health Outcomes Associated with Higher Allostatic Load in Zoo-Housed Western Lowland Gorillas (*Gorilla gorilla gorilla*)

ASHLEY N. EDES^{1,2}, BARBARA A. WOLFE³ and DOUGLAS E. CREWS^{2,4}

¹Endocrinology Laboratory, Smithsonian Conservation Biology Institute, ²Department of Anthropology, The Ohio State University, ³Department of Veterinary Preventive Medicine, The Ohio State University, ⁴College of Public Health, The Ohio State University

As it is in humans, the number one cause of death for zoo-housed great apes is cardiovascular disease (CVD). The development of CVD and other chronic conditions is likely mediated through stress-induced physiological dysregulation, or allostatic load (AL). Multi-system scales for estimating allostatic load, or allostatic load indices (ALIs), have been developed in humans to predict risk of poor future health outcomes. ALIs are multi-system composites of biomarkers from the metabolic, neuroendocrine, cardiovascular, and immune systems. Applied only to humans for two decades, we recently developed ALIs for gorillas. Continuing this previous research, we have now analyzed 69 different ALIs using various biomarkers and methods. Synthesizing these models, we developed a proposed baseline ALI with seven biomarkers and examined associations with markers of cardiovascular health (e.g., cholesterol, triglycerides), presence or absence of chronic degenerative condition, and mortality risk in gorillas from three zoos (n=63). AL ranged from 0-6 (=1.84, SD=1.71). AL was positively associated with triglycerides (linear regression, p=0.004, R²=0.211), but not cholesterol (linear regression, p=0.797, R²=-0.121). Gorillas with at least one chronic degenerative condition had two-fold higher AL (t-test, p=0.003). Each unit increase in allostatic load was associated with a 44% increase in mortality risk (odds ratio, p=0.029, OR=1.438, 95% CI=1.038-1.991). This research demonstrates AL is associated with indicators of cardiovascular risk, the presence of chronic conditions, and mortality risk. Given the number of models tested, this work also provides a foundation for future studies on the long-term consequences of physiological dysregulation on health and longevity in great apes.

This work was supported by the Columbus Zoo and Aquarium and the Department of Anthropology at The Ohio State University.

NMDID: A new research resource for biological anthropology

HEATHER J.H. EDGAR¹ and SHAMSI R. DANESHVARI BERRY²

¹Anthropology, Office of the Medical Investigator, University of New Mexico, ²Health Informatics and Information Management, University of Mississippi

The New Mexico Decedent Image Database (NMDID) is a free-access, searchable dataset of whole-body decedent CT scans and associated metadata. The development of this database provides opportunities to address research challenges previously impossible. Applications include anatomy, pathology, growth and development, biomechanics, forensic anthropology and medicine, public health and other fields. The database is available at NMDID.UNM.EDU.

The sample includes 15,249 individuals who died 2010-2017, approximately 11% of deaths in New Mexico. There is no decomposition detectable

77% of the scans. Two-thirds of the sample were male; one-third were Hispanic/Latino; 872 were aged 1-18; 299 were under 1-year old at death. Natural causes of death account for 5,506 individuals; the remainder include deaths due to accident, suicide, and homicide. Each individual is described by extensive associated descriptive data that derives from the death investigation and autopsy records as well as telephone interviews with next of kin. Information available varies greatly among individual, but can include education, occupations, habitual activities, number of children, country of origin for decedent, parents, and grandparents, health history, medications, socioeconomic status, and more. The metadata alone is an important new source for research.

Each CT dataset consists of two sets of images, one optimized for displaying soft tissue and one optimized for displaying bone, totaling 7GB of information per individual. Each image set consists of approximately 12,000 image slices, each with high resolution and thickness of 1mm, with 0.5mm overlap. The resulting database provides over 85TB of images and documentation for research and education.

Funded by National Institute of Justice 2016-DN-BX-0144. Statements made are solely the responsibility of the authors.

Age and pathology-related changes in neuron density in the chimpanzee cortex

MELISSA K. EDLER^{1,2}, EMILY L. MUNGER², PATRICK R. HOF^{3,4}, WILLIAM D. HOPKINS^{5,6}, JOHN J. ELY⁷, JOSEPH M. ERWIN⁸, RICHARD S. MEINDL⁹, ELLIOTT J. MUFSON¹⁰, CHET C. SHERWOOD⁸ and MARY ANN RAGHANT^{1,9}

¹Pharmaceutical Sciences, Northeast Ohio Medical University, ²School of Biomedical Sciences, Kent State University, ³Fishberg Department of Neuroscience, Ronald M. Loeb Center for Alzheimer's Disease, and Friedman Brain Institute, Icahn School of Medicine at Mount Sinai, ⁴New York Consortium for Evolutionary Primatology, ⁵Division of Developmental and Cognitive Neuroscience, Yerkes National Primate Research Center, ⁶Neuroscience Institute, Georgia State University, ⁷MAEBIOS, ⁸Department of Anthropology and Center for the Advanced Study of Human Paleobiology, The George Washington University, ⁹Department of Anthropology, Kent State University, ¹⁰Departments of Neurobiology and Neurology, Barrow Neurological Institute

In the absence of disease, aging in humans is accompanied by gradual volumetric atrophy of several brain regions and cognitive impairment, but an absence of significant neuronal loss. Although nonhuman primates have mild cognitive deficits, they lack neuron death and cortical atrophy with aging. Conversely, human pathologic age-related conditions, such as Alzheimer's disease (AD), display extensive neocortical and hippocampal neuronal loss and severe cognitive decline. While humans are considered uniquely

ABSTRACTS

susceptible to age-associated neurological disorders, recent studies have revealed AD-like plaques and vasculature containing amyloid-beta ($A\beta$) and tau-related neurofibrillary tangles in chimpanzees and other mammalian species. In this analysis, we investigated the effect of age and AD-like pathology on regional neuron and glia densities in a sample of postmortem chimpanzee brains ($n = 29$, 12-62 years). Utilizing $A\beta$ and tau data previously collected in these apes, we employed stereological methods to quantify neuron density, glia density, and glia/neuron ratio in the prefrontal cortex (PFC), middle temporal gyrus (MTG), entorhinal cortex, and hippocampal subfields CA1 and CA3 from Nissl-stained sections. Aging was associated with decreased CA1 and CA3 neuron densities and MTG glia/neuron ratio (CA1: $R^2 = 0.18$; CA3: $R^2 = 0.20$; MTG: $R^2 = 0.17$, p 's ≤ 0.02). Additionally, increased volume of $A\beta_{42}$ -containing vessels correlated with reduced MTG neuron density ($R^2 = 0.23$, $p \leq 0.04$). These data suggest that both aging and $A\beta$ pathology contribute to neuronal loss in chimpanzees, which appears to differ from normal aging and AD in humans.

NSF (BCS-1316829, MAR), NIH (NS042867, NS073134, NS092988, WDH, CCS; AG017802, JJE; AG014308, JME; AG005138, PRH; P01AG014449, AG043375, EJM), James S. McDonnell Foundation (220020293, CCS), Sigma Xi, KSU RC and GSS

Dental Microwear Texture Analysis of Archaic Period Groups in Indiana and Kentucky

ERIN EDWARDS, ALEXANDRIA MCDANIEL, CHRISTOPHER SCHMIDT and CHRISTOPHER MOORE

Anthropology, University of Indianapolis

Dental microwear texture analysis (DMTA) is the study of microscopic wear on teeth expressed as dental surface relief at submicron scales. DMTA is applied to Phase II facets on first and second molars in order to compare diets of pre-contact humans from the US eastern woodlands. The current study addresses inter-spatial dietary variation in 103 adults from Archaic sites in Indiana (12FI73, Bluegrass, Kramer, Meyer) and Kentucky (Carlston Annis, Barrett, Butterfield, Indian Knoll, Ward). Dental replicas were analyzed with a white-light confocal profiler at a magnification of 100X. Data were leveled and cleaned and then imported into scale-sensitive fractal analysis software, Toothfrax® and Sfrax®, for study of the texture variables: complexity and anisotropy. Our results found statistically significant differences ($df = 6$, $F=2.267$, $p = .044$, partial $\eta^2 = 0.135$) for complexity between Butterfield (mean = 1.50) and the other Kentucky sites (mean: Barrett 1.04; Carlston Annis, 1.01; Indian Knoll, 1.12). No other differences were found. This

study indicates a statistically significant variation in dietary hardness and is consistent with paleobotanical syntheses that identify Archaic diets as diverse and situationally varied.

Complex Clavicles: A novel method for landmark collection on structures lacking clearly defined features

DANIEL E. EHRLICH¹, BIREN A. PATEL² and DAVID J. GREEN^{1,3}

¹Department of Anatomy, Midwestern University, ²Department of Integrative Anatomical Sciences, University of Southern California, Keck School of Medicine, ³Department of Anatomy, Campbell University School of Osteopathic Medicine

Hominoid clavicles exhibit torsion and a sinuous curvature in three dimensions. However, a limited number of homologous anatomical landmarks forces researchers to rely on linear and angular measures in predefined, two-dimensional planes. Such approaches are hampered by selection bias, which may under-represent the true extent of variation. Here, we present a novel method for evaluating clavicle shape that minimizes the subjectivity of landmark placement and clavicle orientation.

Using either surface or CT scan data, a standardized, objective orientation is first established based on the principal axis of the bone. Next, landmark coordinates (including centroid, equally-spaced semi-landmarks, or curvature maxima) are derived from a series of cross-sectional slices. These points effectively create a series of homologous semi-landmark contours or point clouds that may be analyzed using standard geometric morphometric methods.

We demonstrate the utility of this approach on a subsample of human and African ape clavicles, using contour curves derived from the centroid, anterior, posterior, superior, and inferior points of 100 cross-sectional slices. A principal components analysis of Procrustes-aligned coordinates clearly distinguished taxa across the first three PC axes. Eigenvector loadings of landmarks highlight patterns of distinct morphology for each PC, including mid-shaft curvature (PC1) as well as more subtle deflections of the sternal and acromial ends (subsequent PCs). This method removes much of the subjectivity involved in landmark definition and placement, while achieving high coverage and sensitivity to shape change. Further, it can be easily applied to other structures with similarly complex morphology as well as incomplete fossil material.

Funding for this study was provided by Midwestern University.

After Theranos: Next-generation biomarkers and technologies

GEETA N. EICK and J. JOSH SNODGRASS
Anthropology, University of Oregon

What can a drop of blood really do? According to the now-defunct health start-up Theranos, provide results for over 200 analytes within minutes! Although this claim was found to be false, and founder Elizabeth Holmes faces criminal charges, the hundreds of millions of dollars of investment Theranos attracted speaks to the huge demand for finger-prick diagnostics. Start-ups that were developing proprietary technologies in the shadow of Theranos have now been exposed to the full glare of skepticism left in the wake of its collapse, which can only benefit science, as the emphasis has shifted to transparency of technology and clinical trials. Because the biomarkers of greatest interest clinically are often those present in the lowest concentrations in blood (e.g., interleukin-6), which is exacerbated when sampling only a few drops of capillary blood, novel assay technologies are of paramount importance. In this poster, we review the potential and pitfalls of technologies currently under development, such as antibody-coated magnetic particles, viscoelastic focusing, vibrational spectroscopy, nanofluidic biosensors, and multiplexed nanostrips. The huge drive to revolutionize the antiquated blood-diagnostics industry with a focus on microsampling is likely to benefit biological anthropologists tremendously. However, this optimism should be tempered by the tradeoff between the number of analytes assessed and cost, the focus on biomarkers of clinical interest, and the unfeasibility of developing next-generation assays in most biological anthropological laboratories. Nevertheless, the ability to obtain results in field settings from a few drops of blood within minutes has the potential to revolutionize biological anthropological research.

NSF BCS-1638786 and University of Oregon

Paternal age at conception effect on offspring telomere length as a potential adaptive intergenerational signaling mechanism: testing of transmission across four generations in the Philippines

DAN T.A. EISENBERG^{1,2}, NANETTE R. LEE^{3,4}, PETER H. REJ¹, M. GEOFFREY HAYES^{5,6,7} and CHRISTOPHER W. KUZAWA^{7,8}

¹Department of Anthropology, University of Washington, ²Center for Studies in Demography and Ecology, University of Washington, ³USC-Office of Population Studies Foundation, Inc., University of San Carlos, Cebu City, Philippines, ⁴Department of Anthropology, Sociology and History, University of San Carlos, Cebu City, Philippines, ⁵Division of Endocrinology, Metabolism and Molecular Medicine, Department of Medicine, Northwestern University Feinberg School of Medicine, ⁶Center for Genetic Medicine, Northwestern University Feinberg School of Medicine, ⁷Department of

ABSTRACTS

Anthropology, Northwestern University, ⁹Institute for Policy Research, Northwestern University

Telomeres are repeating non-coding DNA sequences at chromosome ends. Telomere length (TL) is of growing interest because of its potential role in senescence and life history allocations. In particular, TL declines with age in most tissues, and shorter TL is thought to contribute to accelerated senescence. Although age-related shortening of TL occurs in most tissues, TL increases with age in sperm. Correspondingly, older paternal age at conception (PAC) leads to the inheritance of longer TL in offspring. We have hypothesized that the PAC effect on TL persists across multiple generations, and thereby is a unique form of transgenerational genetic plasticity that increases expenditures on somatic maintenance as average age at reproduction is delayed within a lineage. By being transmitted across multiple generations, the PAC effect may effectively convey a weighted average signal of reproductive ages of recent male ancestors. Prior work of ours in the Philippines demonstrated a persistent, additive effect of PAC across two offspring generations, but only among paternal grandfathers (n=234) and not maternal grandfathers. Here we use an expanded dataset to link TL to PAC across four generations. We find the expected positive PAC effect on TL (n=3,282; p<0.001) and grandpaternal age effect (n=2,913; p<0.05)—equally among maternal and paternal grandfathers. Possibly due to limited statistical power, we fail to find significant great-grandpaternal or great-great-grandpaternal age effects (ns=1,278 and 32; ps>0.52). These results are consistent with the PAC effect persisting across generations and having a potential intergenerational signaling effect.

Funding from NSF (BCS-1519110 and BCS-0962282), the Wenner-Gren Foundation (Gr. 8111), and NIH (TW05596, DK078150, RR20649, ES10126, and DK056350).

EMPHASIS: Environmental Mismatch in Primates and Humans, Anthropogenic Impacts and Settings Survey

ANDREA R. ELLER¹, STEPHANIE CANINGTON², RITA M. AUSTIN^{3,4}, COURTNEY A. HOFMAN^{3,4} and SABRINA B. SHOLTS¹

¹Anthropology, Smithsonian Institute National Museum of Natural History, ²Center for Functional Anatomy and Evolution, Johns Hopkins University, ³Anthropology, University of Oklahoma, ⁴Laboratories of Molecular Anthropology and Microbiome Research, University of Oklahoma

Environmental mismatches, where advantageous traits evolved in one environment are disadvantageous in another, create trade-offs in health profiles which may have evolutionary implications. To investigate the influence of environmental mismatches, the EMPHASIS project documents health markers in human and nonhuman primate crania associated with a

range of anthropogenic environments. Individuals with known demographic information are scored for skeletal pathology, dental calculus, and developmental stage. To distinguish managed (captive) spaces from wild ones, two scales are applied to each nonhuman primate individual: a life history scale, indicating when (if ever) an individual entered human management, and an environmental conditions scale, indicating the probable ecological conditions within that locale. EMPHASIS has to date surveyed 2181 individuals, including 1104 nonhuman primates comprising all hominoids and macaques at the NMNH. Among apes, bony pathologies presented in 30% of wild-shot specimens and 54% of captives; among macaques, pathologies presented in 22% of wild-shot and 19% of captives. Chi-square tests indicate there is a significant correlation between pathologies and environmental condition among apes (n=452; p=0.032, a=0.05), but not macaques (n=652; p=0.875, a=0.05). Dental calculus presented in 42% of the wild-shot apes, and 57% of captives; results for this chi-square did not indicate a significant correlation between calculus and environment (n=432; p=0.411, a=0.05). Among macaques, dental calculus was found to be significantly correlated with environmental condition (n=652; p=0.000, a=0.05) and presented in only 16% of wild-shot specimens but 61% of captives. Ongoing EMPHASIS research explores why there are apparent differences in captive health profiles between primate taxa.

Flexible grouping patterns of lowland woolly monkeys (*Lagothrix lagotricha poeppigii*): evidence of a multilevel society in a New World primate?

KELSEY M. ELLIS^{1,2}, LAURA ABONDANO¹ and ANTHONY DI FIORE¹

¹Department of Anthropology, University of Texas at Austin, ²Department of Anthropology, Miami University

The ability to accurately characterize how association patterns among conspecifics vary over time and space is critical in evolutionary studies of behavior, given that this aspect of social structure directly influences individuals' opportunities for mate choice and cooperation, the intensity of competition over resources, and the transmission of knowledge and disease within a population. We explored the association patterns and emergent social structure of woolly monkeys living in a primary tropical forest in lowland Ecuador using social network analysis. We constructed association networks for 52 adults and subadults from four neighboring groups based on records of party composition (N=8,302) and close spatial proximity (< 5m, N=20,581) collected during focal animal follows over two four-month periods. Within groups, the degree of substructuring seen based on party-level associations varied with group size, with larger groups exhibiting

greater modularity than smaller groups, likely due to their higher rates of group fissioning. For all social groups, network modularity scores were even higher when close proximity association indices were used, suggesting that animals typically found in the same parties may further associate preferentially with particular others. Peaceful associations of animals from more than one social group were not uncommon, occurring every ~3-20 days and lasting, on average, ~154 mins (range: 15-mins to 2-days). While the clusters revealed through network analysis often contained animals of both sexes, there was no evidence that social groups were made up of aggregations of recognizable one-male units, as is typical of other primates living in tiered, multi-level societies.

Funded by NSF BCS-1540403, the Leakey and Wenner-Gren Foundations, and the National Geographic Society/Waite Grants Program.

Urbanizing Childhood: The Children of the Spring Street Presbyterian Church and the Changing Landscape of Lower Manhattan

MEREDITH AB. ELLIS

Anthropology, Florida Atlantic University

This presentation will look at the skeletal and historical data for subadults, birth to 14.5 years of age (MNI=70), buried at the Spring Street Presbyterian Church in lower Manhattan between 1820 and 1850. It will consider how the forces of urbanization in New York City are reflected in their life histories. In particular, this presentation will examine urban forces in the 19th century—disease outbreaks, urban growth, environmental pollution, and movements of people—as structuring forces in childhood experience. These forces will be presented in conjunction with disease rates recorded in the bone: 52% of the subadults have rickets, 71% of the infants have scurvy and 22% have nonspecific cranial lesions, and 8% of subadults have periostitis. In addition, there are 6 interesting cases of trauma. In order to further contextualize these health markers, data from the 399 death records for children's burials at the site will be presented alongside the skeletal data. Correlations between symptoms recorded in the death records—diarrheas, inflammations, swellings, convulsions—will also be connected to the social conditions of the city. These lived experiences are hallmarks of urbanization, and reflect the poor quality food, decreasing quality of living conditions, and increasing instances of infectious disease endemic in the first half of the 19th century in Manhattan. The subadult remains clearly highlight for us how urbanization, a social, environmental, political and economic system, affects biology and experiences for growing bodies.

ABSTRACTS

Foraging in a landscape of fear: chacma baboons (*Papio hamadryas ursinus*) in the anthropogenic habitats of Hemel-en-Aarde Valley, South Africa

AMANDA L. ELLWANGER^{1,2} and JOANNA E. LAMBERT³

¹Department of Anthropology, University of Texas at San Antonio, ²Department of Cultural and Behavioral Sciences, Georgia State University Perimeter College, ³Program in Environmental Science and Department of Ecology and Evolutionary Biology, University of Colorado Boulder

Prey behavior is shaped by actual predation and perceived predation threat. Though consideration of predation as a selective pressure has a long history in primate studies, evaluation of how perceived risk impacts habitat use has received considerably less attention. For chacma baboons (*Papio hamadryas ursinus*) in Hemel-en-Aarde Valley, South Africa, fear is primarily structured by the presence of humans and leopards (*Panthera pardus melanotica*). We evaluate how baboons navigate a so-called landscape of fear in habitats varying in anthropogenic conversion, food availability, and predation risk. We hypothesized that (1) if humans present a greater perceived risk than leopards – and hence a greater role in structuring the fear landscape – then baboons would be more vigilant in open and anthropogenic habitats and that (2) if risky anthropogenic habitats provide high-food rewards, then baboons would prioritize feeding over risk mitigation (i.e., avoidance) and other activities in these habitats. We collected data (June 2016–April 2017) on behavior (805hrs), habitat type, visibility, nearest refuge, and food availability using 10-minute focal follows, 30-minute scans, and phenological sampling. A one-way ANOVA revealed significant differences in vigilance rate among habitats ($F=2.695$, $p=0.013$). Two-way ANOVAs indicated that habitat use is affected by season ($F=62.78$, $p<0.001$) and animals behave differently in different habitats ($F=8.464$, $p<0.001$). Baboons prioritized feeding in food-rich, risky habitats (identified by vigilance rate). Results partially support our hypotheses and demonstrate that differentially-converted anthropogenic landscapes present baboons with varying levels of risk and reward, suggesting that fear at least partially shapes behavior.

This research was supported by the National Science Foundation's Doctoral Dissertation Research Improvement Grant (Award: 1455675).

Feeding and foraging behavior of chacma baboons (*Papio hamadryas ursinus*) in a temperate and anthropogenically-altered habitat in South Africa

NICHOLAS W. ELLWANGER^{1,2} and THAD Q. BARTLETT¹

¹Department of Anthropology, University of Texas at San Antonio, ²Department of Geography and Anthropology, Kennesaw State University

The activity patterns of free ranging primates are constrained by a variety of abiotic and biotic variables. Here we explore how day length, temperature, and diet impact the feeding and foraging behavior of baboons living in the extreme southern latitudes of the Hemel-en-Aarde Valley, Western Cape, South Africa, which is characterized by a mosaic habitat of endemic fynbos, invasive trees, colonizing grasses, and agricultural farms. We studied one group of baboons for 84 full days over 10 months. We recorded activity, food item consumed, and food biomass intake of all adults ($n=16$). Because day length is highly variable across seasons (latitude = $S\ 33^{\circ} 22' 22''$), we report feeding effort as both percentage of daily activity and estimated hours spent feeding per day. Proportional feeding time was a negative function of daylight hours ($r^2 = .219$, $p<.000$). However, number of hours/day spent feeding was not explained by daylight or temperature ($p=.206$). Feeding hours remained relatively consistent during months of low daylight availability, suggesting that baboons increased the percentage of time spent feeding to maintain the same amount of feeding effort. Proportional feeding time ($r^2 = .259$, $p<.000$) and number of feeding hours ($r^2 = .269$, $p<.000$) were positive functions of the percentage of biomass obtained from invasive tree foods. Seeds of invasive trees (e.g., *Pinus* and *Acacia*) are important foods for baboons in this habitat due to their relatively high availability in their home range and across seasons, but the biomass intake rate of these foods is low, requiring more processing time.

This research was funded by the Department of Anthropology at the University of Texas at San Antonio.

Physical frailty, aging, and mortality in wild chimpanzees

MELISSA EMERY THOMPSON^{1,2}, ZARIN P. MACHANDA^{2,3}, EMILY OTALI², MARTIN N. MULLER^{1,2} and RICHARD W. WRANGHAM^{2,4}

¹Department of Anthropology, University of New Mexico, ² Kibale Chimpanzee Project, ³Department of Anthropology, Tufts University, ⁴Department of Human Evolutionary Biology, Harvard University

Frailty is a syndrome of human aging characterized by multiple symptoms of physical decline, such as loss of body condition, weakness, slowing, exhaustion, and lethargy. While declining physical condition has long been recognized to accompany the aging process, frailty has emerged as an important predictor of

broader adverse outcomes, including disability, poor response to medical treatment, and death. In non-human primates, where internal health status is difficult to assess, signs of frailty could therefore provide an outward approximation of overall health. Additionally, in the absence of medical care or support from caregivers, frailty itself is expected to be a critical determinant of survival. Here, we examine features approximating physical frailty in a community of wild chimpanzees at Kanyawara, Kibale National Park, Uganda. Muscle mass was estimated for 49 adult chimpanzees studied over 21 years using urinary creatinine (21,224 samples). Moderate but significant age-related declines were evident in both sexes by ages 35–40, a time when mortality rates accelerate. These changes were accompanied by other potential indicators of frailty: decreased resting respiratory rate, increased time spent resting, and reduced climbing behavior. However, there was substantial individual heterogeneity in these measures, along with broad overlap between younger and older adults. Our results suggest that chimpanzees with long lifespans maintain robust physical condition, but that those who survive past 50 are conspicuously frail. Chimpanzee lifespan may be ultimately limited by ability to meet daily needs in the face of physical constraints.

Funding: National Institutes of Aging/Office for Research on Women's Health (R01-049395), National Science Foundation (Grants 1355014, 0849380), Leakey Foundation, Wenner-Gren Foundation, University of New Mexico, Harvard University, Tufts University.

Oral health and osteoarthritis: impacts from social and environmental variation among Iron Age steppe groups of southern Siberia and Inner Asia

JACQUELINE T. ENG¹ and MICHELLE MACHICEK²

¹Biological Sciences, Western Michigan University, ²Institute of Intercultural and Anthropological Studies, Western Michigan University

Given the geographic diversity in the extensive Eurasian steppe, variability in past subsistence strategies may be expected, as recent archaeological studies suggest. This study compares bioarchaeological data from three contemporaneous (Iron Age/Xiongnu, c. 1000 BC–AD 100) steppe sites to analyze the influence of environmental conditions and associated subsistence practices upon dental disease and osteoarthritis. The southern Siberian kurgan site of Pazyryk ($N=87$) and the Xiongnu period ring tombs of Egiin Gol ($N=51$) in Mongolia are upper status burials, while the Xinjiang burials of Heigouliang ($N=80$) also show signs of social differentiation. The expectation is that environmental variability across these geographic settings, as well as variation in cultural factors will be evident in differences of markers of oral health and joint disease between sites.

ABSTRACTS

The rates of oral disease and osteoarthritis (at the shoulder, elbow, hip, and knee) increase in older adult categories, as expected, while variation exists between sites and the sexes in which joints are most affected. Inter-site chi-square comparisons show that Heigouliang has significantly higher rates of antemortem tooth loss (χ^2 (2, N=2834)=79.911, $p<0.001$) and in teeth that are carious (χ^2 (2, N=1525)=39.671, $p<0.001$), which is also true when considered by sex, although abscess rates are highest among Pazyryk males (χ^2 (2, N=1689)=6.295, $p=0.043$) and Egiin Gol females (χ^2 (2, N=1090)=12.198, $p=0.002$). The childhood stress marker of enamel hypoplasia is significantly highest among Egiin Gol individuals (χ^2 (2, N=87)=10.852, $p=0.004$). These results suggest variation in gendered activities, dietary practices, and childhood stress among early societies across the steppe.

Funding for JE: Fulbright-Hays Doctoral Dissertation Abroad program & University of California Pacific Rim Award. Funding for MM: Smithsonian Institution (Council for American Overseas Research Centers) and Wenner Gren.

Competitive ability complements coalition formation in wild male chimpanzees

DREW K. ENIGK¹, MELISSA EMERY THOMPSON^{1,2}, ZARIN P. MACHANDA^{2,3}, EMILY OTALI², RICHARD W. WRANGHAM^{2,4} and MARTIN N. MULLER^{1,2}

¹Department of Anthropology, University of New Mexico, ²Kibale Chimpanzee Project, Fort Portal, Uganda, ³Department of Anthropology, Tufts University, ⁴Department of Human Evolutionary Biology, Harvard University

Adolescence is a life history period during which individuals are sexually mature but continue to undergo physical growth. Adolescent males are poorly equipped to compete on their own, so they stand to gain substantial benefits from cooperating in coalitions. Accordingly, in some mammals, low-ranking males who form long-lasting alliances with dominant males achieve greater reproductive success than low-ranking males who adopt individual sneak mating tactics. Because smaller, younger individuals are likely to be less effective competitors, however, adolescent males may not be chosen by others as coalition partners. Here we test whether adolescent male chimpanzees form coalitions at higher rates than do adult males, and whether younger, smaller adolescents form them at higher rates than do older, larger adolescents. Our analyses utilized nearly 13 years of aggression data, which included 888 coalitions across 12 adolescent males, from the Kanyawara chimpanzee community in Kibale National Park, Uganda. We found that adult males formed coalitions at higher rates than did adolescent males (GLMM: $\beta=1.35$, $SE=0.23$, $p<0.001$). Furthermore, within adolescence, males formed more coalitions if they were older ($\beta=1.09$, $SE=0.22$, $p<0.001$) and larger ($\beta=0.87$, $SE=0.24$, $p<0.001$) than if they were

younger and smaller. Our findings indicate that coalition formation among male chimpanzees does not primarily involve the weakest individuals. Rather, the largest and strongest males are most likely to form coalitions, suggesting that the ability to obtain a coalition partner in chimpanzee society is largely limited to the most effective competitors.

This material is based upon work supported by the National Science Foundation Graduate Research Fellowship Grant No. DGE-0237002, National Science Foundation Grants No. 1355014, 9807448, 0416125, and the Leakey Foundation.

Patterns of Skeletal Asymmetry in the Human Pelvis

AMANDINE ERIKSEN and NOREEN VON CRAMON-TAUBADEL

Department of Anthropology, University at Buffalo-SUNY

Previous studies of human bilateral asymmetry tended to focus on single skeletal elements and made different *a priori* assumptions about the sources of asymmetry, thereby limiting the ability to differentiate between genetic/developmental and behavioral causes such as the effect of hand lateralization. Here, we investigate differences in fluctuating asymmetry (FA) and individual (IA) asymmetry in the pelvis for a modern sample of 43 males and females for whom hand preference was documented. Sacral and os coxa shape was quantified using landmark configurations on 3D bone models. FA was calculated from landmark configurations and all possible interlandmark distances for the left and right sides of each bone were used to calculate average sacral and os coxa IA. The results found that while FA of the os coxa and sacrum was correlated ($r=0.43$, $p=0.004$), IA for the two bones was not ($r=0.01$, $p=0.95$), suggesting that more asymmetrical individuals did not necessarily display the same patterns of left or right side dominance. Kruskal-Wallis and Mann-Whitney U tests found no significant differences in IA across sex or handedness groups for the sacrum but right-handed males had higher right side dominance in the os coxa than left-handed males, while females showed no differences between handedness groups. Therefore, the results suggest that handedness can affect asymmetry in parts of the skeleton not directly linked to the upper limb. Further comparisons across skeletal regions will elucidate the relative effects of genetic/developmental factors and handedness in shaping human skeletal asymmetry patterns.

This project was funded by the Wenner-Gren Dissertation Fieldwork Grant (Grant #9641), the Mark Diamond Research Fund (SP-18-19), and the 2017 Morris E. and Lucille R. Opler Dissertation Research Scholarship.

Closing the gap: Examining sex differences in oral health

GINA ERRICO^{1,2}, GENE HUNT³ and DAVID HUNT¹

¹Anthropology, Smithsonian Museum of Natural History, ²Anthropology, The College of New Jersey, ³Paleobiology, Smithsonian Museum of Natural History

Sex-based oral health differences seem to have occurred around the same time as agricultural practices developed. In the bioarcheological record, females have higher rates of oral pathologies, linked to biological, environmental and/or sociocultural effects. These differences manifest across cultures and geographic areas throughout time, but has there been a relaxation of the pressures that stimulate these differences in modern society? To investigate this question, a sample of Euro males and females (between 20-87 years old) who still retained most of their dentition, were selected from the Robert J. Terry Anatomical Skeletal Collection. Coding of wear and pathologies followed standard protocol. The results gauge whether industrialized individuals from the U.S. follow the trend of females having greater oral health problems than men.

The relationship between the proportion of damaged or missing teeth and age was similar between the sexes. Locally-weighted (lowess) regressions followed similar trajectories in males and females, except age 60-70, at which point females have a higher proportion of missing or damaged teeth. The confidence intervals for the lowess curves just barely overlap at these ages. Statistical power was hampered by the low number of Euro females with dentition providing low sample sizes for the age categories. This present study indicates that the differences between the sexes is less noticeable than seen in pre-historic and pre-industrial societies. This agrees with other modern population studies which have identified decreased disparity in oral health between the sexes. This variation is attributable to environmental and sociocultural influences as well as biological effects.

NSF REU Site, OCE-1560088

Expression of Sexual Dimorphism Among the German, Irish, and Italian Ancestry Groups in the Huntington Collection

ASHLEY ESPINOZA^{1,2}, DAVID R. HUNT² and GENE HUNT³

¹Applied Forensic Science, Mercyhurst University, ²Physical Anthropology, Smithsonian Institution, ³Paleobiology, Smithsonian Institution

Various research has suggested that environmental factors have an impact on the expression of sexual dimorphism in a population. One of these environmental factor is nutrition. The access of nutrition, in industrial societies, is often correlated with social economic status. Migration waves to the U.S., during the late 1800's early

ABSTRACTS

1900's, demonstrate social mobility and stratification. These waves brought various European groups such as the Germans, Irish, and Italians to the U.S. The Huntington collection is composed of unclaimed immigrant bodies from 1893-1921 and are of known age, sex, and ancestry. The sample size for this study consisted of 252 individuals: German females (28), German males (50), Irish females (50), Irish males (50), Italian females (24), Italian males (50). The femora and humeri were selected, to be measured for this study, due to being valuable indicators of sexual dimorphism. The data collected from the measurements were analyzed using the programs *R* and *PRISM*. Sexual dimorphism in terms of robusticity was assessed by regressing robustness-related variables against bone length, and using sex as a factor. Significant sexual dimorphism was detected in the three populations, independently. However, the magnitudes of sexual dimorphism across ancestry groups was not significant. These results, may be due to the low sample size of Italian and German females. Coincidentally, the lack of Italian and German females in the collection is reflected on the activities of these immigrant groups. Which in terms, allows us to better understand the "American Experience" of these immigrant groups.

Funding was provided by the National Science Foundation (NSF), REU Site, OCE-1560088.

The Relationship Between Localized Bone Density and the Area and Perimeter of Exit Wounds

ELIZABETH A. EVANGELOU, TESSA SOMOGYI, KEVIN E. SHERIDAN and ELIZABETH A. DIGANGI
Anthropology, Binghamton University

Bone density data has the potential to be a valuable tool in ballistic trauma analysis due to its effect on size and shape of entrance and exit wounds. Bone density is often measured via DEXA scans, but can also be measured from CT scans. Here, we tested the relationship between the size of cranial gunshot exit wounds and localized bone density (i.e., bone density directly adjacent to an exit wound). Thirty-seven donated human heads sourced from an anatomical tissue supply company were subjected to gunshot trauma as part of a larger project. Prior to shooting, each head was placed on a shooting stand at approximately adult male height. Each head was then shot once with a 0.38 revolver either through the frontal or temporal/parietal bone. Bullets were either full metal jacket or jacketed hollow points. Following the experiment, heads were CT scanned, autopsied, and processed using standard maceration techniques. Bone density measurements were collected from the CT scans (using Mimics 20.0) in an area of bone measuring 31-33 mm² located immediately superior to the exit wounds. Area and perimeter measurements of exit wounds were collected using ImageJ. All

data were then subjected to Pearson product moment correlation tests. Preliminary results revealed a medium strength correlation (.510) between bone density and exit wound perimeter. These results indicate that bone density likely has a significant effect on the size of gunshot exit wounds, and this has implications for how we can make interpretations about such wounds moving forward.

This project was supported by an award from the National Institute of Justice: 2016-DN-BX-0155.

The Potential Effect of Climate Adaptation on the Morphology of the Pelvis

JENNIFER EYRE

Department of Anthropology and the Center for the Study of Human Origins, New York University, The New York Consortium in Evolutionary Primatology, NYCEP

Human birth is difficult due to the tight correspondence between the size of the birth canal and baby. The question of why evolution has not acted to increase the size of the birth canal, which would be evolutionarily advantageous due to a reduction in obstructed labor and mortality, is termed the obstetric dilemma. One hypothesis, based on Bergmann's Rule, is that effective thermoregulation in hot climates where hominins evolved required a narrow body and thus a narrow pelvis. Here, I test the hypotheses that i) the bony birth canal expresses a different morphology based on climatic adaptation and that ii) the morphology of the superior pelvis differs more than that of the birth canal as it is not subject to the same constraints.

3D scans of females from the following populations were utilized: Point Hope Inuit (cold climate), South African Zulu (temperate climate), modern Ugandan (hot climate), and historical Sudanese (hot climate). Two sets of landmarks collected; the first captured the morphology of the bony birth canal, the second the superior pelvis. Each set of landmarks was submitted to a generalized Procrustes analysis and visualized using a principle components analysis. Pelves did not separate by population in either analysis on any of the PC axes, suggesting that thermoregulatory adaptation due to climate did not significantly affect the morphology of either the birth canal or the superior pelvis in these populations, which does not provide support for Bergmann's Rule playing a significant role in determination of pelvic morphology in modern humans.

This material is based upon work supported by the National Science Foundation Graduate Research Fellowship Program under Grant No. 1650895.

Diversity in Tudor England: Exploring Origins and Ancestry in the Crew of Henry VIII's flagship, the Mary Rose

KATIE E. FAILLACE, JESSICA SCORRER and RICHARD MADGWICK
Archaeology, Cardiff University

The tragic sinking of Henry VIII's vice flagship, the Mary Rose, on 19th July 1545 caused the deaths of approximately 380 men on board. Excavations of the wreckage in the 1980s revealed the remains of 179 crew members, resulting in a rare life assemblage which can improve our understanding of sailors' lives in later medieval England. A recent, exploratory multi-isotope and craniomorphological analysis of a sample (n=8) of these individuals has led to unexpected revelations of diversity on this Tudor warship. The majority of the sample had isotope values expected for a British population and cranial morphology that would be classified as "White" (Hefner and Ousley 2014). However, two individuals stood out with interesting combinations of isotope signatures and cranial morphologies. Although I9 had isotope values falling comfortably within the ranges for Britain (87Sr/86Sr = 0.71070, $\delta^{18}O_p$ = 18.4‰), his cranial morphology was characterized as "Black" by the Decision Tree and Optimized Summed Scores Attributes (OSSA) methods of Hefner and Ousley (2014). I70 ("the Royal Archer") had a $\delta^{18}O_p$ value of 21.2‰, significantly higher than the estimated British range of 15.9 to 19.2‰ (Evans et al. 2012), most likely from the Mediterranean Sea region. Despite postmortem damage to his cranium, the Decision Tree of I70's craniomorphology suggests he was non-white, probably "Black" or "Hispanic". The individuals highlighted in this study demonstrate a more colourful picture of diversity in Tudor England than typically assumed.

Cardiff University Archaeological Science MSc Programme and Channel 4.

Maternal stress, anxiety, and fear of childbirth among planned homebirth mothers: results from a mixed methods study

NICOLE L. FALK-SMITH and LORENA MADRIGAL
Anthropology, University of South Florida

The aim of this project is to create a better understanding of the hormonal physiology of childbirth using a mixed methods approach. Specifically, interviews, standardized questionnaires, and salivary cortisol samples were collected to analyze the maternal stress response to labor and childbirth when the mother intended to have a homebirth. Homebirths are imperative to study because the home is where our species has given birth for most of human history. Further, maternal cortisol is imperative to study because in-hospital research indicates this hormone must remain within an optimal, normal range for labor and childbirth to progress unimpeded. Yet, the

ABSTRACTS

optimal, normal range for cortisol has yet to be established in a homebirth setting. Thus far nine women who intended to give birth at home in the Tampa Bay area of Florida have participated in the study. Altogether 113 saliva samples have been collected and analyzed to establish baseline cortisol in the third trimester, labor cortisol, delivery cortisol, and post-partum cortisol levels. On average, maternal salivary cortisol levels rose four to six fold from early labor to delivery (0.5 to 2.5 ug/dL) returning to normal, pre-labor levels within twelve hours after delivery. For comparison, other research has indicated that salivary cortisol levels rise two to three fold in Combat Casualty Stress Scenarios. Thus, maternal cortisol level rise is a major and significant event. Gaining a better understanding of the role cortisol plays in childbirth may lead to better childbirth outcomes. Further research is needed to establish maternal cortisol levels cross-culturally.

Funded by the University of South Florida's Creative Scholarship Grant

Frequency of enamel chipping in Tai Forest cercopithecids: Implications for dietary reconstruction in paleoanthropological contexts

LUKE D. FANNIN¹, DEBBIE GUATELLI-STEINBERG¹, ELISE GEISSLER², PAUL CONSTANTINO³ and W. SCOTT. MCGRAW¹

¹Anthropology, The Ohio State University,

²Anthropology, University of Florida, ³Biology, Saint Michael's College

Tooth enamel records evidence of dietary behavior in numerous ways, one of which is edge chipping. Prior research has shown that hard-object foods such as seeds and nuts are capable of chipping and/or fracturing enamel. The presence of chipped enamel has been used as evidence of hard-object feeding in paleoanthropological contexts; however, few studies have evaluated whether chip frequency and size reliably track durophagy in groups of extant taxa with different diets living sympatrically. We examined dental chipping and diet within the cercopithecoid community inhabiting the Ivory Coast's Tai Forest, testing the null hypothesis of no relationship between chipping and dietary hardness. We quantified chip frequency and size on 1105 P4s and M1s from naturally deceased specimens of *Ptilocolobus badius*, *Colobus polykomos*, *Procolobus verus*, *Cercocebus atys*, and *Cercopithecus* spp. Based on degree of durophagy, we predicted that chip size and frequency would be greatest in *Cercocebus atys* and least in *Procolobus verus*. *C. atys*, a hard-object feeder that forages primarily on the forest floor, exhibited the most and largest chips; however, there was no obvious relationship between diet and chip frequency or size in the remaining taxa. There was a strong association between the frequency of enamel chips

(of all sizes) and canopy use, suggesting that exogenous grit may play a role in chip formation. We conclude that food material properties and feeding context must be considered when interpreting dental chipping in fossil taxa.

Evolution of the Epigenome in Ultraconserved Non-coding Elements in Animals over 300 Million Years

CHRISTOPHER FAULK

Animal Science, University of Minnesota

Ultraconserved noncoding elements (UCNEs) are a unique group of sequences that exhibit >200 nt length with >95% identity across vertebrates, conserved for over 300 million years. UCNEs fall in both intergenic and intronic regions, and most cluster near transcription factors and important developmental loci. Despite this conservation the physiologic function of UCNEs remains mysterious, however these sequences represent valuable genetic markers whose features can be compared across species and populations. DNA methylation is a heritable epigenetic mark that affects gene transcription and chromatin architecture and can be modified by environmental factors. Epigenetic biomarkers are valuable tools to assess both current and historic environmental exposures. Yet, most inter-species epigenetic comparisons of exposure assess different target regions by necessity, limiting the strength of inferences. Here we present the use of ultraconserved non-coding elements (UCNEs) as cross-species, conserved target elements harboring interindividual epigenetic variation. Despite the extreme sequence conservation, we show that both inter-species and interindividual variation in DNA methylation is present. We assessed 13 UCNEs in a panel of 56 different vertebrate species and 5 UCNEs in a panel of 96 humans. The mean DNA methylation ranged from 4% to 91% with standard deviations ranging from 2 to 15 and are consistent with methylation in ancient hominids. Most exhibit significant clade specific methylation (Pagel's lambda). We propose the use of UCNEs as target loci for use as epigenetic biomarkers where the identical assay can be used for any vertebrate species.

Social influences on reproductive development and maturation in female geladas

JACOB A. FEDER¹, JACINTA C. BEEHNER^{2,3} and AMY LU^{1,4}

¹Interdepartmental Doctoral Program in Anthropological Sciences, Stony Brook University,

²Department of Anthropology, University of Michigan, ³Department of Psychology, University of Michigan, ⁴Department of Anthropology, Stony Brook University

In primates, the early life environment can strongly affect the onset of reproductive maturation, thereby influencing lifetime reproductive success.

In species with maternal rank inheritance, daughters of high-ranking females often mature earlier than those of lower rank. However, increased group size may delay maturation because of within-group competition. Differences in female developmental trajectories can be investigated by examining morphological and hormonal indicators of maturation. Here, we examined how maternal rank and unit size influenced the age at first sex skin swelling for 15 juvenile female geladas (*Theropithecus gelada*) from seven reproductive units in the Simien Mountains National Park, Ethiopia. In addition, we determined whether the onset of first swelling was presaged by a rise in fecal estrogens (n=726). We found that daughters of high- (t=-10.25, p<0.05) and mid-ranking (t=-8.90, p<0.05) mothers developed their first sex skin swellings earlier than daughters of low-ranking mothers. Furthermore, contrary to expectation, females in larger units matured earlier than those in smaller units (t=-5.28, p<0.01). Fecal estrogen concentrations increased rapidly during the four months prior to an individual's first sex skin swelling, suggesting that both hormonal and physical measures mark the same developmental processes. Although our results for maternal rank are consistent with previous studies, our finding of accelerated maturation in larger groups may be attributed to increased male takeover risk triggering faster life histories.

Fieldwork was supported by National Science Foundation (grant numbers BCS-0715179, IOS-1255974, BCS-1723228); Leakey Foundation; National Geographic Society (grant number 8100-06, 8989-11); the Wildlife Conservation Society; and the University of Michigan.

Nepotistic cooperation among maternal and paternal kin in male chimpanzees from Gombe National Park, Tanzania

JOSEPH T. FELDBLUM¹, KARA K. WALKER², IAN C. GILBY³ and ANNE E. PUSEY²

¹Department of Anthropology, University of Michigan, ²Department of Evolutionary Anthropology, Duke University, ³Institute of Human Origins & School of Human Evolution and Social Change, Arizona State University

Although kin selection theory predicts nepotistic biases in cooperation among group-living animals, evidence for nepotism among adult male chimpanzees is equivocal. Preferential cooperation has been detected among maternal, but not paternal brothers. Possibly, chimpanzees recognize maternal kin through extended association with their mothers but are unable to recognize paternal kin because of their promiscuous mating system. However, the recent finding that fathers bias their behavior toward their infants in Gombe provides evidence of paternal kin discrimination, which may extend to cooperative contexts. Another reason for negative results may be that previous studies in chimpanzees relied on limited observation periods and did not

ABSTRACTS

account for some statistical interdependencies inherent to relational network data. Here we use 21 years of behavioral data from Gombe from 23 adult males with known mothers, 10 of whom also had known fathers assigned via genetic sampling, to investigate the effect of kinship on cooperation. Employing additive and multiplicative effects (AME) models, a Bayesian random effects regression framework for relational data, we found that, as well as maternal brothers, both father-son and paternal brother dyads associated and groomed preferentially, and groomed more equitably, than unrelated dyads, even after accounting for individual age and rank, dyadic age and rank similarity, and individual grooming and association tendencies. Paternal and maternal kinship effects were of a similar magnitude. These results suggest that the ability to recognize paternal kin may be widespread in chimpanzees, and that kin selection likely plays a larger role in cooperation among male chimpanzees than previously thought.

Data collection supported by the Jane Goodall Institute, construction of the long-term database supported by NSF (DBS-9021946, SBR-9319909, BCS-0452315, IIS-0431141, IOS-LTREB-1052693), genetics work supported by NIH (R01 AI058715).

Phylogeny of Extant Colobines Using Morphological Data

AILEEN FERNANDEZ and STEPHEN R. FROST
Anthropology, University of Oregon

We conducted a cladistic analysis of extant colobines using morphological data, as the last such analysis was published twenty years ago by Jablonski (1998). The sample included all commonly recognized extant African and Asian genera including *Colobus* (n=51), *Procolobus* (n=9), *Ptilocolobus* (n=58), *Simias* (n=20), *Nasalis* (n=21), *Rhinopithecus* (n=11), *Pygathrix* (n=9), *Presbytis* (n=110), *Trachypithecus* (n=60), *Semnopithecus* (n=11) and *Kasi* (n=13) treated as a separate OTUs. *Macaca* (n=199), often considered the most morphologically primitive papionin, was the outgroup. We included all of the characters that could readily be applied to colobines from Gilbert's (2013) cladistic analysis of papionins, including 52 quantitative dental, 33 quantitative cranial, and 67 qualitative characters. Quantitative characters were scored with gap weighted coding. We tested all characters for allometry, and affected characters were treated as described by Gilbert (2013). Three analyses were conducted: males only, females only, and sexes pooled. Matrices were assembled with Mesquite and analyzed in TNT using parsimony. The pooled sex analysis recovered a single most parsimonious tree with a monophyletic *Presbytina*, but *Colobina* was paraphyletic. The Asian colobines included an odd-nosed clade, but the langurs were paraphyletic. *Kasi* was sister to *Trachypithecus*. Sex-specific results were similar,

except in the male analysis *Ptilocolobus* was basal to the odd-nosed clade within *Presbytina*; and in the female analysis *Colobus* was basal to the odd-nosed clade within *Presbytina*. The position of *Kasi* in the sex specific analyses was unstable, but always among the other langurs. Future research involves increasing outgroup diversity to include more cercopithecines and incorporating fossils.

Investigating fossil hominin climbing behaviors: Novel applications of existing technology

ELEN M. FEUERRIEGEL^{1,2} and PATRICIA A. KRAMER¹

¹Department of Anthropology, University of Washington, ²Evolutionary Studies Institute, University of Witwatersrand

The retention of climbing-adapted features in the upper limb of some species of fossil hominins have historically been interpreted to indicate the continued relevance of arboreal climbing in the human lineage. Recent paleoenvironmental reconstructions for two major hominin-bearing landscapes in Africa have found that fossil hominins were preferentially utilizing landscapes featuring a mosaic of habitats in close geographical proximity, including dry, uplifted flanks with rocky cliffs. Many extant species of primate use rocky and cliff habitats as sleeping, foraging, and refuge sites. This raises the question: could the retention of climbing-advantageous morphologies in fossil hominins relate to behaviors other than tree climbing, such as rock climbing?

Five healthy, experienced rock climbers were recruited to perform two rock climbing and two suspensory grips on a custom rig. Kinematic analysis (Qualisys Motion Capture Systems, Gothenburg, Sweden) was used to quantify differences between suspensory and rock climbing grips in terms of joint angles, or grip shape. Pilot data was analyzed using principal components analysis and canonical variate analysis to assess variation within the samples. Results indicate significant differences between angular joint configurations according to grip type ($p < 0.007$). The only paired grip comparison with-outsignificant effects was the Hook-Power grip comparison.

The pilot study justifies a more detailed exploration of force distribution and kinematics between rock climbing and arboreal climbing/suspensory grips. We also present a novel approach to instrumenting complex vertical substrates using 3D printing technology to accurately collect kinetic data during non-arboreal climbing behaviors in modern humans.

This pilot study was supported by funding from the Quaternary Research Center.

Exploring age-related variations during talar growth

CARLA FIGUS¹, NICHOLAS B. STEPHENS², RITA SORRENTINO^{1,3}, EUGENIO BORTOLINI¹, LUCIA M. SCALISE¹, GAIA GABANINI¹, MATTEO ROMANDINI¹, FEDERICO LUGLI¹, SIMONA ARRIGHI¹, FEDERICA BADINO^{1,4}, GIULIA MARCIANI¹, GREGORIO OXILIA¹, DANIELE PANETTA⁵, MARIA G. BELCASTRO^{3,6}, WILLIAM HARCOURT-SMITH^{7,8,9}, TIMOTHY M. RYAN² and STEFANO BENAZZI^{1,10}

¹Department of Cultural Heritage, University of Bologna, ²Department of Anthropology, Pennsylvania State University, ³Department of Biological, Geological and Environmental Sciences, University of Bologna, ⁴CNR - Istituto per la Dinamica dei Processi Ambientali, National Research Council, ⁵CNR Institute of Clinical Physiology, National Research Council, ⁶ADES AMU-CNRS- EFS: Anthropology and Health, Aix-Marseille Université, ⁷Graduate Center, City University of New York, ⁸Department of Anthropology, Lehman College, ⁹Division of Paleontology, American Museum of Natural History, ¹⁰Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology

Age estimation is a fundamental aspect in juvenile osteological studies and, as such, there are many methods that rely on ontogenetic-related changes to bone morphology. The talus, being a small and compact bone, is generally well preserved in archaeological contexts, but little is known about its morphological trajectory during growth. To better understand this we apply a (semi)landmark-based approach to an ontogenetic sample of 26 modern human juvenile tali (known age/sex = 12; unknown age/sex = 14), grouped by 5 age categories ranging from 0 to 15 years.

A template of 11 landmarks and 205 semilandmarks were applied to 26 microCT-based digital models of the juvenile tali. These were superimposed by Generalized Procrustes Analysis with the semilandmarks freely sliding against recursive updates of the Procrustes consensus. Finally, individuals of unknown age/sex were projected into the form-space determined from a Principal Component Analysis of the known sample.

Our results show that most of the morphometric variation is explained by PC1 (91%), which is highly correlated with size and accounts for ontogenetic allometry. Negative scores (i.e., youngest) are related to a small and globular morphology. The positive scores (i.e., oldest) account for an elongation of the talar body, which is mainly related to the development of the neck and growth of the lateral malleolar facet.

ABSTRACTS

Overall, our preliminary results suggest that age-related morphological variations of the talus may be used to determine the general age of juvenile skeletal remains, which could be valuable to many archaeological and forensic researchers.

This project is funded by the European Research Council (ERC) under the European Union's Horizon 2020 research and innovation programme (grant agreement No 724046 - SUCCESS); website: <http://www.erc-success.eu/>

ED-XRF study of Oldowan artifacts documents raw material selection and transport through time on the Homa Peninsula, Kenya

EMMA M. FINESTONE^{1,2}, THOMAS W. PLUMMER^{1,2,3}, DAVID R. BRAUN⁴, PETER DITCHFIELD⁵ and JONATHAN S. REEVES⁴

¹Anthropology, CUNY Graduate Center, ²NYCEP, New York Consortium in Evolutionary Primatology, ³Anthropology, CUNY Queens College, ⁴The Center for the Advanced Study of Human Paleobiology, George Washington University, ⁵School of Archaeology, University of Oxford

At the earliest Oldowan occurrences (2.6 – 2.3 Ma) the degree of raw material selectivity is variable and materials were transported over relatively short distances. This is in contrast with sites 2.0 Ma and later where hominins frequently selected and transported materials from further afield. This shift is apparent at Kanjera South (KJS), Kenya (ca. 2 Ma) where toolmakers preferentially selected durable lithologies from non-local sources providing evidence for the earliest habitual transport of raw materials over long distances. At Nyayanga, an older locality that is also on the Homa Peninsula, hominins also selected durable materials such as rhyolite (40.4% of assemblage), quartz (29.9%), and quartzite (27.2%). Trace element geochemistry obtained from X-ray fluorescence spectroscopy indicates that rhyolite and quartzite artifacts came from the same primary sources as those previously identified for KJS. While some rhyolites may have been locally available to KJS and Nyayanga hominins, previous research suggests that quartzite was not locally available. A 2018 survey of nine paleo-conglomerates confirmed that secondary drainages carried quartzite in low frequency (<2%) four kilometers away from Nyayanga, and quartzite was not represented in conglomerates surveyed within the four-kilometer radius. Thus, Nyayanga toolmakers exhibited similar raw material preferences to KJS hominins, choosing durable lithologies that link to the same primary sources and traveled surprisingly long distances to obtain these materials. This reveals continuity in the raw material selection and transport behaviors of hominins on the Homa Peninsula through time, and extends the record of habitual transport of non-local materials for flake production.

This research was supported by the Leakey Foundation and the National Science Foundation DDIG (BSC-1836669).

Evaluating Osteon Cement-Line Interface Distances for Advancing Understanding of Bone Adaptation

ETHAN D. FINLINSON¹, BRODY W. KING¹, MARSHALL K. HENRIE¹, ZOE M. LOHSE² and JOHN G. SKEDROS¹

¹Othopaedics, University of Utah, ²Biology, University of Florida

Secondary osteons (SOs) help avoid fracture because their cement lines (CLs) slow microcrack propagation. At the 2018 AAPA meeting we reported a new characteristic for evaluating this function: distances between the CLs of SOs, in net compression on one cortex and tension on the other (tension is more deleterious). CL interface distances (CL-Int-d) might evaluate this 'toughening mechanism' more adequately than only osteon population density (OPD), size, and shape because it accounts for osteonal variants (e.g., drifting SOs) and fragments. In 2018 we evaluated only medial (compression-region) and lateral (tension-region) cortices of chimpanzee femora (subtrochanteric) where bending is high. Here we also evaluate anterior (A) and posterior (P) cortices (these approximate a neutral axis). We also evaluated CL-Int-d with a denser grid and two orthogonal orientations; hence a more robust analysis. 12 adult femora (subtrochanteric) were also evaluated. Circularly polarized light images were used and CL-Int-d measured from CL tracings. Data were compared to regional variations in OPD, osteon size, and predominant collagen fiber orientation (CFO). Surprisingly, the chimpanzee femora had CL-Int-d that were greater in the medial cortex vs. the lateral cortex (in 2018 we reported these as equivalent)—this can be explained by the more robust analysis. The findings are now more logically related to the smaller SOs in the medial cortex. Human femora had equivalent CL-Int-d's in M-L cortices, which logically corresponds to their similar osteon size/OPD. Therefore, the new characteristic might not supplant conventional osteon-related measures as correlates for studies of bone adaptation in a bending environment.

Diet and Catastrophe: Dental Microwear Analysis of a Population Under Siege at the Ancient Greek Colony of Himera

ELIJAH C. FLEMING¹, LAURIE J. REITSEMA², KATHERINE L. REINBERGER², STEFANO VASSALLO³ and BRITNEY KYLE⁴

¹Department of Classics, University of Texas at Austin, ²Department of Anthropology, University of Georgia, ³Soprintendenza archeologica regione palermo, Italia, ⁴Department of Anthropology, University of Northern Colorado

We analyze the occlusal dental microwear of individuals believed to have died during the siege and subsequent destruction of the ancient Greek colony of Himera, Sicily, in 409 BCE to evaluate diet disruptions in times of warfare. Occlusal

microwear features, caused by mastication, reflect diet at the end of an individual's life, and in this case likely reflect diet of individuals affected by the Carthaginian invasion in 409 BCE. We examine molars from nine soldiers who died in the 409 BCE battle and nine citizens whose skeletal trauma and hasty graves suggest they were battle casualties (the catastrophic assemblage), as well as 14 individuals in tile-capped graves who died in the late 6th to 5th centuries BCE unassociated with destruction of the city (the attritional assemblage). Sputter-coated epoxy casts of molars were viewed at 500X with a Teneo field emission scanning electron microscope. Micrographs of the disto-occlusal facets were analyzed using Microwear 4.02 software. Results indicate that number of pits is greater in soldiers and citizens who died during the city's destruction than citizens in the attritional sample, suggesting that leading up to battle, people consumed a harder diet. This difference in diet between times of war and peace is likely due either to disruption of resource supply, or seasonal differences in resource availability. This study supports the interpretation of hasty graves as catastrophic deaths, expands knowledge of the last days of Himera, and contributes to our understanding of the strategies of ancient communities in the face of warfare.

This research was funded by National Science Foundation Research Experience for Undergraduates award numbers 1560227 and 1560158, the University of Georgia, and the University of Northern Colorado.

Neanderthal Hypercarnivory Revisited – Experimental Study of $\delta^{15}\text{N}$ Shifts in Dietary Items Produced by Various Cooking Techniques

KIMBERLY K. FOECKE¹, ALISON S. BROOKS¹ and CHRISTINE FRANCE²

¹Anthropology, George Washington University, ²Museum Conservation Institute, Smithsonian Institution

Nitrogen isotope ratios are used frequently in paleoanthropology and archaeology as an indicator of dietary composition. When this method is applied to collagen preserved in Neanderthal long bones, results show a highly enriched $\delta^{15}\text{N}$ signal across multiple individuals and sites. Traditionally, paleoanthropologists have attributed this to hypercarnivory, in line with or exceeding the $\delta^{15}\text{N}$ values of contemporaneous carnivores in the same sites. However, recent work on Neanderthal dental calculus and other dietary proxies indicates that the Neanderthal dietary repertoire is much more varied, including a number of plant foods. Reconciling the $\delta^{15}\text{N}$ isotopic results with other dietary indicators necessitates an alternative explanation for the highly enriched $\delta^{15}\text{N}$ signal. This study explores an alternative dietary mechanism from which a $\delta^{15}\text{N}$ signal akin to those seen in Neanderthals could result. We

ABSTRACTS

hypothesize that various methods of cooking animal and plant foods will cause the $\delta^{15}\text{N}$ value of the food items to enrich. If Neanderthals were to consume cooked food items, their $\delta^{15}\text{N}$ values would be accordingly enriched. This study tested relative $\delta^{15}\text{N}$ enrichment through four cooking conditions in animal and plant food items likely consumed by Neanderthals. Samples were analyzed by isotope ratio mass spectrometry (IRMS) at the Smithsonian Institution Museum Conservation Institute. Initial results show significant bi-directional variation in $\delta^{15}\text{N}$ between cooking methods. This result provides insight into a possible enrichment mechanism for the observed $\delta^{15}\text{N}$ values in Neanderthal collagen, and more work is underway to understand the drivers of isotope fractionation under these conditions.

To cook or not to cook: shellfish feeding in tufted capuchins

MARIANA D. FOGACA^{1,2}, MYRA F. LAIRD³, BARTH W. WRIGHT⁴, ROBERTA SALMI⁵ and RICARDO R. SANTOS⁶

¹Research, Neotropical Primates Research Group, ²Biodiversity and Conservation, Federal University of Maranhão, ³Department of Organismal Biology and Anatomy, University of Chicago, ⁴Anatomy, Kansas City University of Medicine and Biosciences, ⁵Department of Anthropology, University of Georgia, ⁶Center for Agrarian and Environmental Sciences, Federal University of Maranhão

Cooking reduces a food's material properties, such as toughness, decreases chewing time, facilitates digestion, and increases energy extraction. Shellfish are thought to be a major calorie source for some fossil hominins, and at some sites, the shellfish may have been thermally processed. Previous studies have examined changes in feeding associated with thermal processing, but shellfish data from non-human primates are limited and have rarely been associated with mechanical and nutritional data. We examined differences in food material properties and chewing sequence duration for provisioned raw and cooked crab (*Ucides cordatus*) in a wild mangrove-living tufted capuchin (*Sapajus libidinosus*) group in Maranhão, Brazil. Feeding was recorded using a Sony hand-camera and resulted in 12 chewing sequences. The number of complete chewing cycles and total feeding duration were counted for each chewing sequence. Our results show that tufted capuchins have double the chewing cycles, but shorter chewing sequence duration when eating cooked crabs relative to raw crabs. Cooked crab meat had higher nutritional values (66 kcal) but also higher toughness values (18.5 Jm⁻²) than raw crab meat (61 kcal and 3.0 Jm⁻²). These results demonstrate that there are both costs and benefits to cooking. Additional analyses are needed to test whether cooked crab has a higher net energy gain

despite requiring longer processing times. The results of this project have implications for estimating the energetics of shellfish food sources for fossil hominins.

Founded by CAPES 8887.162125/2017-00, NSF BCS 1440545 and FAPEMA AUX-08365/17 and Universal 0613/15.

With People, came Parasites: An examination of human intestinal parasites and urbanization at the 18th century Fortress of Louisbourg

MATTIA FONZO¹, AMY B. SCOTT¹ and MICHAEL DUFFY²

¹Anthropology, University of New Brunswick, ²Biology, University of New Brunswick

The Fortress of Louisbourg thrived between the years of 1713 and 1758 and within seven years of its founding, this French colonial site housed over 600 permanent residents and hundreds more who fished or did seasonal business. By mid-century, Louisbourg's population swelled to include over 2500 civilians and almost 4000 military personnel. This population boom led to overcrowded living conditions, differential access to foodstuffs, and saw the development of new medical treatments; all of which exposed those living at Louisbourg to a variety of human intestinal parasites. Each parasite species has a distinct mode of transmission and impact on the health of their host, providing further insights into the daily life of the community members at the Fortress. This study examines pelvic soil from seven excavated burials (six adults and one subadult) from the Rochefort Point cemetery (1738-1758). For each of the seven burials, individual parasite load was collected and determined from the pelvic soil (using micro-sieves of 300 μm , 160 μm and 20 μm mesh sizes) with consideration of individual sex, age, and indicators of stress. Multiple species were identified within the adult and subadult samples including the *Ascaris* species (roundworm) and *Enterobius vermicularis* (pinworm). It is hypothesized that the rapid urbanization of Louisbourg directly contributed to the flourishing of these particular parasites within this Atlantic Canadian population.

This research is supported by a SSHRC CGS Master's Award (MF) and a SSHRC Partnership Development Grant (890-2017-0049) (AS)

Spring function of the Achilles tendon in walking and running gaits

ADAM D. FOSTER¹, JESSE W. YOUNG², FLORIAN F. CAPOBIANCO III³, JOHN T. PEABODY³ and NICHOLAS A. PULEO³

¹Anatomy, Campbell University School of Osteopathic Medicine, ²Anatomy and Neurobiology, NEOMED, ³MS-II, Campbell University School of Osteopathic Medicine

Previous research suggests that the moment arm of the Achilles tendon is negatively correlated with energy costs of locomotion during endurance running in athletically trained individuals. This is a counterintuitive relationship given that longer moment arms result in greater leverage and less requisite muscle force, potentially lowering locomotor costs. This discrepancy has been argued to result from the presumed spring-like function of the Achilles tendon – shorter ankle moment arms place larger loads on the Achilles tendon – which results in a greater amount of elastic energy storage and return. However, this presumed spring-like function has not been directly investigated. In this study, we test this hypothesis using inverse dynamics in human subjects (n=17) at speeds ranging from walking to a sprint. The spring function of the Achilles tendon was modeled using specific net work (SNW; net work/total work), a continuous variable that can range from zero (a perfect spring) to one (a perfect motor, lacking energy storage and return). Our preliminary data shows that size-adjusted SNW is greatest during walking and lowest during running, suggesting that the ankle transitions to spring-like mechanics at higher speed. Contrary to predictions, the Achilles tendon moment arm length is not significantly correlated with SNW at walking to running speeds. However, there is a weak correlation during sprinting (Pearson's $r=0.44$, $p=0.10$). Broadly, our results suggest though the ankle may exhibit spring-like behavior during running, overall the relationship between ankle anatomy and energy return is complex and other variables may play an important role.

Funding provided by the CUSOM Medical Student Summer Research Scholars Program.

Function and variation in the mechanical properties of *Papio anubis* tooth enamel

FREDERICK R. FOSTER

Anthropology, Rutgers, the State University of New Jersey

Tooth performance is an important component of dietary adaptation. One measure of performance is the ability of a tooth to withstand failure due to fracture, which occurs when tensile stress within enamel exceeds a critical threshold related to its mechanical properties. Two of these properties, hardness and elastic modulus, grade substantially between the enamel-dentine-juncture and the occlusal surface in primates. These mechanical property gradients reflect the ability of enamel to internally distribute the tensile stress generated during chewing, keeping it below the threshold for fracture. Mechanical property gradients have been compared across primate species that chew different mechanically challenging foods to assess their role in tooth performance. However, inferences made from these comparisons are tenuous because individual species are typically characterized by

ABSTRACTS

fewer than three samples. Additionally, these comparisons do not consider critical regions of enamel where high tensile stresses are expected to occur during chewing, increasing the likelihood of fracture. This study addresses these shortcomings by mapping gradients for hardness and elastic modulus through critical regions of enamel in a sample of ten *Papio anubis* lower second molars, using nanoindentation. Within-tooth comparison of mechanical properties was done using a modified ANOVA test, suitable for comparing gradients. Results show that mechanical property gradients differ in critical regions compared to elsewhere in enamel, suggesting these regions are better at coping with high tensile stresses. This study illustrates the importance of using larger sample sizes in assessing mechanical behavior in primate tooth enamel, and the relevance of mechanical properties to tooth performance.

This work was funded by a grant from the Center for Human Evolutionary Studies at the Department of Anthropology, Rutgers, the State University of New Jersey.

Applying the random encounter model to estimate density of *Cercopithecus lomamiensis* from camera traps in the Lomami National Park and buffer zone of the Democratic Republic of the Congo

CHARLENE S. FOURNIER KORCHIA¹, ERIK G. NOONBURG¹, PABLO AYALI², TERESE B. HART², JOHN A. HART² and KATE M. DETWILER^{1,3}

¹Biology, Florida Atlantic University, ², Lukuru Wildlife Research Foundation, ³Anthropology, Florida Atlantic University

The technological development of camera traps over the past decade has proven to be a highly valuable tool in the study of cryptic and endangered animal species. Since its description in 2012, we conducted three camera trap (CT) surveys on the new guenon species, *Cercopithecus lomamiensis* (lesula)—a terrestrial, cryptic species endemic to the Central D.R. Congo. The objective of this study was to apply the random encounter model (REM), a novel method for estimating animal density from camera trap data, to estimate density of *C. lomamiensis* from multiple sites across its range. We used a systematic grid approach to complete two camera trap surveys inside the Lomami National Park (LNP) (Losekola in 2014; E15 in 2015), and one outside the park (Okulu in 2013), where animals are heavily hunted. We analyzed a total of 598 lesula video events over 5,960 CT days from 92 CTs (Okulu: 143 events, 1551 CT days; Losekola: 282 events, 2430 CT days; E15: 173 events, 1979 CT days) to obtain the required parameters for the REM. Model parameters included: (1) group size, (2) travel speed, (3) activity pattern, and (4) day range. We found similar results of group density inside ($D(g)=4.08\pm 0.13$) and outside ($D(g)=4.28\pm 0.05$)

the national park; however, individual density was smaller in hunted forest ($D(i)=19.92\pm 3.01$) than in protected forests ($D(i)=30.94\pm 2.37$). This study benefits conservation efforts of *C. lomamiensis* by yielding an estimate of total population size, which can be used to monitor the population and detect potential decline due to hunting.

New Digs: Revisiting Paleoanthropology in the Genome Editing Era

KEOLU O. FOX

School of Medicine | Department of Pediatrics, University of California, San Diego

Mining paleogenomic datasets allows us to understand hominin population history at a higher resolution, including the confirmation of previously theorized ancient hominin introgression (Slon et al. 2018). While these analyses/methods have been used to impute ancient hominin disease susceptibility, one particular challenge working with paleogenomic data is that there is scant phenotype information to accompany degraded genome sequences. Intermediary methods have proposed to utilize both *in vitro* and *in vivo* systems to evaluate ancient hominin variations' contribution to the human genepool via "human-Neanderthal hybrid induced pluripotent stem cells (iPSC's) resources" and "Neanderthal transgenic mice." I will discuss methods to functionally evaluate the role of ancient hominin-specific variation (i.e. coding and regulatory variants not found in any modern human population) discovered in publicly available paleogenomic datasets. I will highlight emerging methods to systematically isolate and explore ancient hominin allele function via endogenous introduction of ancient hominid-specific alleles using a precision form of genome editing (i.e. base-editing). Once these ancient hominin-specific mutations are endogenously introduced in diverse cell types (e.g. mesenchymal and iPSC), and differentiated in controlled 3D culture environments, the paleoanthropology community can begin the previously unexplored study of ancient hominin genotype to phenotype relationships, including neurological development, metabolism, immune system variation, and the potential role of each of these in ancient hominin disease susceptibility and "extinction."

Development of gut microbiota and the brain across the first year of life: A longitudinal study of human infants

MOLLY FOX

Department of Anthropology, UCLA

This project addresses the role of the gut microbiome in infant brain development. The human gastrointestinal tract harbors more than 10-times as many microbial cells than are present in the entire human body, contributing 150-times more microbial than human genes in our bodies.

Because the gut microbiome and brain have overlapping critical periods of development and are biologically interconnected systems, it follows that maturation of the gut microbiome may affect brain development. This project investigates how accumulation of microbial communities in the intestine across the first postnatal year of human life affects neurodevelopment of cognitive and emotion regulation systems.

In a prospective, longitudinal study of mother-child dyads, we collected and analyzed fecal samples from infants at 1-3 weeks, 2-months, 6-months, and 12-months postnatal age. Mother-infant dyads partook in study sessions that included standardized and validated measures for evaluating infant cognitive development and emotion regulation at the latter three timepoints. DNA was extracted from fecal samples, the V3-V4 region of the 16S ribosomal subunit was amplified, and a closed-reference taxonomic classification was performed. We measured significant differences in beta diversity between groups using Permutational Multivariate Analysis of Variance (PerMANOVA) on models with beta diversity as the response variable, cognitive and emotional development strata as the predictor variable, stratified by age groups. Three beta diversity metrics were used (Bray-Curtis, Weighted UniFrac, and Unweighted UniFrac). This is the first study involving human subjects, to our knowledge, that has taken a developmental approach to understanding how gut microbiota affect the early-life development of brain systems.

NIH P50/MH096889 (PI Dr. Baram) and 2P2CHD041022-16 (PI Dr. Seltzer) seed grant to Dr. Fox

A consideration of the 'anomalous' narial margin patterning in the Krapina Neandertal maxillae

ROBERT G. FRANCISCUS

Department of Anthropology, University of Iowa

Nearly every anatomical aspect of the extensive Krapina Neandertal sample has been studied or incorporated into numerous publications since its initial description over a century ago – including many contributions by Erik Trinkaus. However, one key feature, the narial margin (NM) configuration on the inferior border of the nasal aperture, has not been sufficiently considered. Here, the original remains of the relevant Krapina maxillary sample (n=4), and the broader available Neandertal sample, augmented in a few instances by casts and published images (n=29), are compared. I employed a detailed 7-category NM crest coding system, as well as a simpler, dichotomized category system contrasting presence vs. absence of nasal guttering. All four of the sufficiently preserved Krapina maxillae show a separate lateral crest with some level of NM guttering, and the two most complete possess a category-3 configuration where the turbinal

ABSTRACTS

and spinal crests are fused and collectively delineate the NM border separately from the lateral crest. This precise pattern is found in no other Neandertals across their known range which possess, instead, either a single, sharp, amalgamated crest, or one in which the lateral crest contributes significantly to the demarcation of the NM. The Krapina NM pattern is closer to that found in putative Neandertal lineage precursors (e.g., Sima de Los Huesos), and many Early- to Mid-Pleistocene *Homo* fossils across Africa and Eurasia, likely reflecting the primitive condition for *Homo*. The Krapina NM configuration, anomalous among Neandertals, raises important questions of chronology and paleobiology in this important hominin sample.

This work was supported by a Leakey Foundation Grant and NSF SBR-9312567.

Assessment of pathological conditions found in Andean Holocene inhabitants of Cuncaicha rock shelter, Peru

MICHAEL FRANCKEN¹, JUDITH BEIER¹, HUGO REYES-CENTENO^{1,2}, KURT RADEMAKER³ and KATERINA HARVATI^{1,2}

¹Paleoanthropology, Senckenberg Center for Human Evolution and Paleoenvironment, University of Tuebingen, ²Center for Advanced Studies 'Words, Bones, Genes, Tools', University of Tuebingen, ³Department of Anthropology, Northern Illinois University

The Cuncaicha rock shelter is a high-altitude (4480 masl) archaeological site in the southern Andes of Peru. The excavation of the site in 2015 provided five partial skeletons (two adult females and three adult males) and isolated bones of a sixth individual, dated to time periods between the early and late Holocene (9000-3000 cal. BP). Human skeletal remains from Late Pleistocene to mid-Holocene archaeological sites are uncommon in the high Andes; therefore, our work focused on a detailed examination of the recovered skeletal material and comparison with data of contemporary burial sites from the Andes and South America in general.

Here we report on the macroscopical analyses regarding degenerative and pathological changes, including bone remodeling, signs of inflammation, trauma, lytic defects, and other pathological abnormalities, as well as degenerative joint diseases. We recorded diverse indicators for physical stress, as well as injuries and infectious diseases, represented by healed trauma, musculoskeletal stress markers, and periosteal reactions. These examinations are supported by diagnostic imaging from computed tomography.

As skeletal data suggest, all five individuals experienced similar pathological conditions independent of the occupational period. The comparison with contemporary sites in the Andean region revealed a wide conformity in the skeletal data. Despite the harsh environmental

conditions resulting from high elevation, we found no distinct skeletal indication for adaptations to extreme living conditions. Instead, the observed skeletal pathologies appear to more generally characterize the wear and tear of hunter-gatherer societies.

This study was supported by the German Research Foundation (DFG grants FOR-2237 and INST 37/706-1).

The Impact of Food Texture Preference on Oral Processing in Modern Humans

ERIN M. FRANKS¹, TREY W. MOBERLY¹, MELISSA JELTEMA², PAIGE J. LUCK³, JACQUELINE BECKLEY², E. ALLEN FOEGEDING³ and CHRISTOPHER J. VINYARD¹

¹Anatomy and Neurobiology, Northeast Ohio Medical University, ²The Understanding and Insight Group LLC, Denville, NJ, ³Food, Bioprocessing, and Nutrition Sciences, North Carolina State University

It is well-known that variation in food properties impacts oral processing within individuals and across species. Thus, food texture, which combines perceptible mechanical, structural, and surface properties of foods, has a significant effect on feeding behavior. Recent work in humans has identified four consumer groups that differ in food texture preferences and corresponding mouth behaviors: 1) Crunchers, 2) Chewers, 3) Smooshers, and 4) Suckers. While these behavioral groups play a role in food selection, it is unknown how groupings relate to physiological variation in oral processing. This largely unknown relationship persists despite evidence from non-human primates that food preference impacts oral processing.

To investigate how Mouth Behavior (MB) grouping relates to oral processing, 85 participants completed an online assessment to determine MB group. We then selected 40 participants distributed among Chewers, Crunchers, and Smooshers for physiological analysis. Participants chewed food samples representing the four MB groups while we recorded jaw-muscle activity and jaw kinematics using surface electromyography and a 3D jaw tracker, respectively. Linear mixed models assessed the effect of MB grouping and food on jaw-muscle and jaw kinematic variables. Preliminary data show that while MB grouping had a significant impact on oral processing, it only accounted for 1-2% of total variation, whereas food accounted for up to 30% of the total variation on average. These findings suggest that individuals, regardless of preferred food texture and feeding style, likely modulate their feeding activity based on differences in food material and structural properties as well as requisite bolus formation.

USDA: NIFA/AFRI 2014-67017-21644

Macroscopic analysis of periosteal new bone in human long bones

ERIC FRAUENHOFER

Chemistry, SUNY Buffalo State

Periosteal new bone (PNB) is a proliferative skeletal lesion that results from the inflammation of the periosteum. As there are limited descriptions of PNB in the literature, I undertook a comprehensive study of PNB affecting 213 human long bones. I studied eighty-nine adult individuals of the Hamann-Todd Osteological Collection, a documented human skeletal collection at the Cleveland Museum of Natural History. I characterized each individual lesion based on its maximum length and width, whether it appeared focal or diffuse, and its maturity and vascularity. The types of long bones are not equally affected (Chi-Square (5) = 75.20, $p < 0.0005$), with the lower long bones affected more often than the upper long bones. The tibia is the most affected bone, accounting for 69 (32%) of the bones affected, consistent with the literature. Additionally, of the 356 lesions studied, 120 (34%) were located on tibiae. The number of lesions were more than expected on tibiae and fibulae (Chi-Square (5) = 154.47, $p < 0.0005$). Tibiae also had a higher proportion (0.53) of diffuse lesions, compared to focal lesions (0.47), than the other types of long bones, which had either an equal or lower proportion of diffuse lesions to focal lesions. Almost half of all lesions (48%) consisted of a mixture of woven and lamellar bone. Additionally, 69% of all lesions were characterized as having mixed vascularization consisting of striations and foramina. This study enhances existing descriptions of PNB, which is one of the most commonly encountered conditions in bioarchaeological remains.

This research was funded by the Undergraduate Summer Research Fellowship Program through SUNY Buffalo State's Office of Undergraduate Research and the Dr. Gerard and Kathleen Wieczkowski Anthropology Research Grant.

Life history underpinnings of East Turkana faunal turnover during the early Pleistocene

JAMES FRAZIER¹ and AMANDA MCGROSKY²

¹Anthropology, Bryn Mawr College, ²School of Human Evolution and Social Change, Arizona State University

Early Pleistocene environmental shifts in East Africa saw the success of *Paranthropus* and early *Homo* corresponding with changes in faunal communities. Research on extant fauna suggests that success or decline at the global level is linked to both extrinsic variables (abiotic or geographic factors) and intrinsic life history variables. Similar dynamics may be detected in the fossil record and at smaller geographic scales. Our research seeks to determine whether population dynamics

ABSTRACTS

of Pleistocene large mammalian and primate fauna in East Turkana can be linked to different intrinsic and extrinsic factors at the sub-regional scale.

The East Turkana Faunal Database and novel field collections were used to calculate rates of population decline for mammalian taxa in three East Turkana sub-regions around the paleo-lake Lorenyang. Fossil life history traits were inferred from their closest living analogues. Environmental data were collected from published literature. Multiple regressions were used to quantify the relationship between percent change in relative abundance, and intrinsic and extrinsic predictor variables (diet, local environment, life history traits, body mass). Results suggest that population changes can be explained by different combinations of variables in different sub-regions. In sub-region farthest from the lake, life history variables explained more variance in population change than in sub-regions closer to the lake (adj. $r^2=0.494$ vs. 0.307 and 0.283 , respectively). In contrast to global studies, our results suggest a greater role for life history strategies at a sub-regional level, and have potential implications for factors influencing human and primate success in the face of climate change.

Bryn Mawr LILAC Summer Internship Funding, Judy Loomis Gould Scholarship, Pauline Austin Adams Fund for Excellence in Anthropology

Culture change in the urban north: The intergenerational effects of dietary and sociodemographic patterns among Alaska Native women and children living in Anchorage, Alaska

RUBY L. FRIED¹ and CHRIS W. KUZAWA^{1,2}

¹Anthropology, Northwestern University, ²Institute for Policy Research, Northwestern University

Shifting from a traditional diet toward consuming primarily store-bought foods due to cultural and societal transitions can impact adult weight gain and biology. The recognition that a woman's diet may also shape the metabolism and health of her offspring via the gestational milieu raises questions about the intergenerational impacts of these social and dietary changes. Here we investigate how maternal consumption of, and access to, traditional foods influences pre-pregnancy and pregnancy metabolism, and birth outcomes among Alaska Native women and children. Maternal diet before and during pregnancy, along with factors contributing to dietary patterns, including urban/rural residence, rural-urban food sharing, income, and education were obtained via interviews of mothers ($n=149$) visiting the Alaska Native Medical Center in Anchorage, Alaska between October 2016-August 2018. Possible intergenerational impacts of these factors were assessed using linked medical records of mother-infant dyads that spanned pre-pregnancy to birth outcomes. Preliminary results show that

life-long residents of Anchorage eat significantly fewer traditional foods (13.8% of total diet) than mothers who have ever lived in rural Alaska (24.1%). Although traditional food consumption predicted lower, healthier, pre-pregnancy weight ($p=0.015$) and body mass index (BMI) ($p=0.069$), as expected, offspring birth weight, length, and gestational age were not impacted (all $p>0.1$). Greater maternal educational attainment, which was associated with lesser traditional food consumption, predicted higher pre-pregnancy BMI ($p=0.03$) and newborn birth weight ($p=0.008$). Our results suggest that traditional food consumption reduces pre-pregnancy weight, and that lifestyle changes associated with maternal education may have intergenerational effects on offspring fetal growth.

RLF was funded by a NSF Graduate Research Fellowship, a Wenner Gren Dissertation Fieldwork Grant, and NSF DDRIG #1613340.

The oldest, most complete skeleton of *Theropithecus*, ARI-VP-1/26 from Woranso-Mille, Afar, Ethiopia

STEPHEN R. FROST¹, NINA G. JABLONSKI² and YOHANNES HAILE-SELASSIE³

¹Anthropology, University of Oregon, ²Anthropology, The Pennsylvania State University, ³Physical Anthropology, Cleveland Museum of Natural History

Theropithecus is the most abundant, widespread, and long-lasting primate genus in the African Plio-Pleistocene. While much of the evolution of the genus is well-known, there are still questions regarding the origins of its specialized form of manual foraging. A partial skeleton, ARI-VP-1/26, which includes much of the vertebral column, several ribs and sternbrae, nearly complete left forelimb and hand, partial right forelimb and hand, partial left and right hindlimbs and feet, was collected from Aralee Issie directly from the Mesgid Dora Tuff (thus 3.57-3.664 Ma) between 2004-2014.

While only a few dental remains are tentatively associated, several criteria clearly allocate ARI-VP-1/26 to *Theropithecus oswaldi* cf. *darti*: diagnostic manual digital proportions, elbow and femoral morphology, as well as size and overwhelming abundance at Woranso-Mille. Morphologically, ARI-VP-1/26 also matches other more fragmentary contemporary postcrania associated with diagnostic cranial material. Some, but not all, epiphyseae are fused. Based on the overall pattern, these suggest ARI-VP-1/26 was subadult. Using a *Macaca mulatta* developmental schedule yields an estimated age at death of 5 – 6 years and implies all teeth other than M3s and canines were in occlusion. Sizes of individual elements suggests the ARI-VP-1/26 was male.

The hand of ARI-VP-1/26 has the long thumb and short digits of *Theropithecus*. Combined with shoulder and femoral morphology, this shows *T. oswaldi* shared specialized terrestrial manual foraging with *T. brumpti* and *T. gelada*, and therefore their common ancestor too, and implies this behavior evolved prior to the highly derived dentition of the genus.

We thank the National Science Foundation (BCS-1124705) and a University of Oregon Faculty Research Award for support.

The Phylogeny of Baboon Social Organization

AMANDA J. FUCHS¹ and JASON M. KAMILAR^{1,2}

¹Department of Anthropology, University of Massachusetts, Amherst, ²Graduate Program in Organismic and Evolutionary Biology, University of Massachusetts, Amherst

Baboons are among the best-known primate taxa in terms of behavioral ecology, yet few studies have examined their social organization in an explicitly phylogenetic context. Therefore, we used several phylogenetic approaches to model their group size and composition. We constructed a population level phylogeny from 31 sites representing five baboon species (*P. anubis*, *P. cynocephalus*, *P. papio*, *P. kindae*, *P. ursinus*). For each site, we obtained four social organization traits: average group size, adult sex ratio, number of females, number of males. First, we calculated the phylogenetic signal in each trait. Next, we examined how well evolutionary models (Brownian Motion, Ornstein-Uhlenbeck, and Early Burst) and a null model fit the variation in each trait. We found moderate phylogenetic signal for group size and number of females. Interestingly, the null model was a similar or better fit to the social organization data than any of the evolutionary models. Our results indicate that evolutionary models do not adequately explain site-level social organization variation in baboons. This may be due to the greater importance of local environmental factors for driving variation in baboon group size and composition. In addition, there has been significant gene flow among baboons. If baboon social organization is generated from individual-level behaviors that have some genetic basis, then gene flow among populations may be associated with the horizontal transmission of traits. This process could mask the vertical transmission of traits, which is assumed in phylogenetic analyses. Our study has important implications for understanding the diversity of baboon societies.

Human Mitochondrial Diversity Across West New Guinea: The Origin and Expansion of Haplogroups Q1 and P3

CHRISTOPHER J. FUGINA¹, EMILY S. JELEN¹, MOLLY C. MORAN¹, SEAN C. VELAZQUEZ¹,

ABSTRACTS

MAURICIO MONTES¹, CALEB A. ALMETER¹, CORINNA N. RONEN¹, AMELIA A. GUYON¹, RALPH M. GARRUTO² and MICHEL SHAMOON-POUR^{1,3}

¹Freshman Research Immersion, Binghamton University, ²Laboratory of Biomedical Anthropology and Neurosciences, Binghamton University, ³Anthropology Department, Binghamton University

The human population history of the New Guinea Island has often been studied by investigating the genetic variation among populations of Papua New Guinea, which comprises the eastern half of this massive island. Here we explore the mitochondrial DNA diversity in the largely understudied West New Guinea (WNG). 207 blood serum samples representing 34 villages of the highlands and southern coastal regions were selected from a larger collection housed in the Binghamton University Biospecimen Archive Facility. Initial analysis of mtDNA HVS-1 sequences produced 84 unique haplotypes of haplogroups P, Q, and the rare M subclade M73⁷⁹. 70 samples were selected for full mitogenome sequencing. The coalescence age estimates revealed older ages for the major Q subclade (Q1= 35kya) than the most common P subclade in both highlands (P1= 20kya) and south coast (P1d= 25kya). The distinct ages of Q and P in WNG indicate their introduction to WNG via separate migrations. The absence of Haplogroup B in both regions suggests that the Austronesian Expansion was limited to the northern coast of WNG. The WNG sample represented some of the most ancestral lineages of Q1 and M73 reported so far. Particularly in regard to Q1, Bayesian and network analysis suggest that this important haplogroup likely originated in WNG or was introduced to WNG soon after its emergence in Sunda. Our sample also includes examples of P3 and P4 lineages that are ancestral to those found among Aboriginal Australians, pointing to their introduction to Australia from WNG no later than 25 kya.

This project was supported in part by: Howard Hughes Medical Institute (HHMI) through the Precollege and Undergraduate Science Education Program, NYS Regional Economic Development Council, SUNY Investment & Performance program.

Investigating symptoms of depression in African Americans by integrating genetic and sociocultural data

KIA C. FULLER^{1,2,3}, CHRISTOPHER MCCARTY^{3,4}, CLARENCE C. GRAVLEE^{2,3} and CONNIE J. MULLIGAN^{2,3}

¹Genetics and Genomics Graduate Program, University of Florida, ²Genetics Institute, University of Florida, ³Anthropology Department, University of Florida, ⁴Bureau of Economic and Business Research, University of Florida

Depression is one of the most common mental illnesses in the United States and around the world. African Americans typically report more severe symptoms of depression than European Americans. This project takes a biocultural

approach to investigate variation in symptoms of depression by integrating genetic and sociocultural data gathered from 138 African Americans in Tallahassee, FL. We measured symptoms of depression using the Center for Epidemiological Studies' Depression scale (CESD). We gathered sociocultural data from in-depth interviews and genotyped SNPs in five genes (*HTR1a*, *GNB3*, *SLC6A4*, *FKBP5*, and *BDNF*) that had been previously associated with depression.

Multiple linear regression was used to test the impact of age, sex, sleep, and money strain (self-reported difficulty paying bills) on CESD score. Preliminary results show that individuals who reported little money strain had significantly lower CESD scores than individuals who reported some or money strain (p-value = 0.02). In contrast to previous studies, there were no significant differences in CESD scores based on age (p-value = 0.84), sex (p-value = 0.61), or average amount of sleep (p-value = 0.56). Genetic studies have found a significant association between the T allele of rs1360780 (in *FKBP5*) and depression in European Americans, but not in African Americans even though the SNP is more common in African Americans (0.42 vs 0.31). We have previously shown that integrating genetic and sociocultural data can reveal new genetic associations. Thus, we will add genetic data to the models to investigate variation in symptoms of depression in our sample population.

Supported by NSF Grants BCS 0820687 and BCS 0724032.

Dental topography metrics from lemurs as ecometrics along spatial environmental gradients on Madagascar

ETHAN L. FULWOOD

Evolutionary Anthropology, Duke University

Tooth shape quantified using topographic metrics in multispecies samples typically covaries with categorical dietary ecology. This relationship is believed to hold because the foods exploited by ecologically dissimilar taxa tend to differ in their material properties. Plant food material properties may also vary along spatial gradients. This variation may result from differences in the plant foods available to primates in different environments and from adaptive responses by plants to abiotic environmental factors, such as aridity, which alter the material properties of their parts. Treating dental topography metrics as ecometrics by examining their spatial relationships to climate may provide a new means of testing relationships between these metrics and food properties.

Higher community values of Dirichlet normal energy (DNE) and orientation patch count (OPC) are expected in colder, drier, and more seasonal environments. Lemur species ranges are taken from IUCN range maps and environmental data

from WorldClim. One thousand sampling points are evenly distributed across Madagascar, with 539 intersecting lemur species ranges. The relationships between topographic metrics and precipitation, temperature, and seasonality are modeled using multivariate regression. The hypotheses are only partially supported. DNE is associated with seasonality as predicted, with strong positive associations with both temperature and precipitation seasonality, and is also highest in hot and arid environments. OPC, alternatively, is highest in cool, wet environments with low seasonality. This suggests that these metrics reflect different aspects of lemur dietary ecology. DNE appears to correspond more closely with adaptation to more demanding fallback foods in environments of greater environmental stress.

Re-evaluating the analysis of dominance: Investigations of dominance in captive chimpanzees (*Pan troglodytes*) and wild Tibetan macaques (*Macaca thibetana*) from a context-dependent perspective

JAKE A. FUNKHOUSER^{1,2}, JESSICA A. MAYHEW^{2,3} and LORI K. SHEERAN^{2,3}

¹Department of Anthropology, Washington University in St. Louis, ²Primate Behavior Program, Central Washington University, ³Department of Anthropology & Museum Studies, Central Washington University

Theoretical definitions of dominance, how dominance is structured and organized in nature, and how dominance is measured have varied as investigators seek to classify and organize social systems in gregarious species. Given variability in behavioral measures and statistical methods used to derive dominance rankings, we conducted a comparative analysis of dominance using existing statistical techniques to analyze dominance ranks, social context-dependent dominance structures (agonistic competitions, lack of agonism, privileged role, and priority access to resources), the reliability of statistical analyses, and rank predictability of dominance structures on other social behaviors (e.g., affiliative, grooming, and nearest-neighbor networks). We investigated these topics using behavioral data from captive chimpanzees (*Pan troglodytes*) and wild Tibetan macaques (*Macaca thibetana*). We used a combination of all-occurrence, focal-animal, and instantaneous scan sampling to collect social, agonistic, and associative data from both species. We analyzed these data with 69 statistical tests across multiple software (R, SPSS, UCINET, SOCPROG) to derive dominance ranks (via DS, I&SI, ELO, ADAGIO, PERC), test rank reliability (via individual median rank calculations and Spearman's ρ correlation coefficients), and assess cross-context predictability (using MR-QAP matrix correlation/regression). These results indicated context-dependent dominance and individual social roles in the captive

ABSTRACTS

chimpanzee group, one broadly defined dominance structure in the Tibetan macaque group, and high within-context analysis reliability but little cross-context predictability across both species. Overall, we suggest this approach is preferable over investigations of dominance where only a few behavioral metrics and statistical analyses are utilized with little consideration of rank reliability or cross-context predictability.

Pete and Sandra Barlow Award (CWU Department of Anthropology and Museum Studies); Debra and Arlen Prentice Award (CWU Primate Behavior Program); CWU School of Graduate Studies and Research

Dental Disease in an Egyptian Colonial Cemetery at Tombos

MARGARET J. FURTNER¹ and MICHELE R. BUZON²
¹Department of Geography & Anthropology, Louisiana State University, ²Department of Anthropology, Purdue University

The purpose of this study is to examine the prevalence of dental disease at Tombos, a cemetery established during the Egyptian colonial occupation of Nubia that was used during the New Kingdom through the Napatan period. Earlier studies conducted on a previously excavated sample of the population reveal significantly high dental wear in comparison to regionally and temporally similar groups, and high levels of antemortem tooth loss in comparison to abscess and caries rates. The current sample reflects similar trends of severe dental wear, high prevalences of AMTL, and low prevalences of abscesses and caries. The average wear score for the M1 totaled 29.33/40, recorded using the Scott method. 18% of the total tooth sample was lost due to AMTL, while only 4% of observed teeth were affected by caries and 5% of associated alveolar bone was affected by abscesses. Overall, the current assemblage under study reports lower frequencies of AMTL, abscesses, and caries than the previous Tombos sample, with slightly higher rates of molar wear, and a higher individual decay rate of 81.82%. The variation between these two assemblages from Tombos may be attributed to socio-cultural differences between the samples, initially evidenced by their distinct burial styles reflecting different cultural traditions and socioeconomic class. These results indicate inter-population variation in the prevalence of dental disease at Tombos, which may be attributed to the political and cultural changes taking place in the region as a result of colonial occupation, which differentially affected various segments of the community.

Exploring age-related variations during calcaneal growth

GAIA GABANINI¹, CARLA FIGUS¹, RITA SORRETINO^{1,2}, NICHOLAS B. STEPHENS³, MARIA

G. BELCASTRO^{2,4}, WILLIAM HARCOURT-SMITH^{5,6,7}, TIMOTHY M. RYAN³ and STEFANO BENAZZI^{1,8}

¹Department of Cultural Heritage, University of Bologna, ²Department of Biological, Geological and Environmental Sciences - BiGeA, University of Bologna, ³Department of Anthropology, Pennsylvania State University, ⁴ADES AMU-CNRS-EFS: Anthropology and Health, Aix-Marseille Université, ⁵Graduate Center, City University of New York, ⁶Department of Anthropology, Lehman College, ⁷Division of Paleontology, American Museum of Natural History, ⁸Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology

Methods for age estimation in juvenile osteological samples are highly accurate compared to those of adults, but little is known about the variation of the foot bones during growth. This study explores the age-related morphological changes of the calcaneus, which is often well preserved even in the case of multiple or damaged burials, using Geometric Morphometric Methods.

A sample of 33 modern human juvenile calcanei (known age/sex= 22; unknown sex/age= 11) was 3D scanned using an Artec3D Space Scanner. 5 age categories (0-15 years) were defined; unknown sex/age specimens were classified as ND.

A template of 15 landmarks and 209 semi-landmarks was applied to the digital models. The (semi)landmark configurations were superimposed by Generalized Procrustes Analysis. A form space Principal Component Analysis (PCA) was computed using the known sample to explore variation during growth, while ND specimens were projected within it.

The analysis shows that PC1 (ca. 93%) is highly correlated with size and accounts for ontogenetic allometry. Negative scores (youngest individuals) are characterized by a compact morphology while positive scores (oldest individuals) show both a greater definition of the *sustentaculum talii* and *sinus tarsii* and more pronounced edges for the talar and cuboid articular facets. The projected sample follows the trajectory of the known sample, which means that our ND specimens can be aged in the 5 categories after being projected. Our results suggest that age-related morphological changes of the calcaneus during growth may be used to estimate the general age of juvenile skeletal remains.

This project is funded by the European Research Council (ERC) under the European Union's Horizon 2020 research and innovation programme (grant agreement No 724046 - SUCCESS); website: <http://www.erc-success.eu/>

The Ethical Exhibition of Human Remains

AUBREE GABBARD
Sociology and Anthropology, Metropolitan State University of Denver

Despite ongoing conversations about the collection and display of human remains, a universally accepted standard for exhibiting human remains does not exist. Who decides what human remains belong on display and how are those conclusions reached? This pilot study examines the display of human remains in museums and cultural institutions by investigating the perspectives of anthropological researchers and museum staff. Interviews and surveys with anthropologists and museum professionals working within the United States were conducted to assess perspectives on the conditions in which human remains may be displayed.

Survey responses were analyzed based on the professional's role in the field as well as their educational, professional, and cultural backgrounds. Preliminary results show common themes centering around the cultural affiliation of the remains, context and purpose of the exhibition, and type of human remains on display (complete, skeletal, replica, print, etc.). Professionals who work with descendent populations were more likely to prioritize their values and beliefs when considering exhibiting human remains. Museum visitors were asked to participate in an oral survey in order to better understand if the expected messages of exhibitions are reaching their intended audience.

Museums have a responsibility to both the general public and the communities whose cultural material they curate. Future research includes using ethnographic methods to find common goals and help facilitate conversations between groups with conflicting perspectives, seeking to answer the question of how anthropology and museum professionals can balance their accountability to both museum visitors and descendent populations.

Weighing the possibilities: Exploring a modified technique for the assessment of frailty in human skeletal remains

KATHERINE GADDIS¹, MARISSA RAMSIER¹, ARKADIUSZ KOPERKIEWICZ², MAREK POLCYN³ and ARIEL GRUENTHAL-RANKIN^{1,4}

¹Department of Anthropology, Humboldt State University, ²Institute of Archaeology, University of Gdansk, ³Department of Anthropology, Lakehead University, ⁴Department of Anthropology, Binghamton University (SUNY)

In recent years, significant progress has been made toward the development of a cumulative index for assessing frailty in archaeological populations. However, current bioarchaeological assessments do not take into consideration variation in the severity of physiological stressors and individual responses to those stimuli. This study proposes a modified method for the assessment of frailty in archaeological remains that involves a weighted analysis of commonly observed non-metric biomarkers of skeletal stress rather

ABSTRACTS

than just scoring as present or absent. This modified index employs a series of weighted scales designed for each of four categories of physiological stressor, including nutritional deficiencies, infections, growth disruption, and trauma. The sample included 36 individuals (males, $n=19$; females, $n=12$; indeterminate, $n=5$) aged approximately 7 to 65 years from the Beżawki archaeological site, a Late Medieval Prussian cemetery located in northeastern Poland. Each individual included in this study was examined for evidence of stress biomarkers, which were scored and weighted by factors such as activity of lesions, size and prevalence of dental caries, and progression of joint disease. Biomarker scores were then used to determine a cumulative frailty score for each individual. These individual cumulative scores were then compared with those previously calculated using a binary index of frailty. Preliminary results of this study indicate that a weighted index can provide additional insight into demographic patterns of frailty that may otherwise be obscured by a presence-absence system. Ongoing research will continue to explore modifications of existing techniques for the assessment of frailty in archaeological assemblages.

Palatine morphological variation associated with diet in lemurs

GLADYS Y. GALDAMEZ and SARAH M. ZALESKI
Anthropology, University of Florida

Previous research has demonstrated differences in cranial morphology among lemurs that are associated with diet. This study assesses differences in palatine morphology among lemur neonates. The sample includes four frugivores (*Lemur catta*, *Cheirogaleus medius*, *Varecia variegata*, and *Eulemur mongoz*), two folivores (*Propithecus verreauxi* and *Hapalemur griseus*), a liquid consumer (*Mirza coquereli*), and *Microcebus murinus* with a varied diet. Qualitative analyses reveal longer, laterally displaced pyramidal processes in folivores. *Mirza coquereli* and *Microcebus murinus* show shorter, posteriorly displaced pyramidal processes. Three-dimensional landmark coordinates representing palatine bone shape and dental arcade border were collected in Amira software. Generalized Procrustes Analysis and Principal Component Analysis (PCA) were completed in the R Geomorph package. Most frugivores clustered together based on PC1 and PC2 scores. *Lemur catta*, however, clusters closer to folivores than expectations based on diet. The liquid consumer did not cluster with any other specimen. Frugivores exhibit a palatine that is relatively larger compared to other specimens and anteriorly displaced relative to alveolar landmarks. Palatine shape differences may be attributed to the medial-lateral breadth

of the bilateral maxillary dentition. This study suggests that dietary differences are associated with variation in palatine morphology and spatial orientation relative to the dental arcade among neonatal lemurs.

Funded by the National Science Foundation (BCS-1231717, BCS-1231350, BCS-0959438, BCS-1728263)

The Bioarchaeology of Urbanisation in Denmark

JULIA A. GAMBLE
Anthropology, University of Manitoba

The period from the 11th to the 16th centuries in Denmark saw increasing urbanisation with the development of towns focused around market centres. This was influenced by population decimation in the mid-14th century with the Black Death epidemic and consequent socioeconomic and political restructuring. It has been suggested that these changes would have influenced population health, with disparity between rural and urban contexts. However, bioarchaeological studies have revealed inconsistent patterns, highlighting the complexity of this period and the need for more in depth study. Using a novel dental enamel microscopic approach, this study examines population difference in health and stress for urban and rural sites in and around the medieval town of Horsens, Denmark. No clear differences in growth are identified between the rural and urban settings, with both overall stature and long bone metrics showing no significant difference, though in the broader population sample beyond that covered in the dental component of this study males at the urban site had significantly higher femoral lengths ($p = 0.012$). Enamel defects were segregated by crown portion and also scored according to severity (reflecting an overall picture of crown involvement). Results suggest that individuals from the urban site developed more severe developmental defects and that this was dominated by the occurrence of a higher number of defects forming between the ages of 2 and 2.9 years of age. Individuals from the urban site also saw reduced survivorship during childhood but improved survivorship as adults, suggesting an age-dependent difference in health experience.

This project was funded in part by a SSRHC Vanier Canada Graduate Scholarship.

Reconstructing Weaning and Childhood Diets at the 6th-5th C. BCE Skeletal Population of the Greek Colony of Himera

ABIGAIL S. GANCI¹, LAURIE J. REITSEMA², KATHERINE L. REINBERGER², STEFANO VASSALLO³ and BRITNEY KYLE⁴

¹Gillings School of Global Public Health, University of North Carolina at Chapel Hill, ²Department of Anthropology, University of Georgia, ³Archaeological Heritage Section, Archaeological

Superintendency of Palermo, ⁴Department of Anthropology, University of Northern Colorado

Adequate nutrition during early childhood influences survival and adult health, yet practices concerning children are systematically overlooked in the literary and archaeological records. By investigating the infant feeding practices of a 6th-5th C. BCE skeletal population from the Sicilian Greek colony of Himera, this research examines ancient childhood lifeways and complements investigations into the morbidity and mortality of the Himieran colonial population. Using stable nitrogen and carbon isotopic ratios ($\delta^{15}N$, $\delta^{13}C$) derived from the bone collagen of 30 infants and juveniles and 10 adults, we determine time of weaning instigation, cessation, and the nature of complementary foods supplied to weaning infants. Through Bayesian analysis conducted using the WARN statistical package in R, we conclude that weaning began at 5 to 6 months after birth and was completed by 4 to 5 years of age. Both nitrogen and carbon values demonstrate clear trophic level enrichments associated with breast-milk consumption as well as declines to adult baselines with the transition to a solid diet. The modeled weaning chronology suggests that weaning lasted longer at Himera than at other colonial case studies and complements investigations into Himieran childhood stress which suggest that children experienced increased vulnerability during weaning. By expanding our understanding of childhood diets, this investigation contributes to a broader discussion of ancient Greek childhoods and the role of juveniles within complex colonial societies.

This research was funded by National Science Foundation Research Experience for Undergraduates award numbers 1560227 and 1560158, the University of Georgia, and the University of Northern Colorado.

Chronic stressors lead to dysregulated endocrine-immune function and diabetes risk in Honduran immigrant women

ANGELA R. GARCIA^{1,2}, SERGIO MURILLO^{2,3}, BENJAMIN C. TRUMBLE^{1,4}, MICHAEL D. GURVEN⁵ and AARON D. BLACKWELL^{5,6}

¹Center for Evolution and Medicine, Arizona State University, ²CESAMO, Utila, Honduras, ³Medicine, Universidad Catolica de Honduras, ⁴School of Human Evolution and Social Change, Arizona State University, ⁵Department of Anthropology, University of California, Santa Barbara, ⁶Department of Anthropology, Washington State University, Pullman

Adverse social conditions are consistently linked to higher risk of metabolic pathologies like type 2 diabetes (T2DM), and marginalized individuals tend to be at high risk of both poor social conditions and T2DM. Depression, discrimination, and other aspects of social adversity are thought to influence disease risk in part through their effect on the neuroendocrine and immune systems, but the mechanisms by which these factors influence

ABSTRACTS

disease risk is not well understood. We hypothesize that adverse social conditions chronically stimulate the hypothalamic-pituitary-adrenal (HPA) system, which results in decreased sensitivity of leukocytes to regulation by cortisol (i.e. glucocorticoid resistance, GCR) and increased glucose due to the opposing action glucocorticoids have on insulin. We evaluate this pathway linking social condition and T2DM risk among marginalized Honduran immigrants (N=123 women) with high rates of metabolic diseases, but substantial variation in individual risk. We find that blunted cortisol is associated with reduced change in count and proportion of lymphocytes over the day ($\beta = -6.99$, $p < 0.001$ and $\beta = -3.14$, $p = 0.01$), and that individuals reporting depressive symptoms (n=59) had significantly higher fasting glucose ($b = 0.114$, $p = 0.001$) and showed evidence of decreased sensitivity of lymphocytes to cortisol signaling ($b = -0.05$, $p < 0.001$). Our findings suggest that metabolic pathologies may be influenced by dysregulation of neuroendocrine-immune interactions. Finally, diverse aspects of social adversity may alter interactions between leukocytes and the HPA axis through effects on glucocorticoid receptor sensitivity, suggesting a pathway by which social factors may be linked to T2DM through influence on neuroendocrine and immune regulation.

Wenner-Gren Foundation Grant #9407

Bioarchaeological Evidence for Canalization in Subadult Body Size and Growth, Colonial Lambayeque Valley, Peru

VIRIDIANA M. GARCIA¹, DANIEL H. TEMPLE¹, HAAGEN D. KLAUS¹, JACLYN A. THOMAS² and STEPHAN N. BALL¹

¹Sociology and Anthropology, George Mason University, ²School of Human Evolution and Social Change, Arizona State University

The postcontact communities of Eten and Mórrope (A.D. 1536-1750) on the north coast of Peru demonstrate evidence for complex responses to Spanish colonization. Eten was located in a unique ecological and economic setting that buffered many stresses of conquest while Mórrope was characterized by sociopolitical marginalization and resource insufficiency. Drastically different responses to colonization in the two samples include greater skeletal evidence for chronic metabolic stress and infectious disease in Mórrope. However, no differences in adult body mass or stature were found between the two samples. This study evaluates differences in infant and childhood growth in body mass and femoral length between Eten and Mórrope to understand if similarity in growth also characterizes these samples (n=119). Lines were fit to the data using forward selection. Standardized residuals of body mass and femoral length were compared between Eten and Mórrope using Mann Whitney U tests. Linear models were fit to

both data sets. This result is normal for samples that do not include individuals older than 10 years. No significant differences in the standardized residuals for growth in body mass were found ($p < 0.11$). Similarly, no significant differences in the standardized residuals for growth in femoral length were found ($p < 0.10$). These results demonstrate that the lack of growth differences between adults paralleled that of infant and childhood growth. This study represents another line of evidence demonstrating deeply canalized growth patterns in north coast populations that likely helped maintain these similarities despite differences in biocultural settings.

The importance of age-at-death in orbital roof lesion analysis

BRIANNA GARDNER and TINA JAKOB
Archaeology, Durham University

Gardner & Jakob (2016) argued the use of the term "cribra orbitalia" promoted observer bias and introduced error in the prevalence of anemia in the medieval Fishergate House, York, UK population. In an attempt to amend this error, Lesion Type 6 was introduced as an additional lesion type to Stuart-Macadam's 1991 orbital roof lesion classification. Furthermore, the amended chart introduced standard differential diagnoses to be considered for each lesion type, which included several metabolic, nutritional deficiency, and nonspecific diseases as potential diagnoses.

Further research has indicated the necessity of considering age when analyzing orbital roof lesions. Failure to do so introduces severity error, as identically sized lesions will appear larger in smaller orbits and vice versa. Lesions within smaller orbits are often interpreted as more severe, while the same sized lesion within a larger orbit would be interpreted as less severe. In an attempt to address this issue, porosity size was removed from consideration of lesion types, resulting in an amended lesion type chart.

Age also influences the manner in which Type 6 lesions will manifest, as well as their appearance. New bone growth associated with disease in adults is primarily localized, while new bone growth in non-adults can be widespread due to the less mineralized nature of immature bones. Scurvy, a potential diagnosis for Type 6 lesions, is an example of such an occurrence. For this reason, the authors have further amended the lesion type chart to include a reference for Type 6 lesions in non-adults.

An experimental study of bone tools from Swartkrans Cave, South Africa

SARA GARDNER¹, FRANK L'ENGLE WILLIAMS¹, JASON HEATON² and TRAVIS PICKERING³

¹Department of Anthropology, Georgia State University, ²Department of Biology,

Birmingham-Southern College, ³Department of Anthropology, University of Wisconsin-Madison

Early Pleistocene deposits from Swartkrans Cave, South Africa, yield the remains of *Paranthropus robustus*, early *Homo*, and ungulate bone fragments that were manipulated through habitual yet short-term use and possibly utilized as multi-purpose tools. An experimental tool set modeled after those from Swartkrans Cave was created using fresh ungulate long bones to demonstrate wear caused by extracting termites, tubers, or both resources, and molded after 30, 60, 90 and 120 minutes of use (n = 12). The number of scratches in an area of 3.65 mm by 2.40 mm under a magnification of 40x range from 8 to 131. Scratch length, breadth, and angle were recorded for the five most prominent scratches. The highest standard deviation of scratch angle is seen in the tools used to dig both termites and tubers, whereas the lowest standard deviation is seen in the tools used for digging only termites. A principal components analysis shows that tools utilized exclusively for termites cluster near zero suggesting they are difficult to classify on the first PC axis (48.2% of the variance). On PC2 (26.9% of the variance), there is an imperfect separation between the tools used in both substrates and those utilized solely for tuber extraction. Comparison of these results to the original tools from Swartkrans suggests that *P. robustus*, and/or early *Homo*, could have utilized the bone tools for termite harvesting, tuber digging or both types of resource extraction. These results have implications for reconstructing the diet of early hominins in southern Africa.

Colonialism and Structural Violence: Implications for Childhood Physiological Stress and Mortality Risk

CAREY J. GARLAND and LAURIE J. REITSEMA
Anthropology, University of Georgia

This study bridges structural violence and the Developmental Origins of Health and Disease (DOHaD) to interpret patterns of indigenous childhood stress and mortality in the context of Spanish missionization in the American Southeast. Spanish missionization in La Florida is associated with changes in indigenous patterns of diet, disease, and demography related to Spain's political-economy. The DOHaD marks an important theoretical shift in bioarchaeology because it shows that adult health and mortality are tied to not only immediate political-economic circumstances, but also to early life physiological stress. Increased morbidity and mortality risks also are associated with repeat allostatic responses. Therefore, the link between early life stress and mortality risk is not simply related to *if* one experienced early life stress, but also *how often* they experienced stress. We examine internal enamel micro-defects as indicators of early life stress histories and predictors of

ABSTRACTS

age-at-death for indigenous Guale individuals interred at Mission Santa Catalina de Guale (n=50) (A.D. 1605-1680) on St Catherines Island, Georgia. In this sample, Guale individuals with observed enamel defects died earlier than individuals without observed enamel defects ($p=0.02$). Furthermore, results reveal a significant negative relationship between age-at-death and defect frequencies ($p=0.01$), suggesting that repeat early life stress was associated with increased risk of early mortality in this study sample. This research turns a spotlight on how structural violence in the context of Spanish imperialism impacted childhood health and mortality risk. This is important as children often suffer the greatest from the affects social inequality and oppression.

Effects of microbial colonization on bone collagen stable carbon and nitrogen isotope values: Results from a long-term diagenesis modelling experiment

SANDRA GARVIE-LOK¹, JILL MORGAN¹, PAMELA MAYNE CORREIA¹ and MINDY PITRE²

¹Anthropology, University of Alberta, ²Anthropology, St. Lawrence University

Here we report results from an experiment modelling microbial degradation in curated archaeological bone. Thirteen modern deer metapodials were inoculated with soil microbes commonly encountered in archaeological bone, incubated for nine weeks, then held at room temperature using different curatorial treatments (e.g. plastic or paper bags). Sections were frozen prior to inoculation and immediately after incubation for comparison to curated sections. SEM after two years of curation confirmed substantial microbial colonization for most treatments. This report discusses collagen stable carbon and nitrogen isotope values after eight years of curation. Six bones were chosen to represent a range of microbial degradation levels at the two year point. For each, collagen was isolated from pre-inoculation, post-incubation and post-curation sections. We expected that stable isotope values would change after incubation and curation, but that this would be accompanied by changes in collagen preservation indicators (collagen yield, C/N ratio, %C and %N) warning of the microbial degradation. The results show modest isotopic alterations for most treatments, some large enough to be interpreted as dietary differences. These were not correlated with curation treatment or microbial alteration at two years. C/N, %C, %N and yield remained within commonly accepted ranges, suggesting that these may not always warn of isotopic alteration. The prospect of microbial alteration of bone during curation is a concern for bioarchaeologists given the reliance of many studies on biochemical analyses of curated bone samples. Our results suggest that further research is needed to examine factors involved in this degradation.

Assessing the potential of ilium outlines, greater sciatic notch metrics, and indices of pubic/ischial length for subadult sex estimation

HEATHER M. GARVIN¹, KIERAN SEVERA^{1,2}, ELIZABETH TERNENT¹, MICHALA K. STOCK³, LAURA CIRILLO⁴ and KYRA E. STULL^{4,5}

¹College of Osteopathic Medicine, Des Moines University, ²College of Pharmacy & Health Sciences, Drake University, ³Department of Exercise Science, High Point University, ⁴Department of Anthropology, University of Nevada, Reno, ⁵Department of Anatomy, University of Pretoria

Previous studies on subadult pelvic sexual dimorphism present varying results depending on the samples, variables, and methods applied. This study used a modern sample of subadult post-mortem CT scans to investigate the utility of ilium outlines, greater sciatic notch (GSN) measurements, and indices of pubic/ischial length in subadult sex estimation. The pelves of 202 subadults (neonate to 10 years of age) were segmented and 3D surface models created. Ilium orientation was standardized and two-dimensional contour outlines were collected and subjected to elliptical Fourier and principal component analyses. GSN length, depth, and angle, along with pubic and ischial lengths, were collected from the 3D models. M/ANCOVA and discriminant function analyses (DFA) were performed on the principal components and pelvic metrics.

ANCOVA results indicate significant ($p < 0.05$) sexual dimorphism in components related to the ilium outline, although DFA correctly classified only 60.4% of the total sample. Systematically re-running analyses excluding the youngest age cohorts at one year intervals (e.g., including all individuals >1yr, all individuals >2yr, etc.), revealed that by the age of four, correct classification increases to 77.4%, although the sample size was limited to 31 individuals. Correct classification using GSN variables did not exceed 64% regardless of the age cohorts or variables included. The pubic/ischial indices displayed no significant sex differences. These results suggest that pelvic sex estimation is unreliable in young children, but that ilium shape may be undergoing sexual differentiation by the age of five. Larger samples of subadults in these mid-childhood ages are needed for further testing.

This project was funded as part of a National Institute of Justice (2015-DN-BX-K409).

Oral processing behaviors of captive mandrills (*Mandrillus sphinx*) at the Columbus Zoo

JOSEPH GEHERTY and SCOTT W. MCGRAW
Anthropology, The Ohio State University

Oral processing behaviors are known to co-vary with aspects of feeding ecology, food material properties, and cranio-dental anatomy. Previous field studies on terrestrial mangabeys (*Cercocebus*) have revealed important age/sex differences in the frequency of incision, isometric biting and chewing frequency related to diet. Here we provide information on the *Cercocebus* sister taxon in order to better understand variation within this clade of African papionins. We examined oral processing behavior of captive mandrills (*Mandrillus sphinx*) at the Columbus Zoo and tested the hypothesis that extreme sexual dimorphism in this species would result in significant age and sex differences in food processing behaviors. We used focal animal sampling on an adult male and female, and two sub-adult males to quantify ingestive and oral processing behaviors associated with different foods available to the monkeys. Kruskal-Wallis tests were performed on a sample of over 1,100 chewing events across subjects. Significance tests identified few age/sex differences in rates of incision or mastication when individuals consumed the same food items. However, among eight food types, five yielded significant differences in incision frequency while two yielded differences in mastication frequency. Foods such as stems and bark tended to require more incisive work than smaller items. We conclude that despite its extreme degree of sexual dimorphism, captive mandrills process their foods in comparatively similar ways across ages and sexes. These results are consistent with those from free-ranging sooty mangabeys and suggest that ingestive and oral processing behaviors are generally conservative across African papionins.

Dentin hardness distribution and chewing frequency in two sympatric colobines

ELISE GEISSLER¹, W. SCOTT. MCGRAW² and DAVID J. DAEGLING¹

¹Anthropology, University of Florida, ²Anthropology, The Ohio State University

Dentin acts to preserve dental structural integrity and to arrest and prevent cracks, although little is known about the effects of fatigue on dentin hardness. Because dentin is sensitive to changes in the oral environment over the lifespan, the question arises as to whether chewing frequency influences dentin microstructure. Sagittal sections of molars from two sympatric African colobine monkeys, *Colobus polykomos* (n = 6) and *Ptilocolobus badius* (n = 5) were sampled, of which the former displays a higher chewing frequency than the latter (McGraw et al. JHE 98: 90-102). Coronal dentin was examined using a Knoop indenter by placing ten clusters of indents at four different angles (0°, 30°, 60°, 90°) throughout the tooth to measure hardness distribution.

ABSTRACTS

Anisotropy (differences among indenter angles) was nonsignificant ($P > 0.09$). Subsequent nested ANOVA found no statistically significant difference between species ($P = 0.2$) in overall indentation hardness. Resampled 95% confidence intervals also overlapped extensively. Heatmaps revealed dentin softening nearer the pulp chamber and towards the dentin-enamel junction in most samples. However, while five of six *C. polykomos* samples showed a significant positive Moran's *I* statistic for spatial autocorrelation ($P < 0.05$), no *P. badius* teeth displayed significant Moran's *I*.

While variation in hardness is not different between the species, spatial dependence of hardness is evident. This finding raises questions concerning fatigue risk and the role of load history in determining the spatial distribution of hardness variation in mature molars.

NSF BCS-0922429 and 0921770.

At the Intersection of Gender, Age, and Race: The Complexity of Social Identity in Early-20th Century Cuba

PAMELA L. GELLER

Department of Anthropology, University of Miami

While bioarchaeological studies of social identity have proliferated recently, few account for the intersectional nature of identity. To do so recognizes identity as a process formed from multiple, cross-cutting facets of lived experience like gender, race, age, class, etc. There are several reasons bioarchaeologists are reticent to conceptualize identity as such. Much writing about intersectional identity comes from feminist and queer scholars who concentrate on its discursive aspects while eliding its material ones. Intellectual labor is needed to make these ideas applicable to bioarchaeology. At the same time, bioarchaeology's emphasis on population-based research fails to adequately explain a group's heterogeneity or the nuances of individuals' life histories. In support, a review of publications demonstrates that investigators often represent "women" and "men" as monolithic and stable categories. There is little attention to the dynamism of gendered identities throughout life or the impact that other dimensions of existence have on their performance. As an example of how to materialize intersectional identities, I discuss the crania of three individuals from Cuba who died in the early-twentieth century. They were buried in a Havana cemetery, disinterred in 1922, and then sent to the Smithsonian's National Museum of Natural History. Skeletal and archival analysis indicate they were females, black (though identified archivally as "mixt race"), middle-aged, and born enslaved. Ultimately, this Cuban example shows that what has historically been "missing"

is consideration of identity's complex intersections—in this case, gender, age, race, class, and nationality—that facilitate more comprehensive and equitable reconstructions of the past.

This work was supported by a Faculty Grant from the University of Miami Institute for Advanced Study of the Americas.

Exploring the population history of modern Latinos through dental morphology

REBECCA L. GEORGE and G. RICHARD SCOTT

Anthropology, University of Nevada, Reno

Latino groups are one of the fastest growing populations within the United States. As a result of this increase, forensic anthropologists have to be familiar with the skeletal variation within these diverse populations as it is likely they will be represented in casework. The current project aims to explore the dental morphological variation of Latino populations through biodistance statistics that trace their population history. Dental morphological variation should be part of the ancestry estimation methods for Latinos for several reasons: 1) they have a unique population history; 2) the shapes and features of teeth are under moderate to high genetic control; 3) certain traits, such as shoveling, exhibit dominance and are expected at certain frequencies in these populations. Pre-contact Native American samples from the United States and Latin America were compared to archaeological European and Africa samples and modern European and Latino samples to examine the changes in dental morphological frequencies through time. Data were collected on modern populations according to the ASUDAS standards, while pre-contact and archaeological populations were sampled from the Turner database. As compared with the pre-contact samples, for example, modern Latinos exhibited lower a lower prevalence of shoveling, hypocone presence, and enamel extensions, but exhibit a higher rate of Carabelli's trait. A preliminary Mean Measure of Divergence analysis showed significant distances between the temporal and nearly all regional samples. These results demonstrate an initial success with utilizing dental morphology to define Latino dental variation.

Adiposity, leptin, and single nucleotide polymorphisms in Kansas Mennonites

CHAD GERHOLD¹, MICHAEL CRAWFORD^{1,3} and MJ MOSHER^{1,2}

¹Laboratory of Biological Anthropology, University of Kansas, ²Department of Anthropology, Western Washington University, ³Department of Anthropology, University of Kansas

Leptin (*LEP*), an afferent protein signal synthesized primarily by adipocytes, moderates energy storage and expenditure by promoting gene expression through leptin receptors (*LEPR*).

Several mutations documented in the *LEPR* are associated with increased obesity. Using results of a whole exome study of individuals of the Kansas Nutrition Project (M97, Fe105), we selected 7 *LEPR* SNPs (rs1045895, rs1137100, rs1137101, rs1805134, rs1805094, rs12067936, rs1805096) previously found to be associated with obesity in genome-wide associational studies. We hypothesized that that variation of DNA methylation (DNAm) along the *LEP* core promoter would correlate with receptor mutations associated with increased adiposity. All selected SNPs were in Hardy-Weinberg equilibrium. Methylation percentages at 7 CpG sites were logit transformed to correct for heteroscedasticity. BMI, serum leptin (log transformed) and *LEPR* SNPs statistical models were constructed using permutation tests and fixed-effect ANOVA tests. Benjamini-Hochberg method for calculating false discovery rate (FDR) was used and statistical significance set as $p = 0.05$ and $FDR = 0.10$. Data extraction and statistical analysis was conducted in the R environment. In both combined and sex-stratified data, we found no evidence to suggest DNAm at these 7 promoter CpG sites associated with BMI, leptin levels or with *LEPR* SNPs amongst Kansas Mennonites. Further adjustment for both age and dietary macronutrients intake percentages did not alter the outcome. These findings suggest that changes in adiposity among Mennonites are not associated with epigenetic methylation patterns in leptin's core promoter region and alternative metabolic pathways are regulating adiposity in Mennonites.

Mortality or Methods: What Do Skeletal Age Estimates Really Tell Us About Past Populations?

SARA M. GETZ¹ and GEORGE R. MILNER²

¹Anthropology, Idaho State University,

²Anthropology, The Pennsylvania State University

Paleodemographic analyses depend on accurate age estimates; however, despite criticisms of commonly used adult estimation methods for the pubic symphysis and iliac auricular surface, they are still often employed. Here the performance of the Brooks and Suchey (1990), Lovejoy et al. (1985), and Buckberry and Chamberlain (2002) procedures are compared using two modern, known-age skeletal collections, Athens (N=201) and St. Bride's Crypt (N=168), and two archaeological samples from Denmark, Klosterkirke (N=166) and Ole Worms Gade (N=317).

No estimated age-at-death distribution approximated the two known-age distributions. Age distributions for single samples do not resemble one another when different age-estimation methods are used. Instead, each method produces its own characteristic age distribution,

ABSTRACTS

regardless of the sample. Method-specific patterns are recognizable even though samples differ in their age and sex composition, source population, and skeletal preservation.

Of particular interest is an inability to capture old-age mortality. These data strongly suggest that the peculiar nature of paleodemographic adult age-at-death distributions, especially many deaths in middle age with hardly anyone surviving past 50 years, is likely the product of method choice, not past mortality experience.

Identifying the effects of these patterns on paleodemographic research and subsequent interpretations is complicated by the frequent use of multiple techniques to age single skeletons, the various ways separate age estimates are combined, and differences in skeletal preservation. In short, age-at-death distributions produced using these techniques should be considered, at best, questionable, and, at worst, pure fiction.

Research funded by NSF Doctoral Dissertation Research Improvement Grant (DDRIG) 1455810.

Heritability of the Body Composition and Blood Pressure association in ethnically distinct indigenous populations

SUDIPTAA GHOSH¹, TASBULAT DOSAEV², JAI PRAKASH³ and GREGORY LIVSHITS³

¹Anthropology, North-Eastern Hill University,

²Anatomy, Asfendiyarov Kazakh National Medical University,

³Anatomy and Anthropology, Tel-Aviv University

The present paper is an attempt to understand ethnic variations in the association of blood pressure with body composition in two geographically and ethnically diverse adult populations, i.e. Santhal, an indigenous group from India and Chuvash, an indigenous population from Russia. In addition, the paper attempts to identify genetic and/or environmental factors that contribute to this association. Pedigree samples were collected from these two ethnically different populations. The multiple and multivariate regression frameworks were used in the paper. Contribution of genetic and shared familial environmental factors to variation and co-variation of the studied parameters were examined by quantitative genetic analysis using the Mendelian Analysis Package.

In somatotype, both the environmentally diverse populations are found to be predominantly mesomorphic irrespective of their sex. According to the multiple multivariate regression analysis results, age but not sex is an important confounder for blood pressure variations in both the samples. In addition, variance decomposition analysis indicates that fat mass, mesomorphic component and fat free mass have considerable influence on the variation of blood pressure. Heritability estimates are significant for all the blood pressure and body composition traits in both the populations

ranging between 0.125 ± 0.058 (Chuvash, ectomorphy) and 0.625 ± 0.084 (Santhal, FFMI), being however as a rule $\geq 0.250 \pm 0.086$. Hence, additive genetic component contribute to a substantial proportion of blood pressure and body composition variance. Resemblances in genetic and other covariates of blood pressure in these two populations perhaps suggest a basic pattern in epigenetic interactions that are possibly shared by the entire human species.

Ministry of tribal affairs, Government of India & Israel Science Foundation.

Effect of infant carriage on joint yield in wild vervet monkeys

DANIEL GIBBONS¹, BIREN A. PATEL^{2,3}, PETER S. HENZI^{4,5}, CHRISTOPHER YOUNG^{4,5,6}, LOUISE BARRETT^{4,5}, JONATHAN JARRETT^{4,5} and NATHAN E. THOMPSON¹

¹Department of Anatomy, New York Institute of Technology College of Osteopathic Medicine,

²Department of Integrative Anatomical Sciences, Keck School of Medicine, University of Southern California,

³Human and Evolutionary Biology Section, Department of Biological Sciences, University of Southern California,

⁴Psychology Department, University of Lethbridge,

⁵Applied Behavioural Ecology and Ecosystem Research Unit, University of South Africa, ⁶Department of Anatomy and Physiology, University of Pretoria

Anthropoid primates exclusively transport infants via infant clinging during locomotion. While carrying likely has advantages over infant parking, it confers a direct locomotor cost to the mother, proportional to the mass of the infant. Given energetic demands of rearing, mothers may be under high pressure to selectively alter gait parameters to minimize locomotor cost. One means to accomplish this would be to utilize greater energy recycling via large oscillations of the center of mass (CoM) during walking. Alternatively, perturbations to the infant and large CoM oscillations may lead to a bumpy ride for the infant, and thus increase costs associated with infant repositioning during travel. If true, mothers may walk with a 'flat' trajectory of the CoM, involving higher joint yield. This would minimize perturbations to the infant, but likely increase metabolic costs to the mother.

Here we test these hypotheses in wild vervet monkeys (*Chlorocebus pygerythrus*) from the Samara Game Reserve, South Africa. Adult females were filmed *ad libitum* while walking through acacia woodland with and without infant carrying. We measured 2D elbow and knee joint angles and joint yield as a proxy for CoM oscillations.

Initial results show mixed support for either hypothesis. Overall, both knee and elbow yield were slightly greater for carrying mothers (knee: carrying: $26.2 \pm 9.8^\circ$, non-carrying: $20.4 \pm 9.8^\circ$; elbow: carrying: $21.7 \pm 6.5^\circ$, non-carrying:

$16.3 \pm 7.0^\circ$). On an individual basis however, this trend was present in $\sim 65\%$ of individuals, suggesting that natural variation exists in infant carrying and mothers may find individualized methods through which to maximize locomotor efficiency.

Funded by the: National Research Foundation (South Africa; S.P.H.), Natural Science and Engineering Council (Canada; S.P.H. and L.B.), University of Pretoria (C.Y.), and National Science Foundation (SMA 1719432; N.E.T.).

Resolving the taxonomic status of *Cercopithecus dryas* Schwarz 1932 and *C. salongo* Thys van den Audenaerde 1977

CHRISTOPHER C. GILBERT^{1,2,3}, ERIC J. SARGIS^{4,5,6}, EMMANUEL GILISSEN^{7,8}, JULIA L. ARENSON^{2,3}, BIREN A. PATEL^{10,9}, MASATO NAKATSUKASA¹¹, KATE M. DETWILER¹², TERESE B. HART^{13,5} and JOHN A. HART^{13,5}

¹Department of Anthropology, Hunter College, CUNY, ²PhD Program in Anthropology, The Graduate Center, CUNY, ³New York Consortium in Evolutionary Primatology, (NYCEP), ⁴Department of Anthropology, Yale University, ⁵Division of Vertebrate Zoology, Yale Peabody Museum of Natural History, ⁶Division of Vertebrate Paleontology, Yale Peabody Museum of Natural History, ⁷BIOCOL, Department of African Zoology, Royal Museum for Central Africa, ⁸Laboratory of Histology and Neuropathology, Université Libre de Bruxelles, ⁹Department of Integrative Anatomical Sciences, Keck School of Medicine, University of Southern California, ¹⁰Human and Evolutionary Biology Section, Department of Biological Sciences, University of Southern California, ¹¹Laboratory of Physical Anthropology, Graduate School of Science, Kyoto University, ¹²Department of Anthropology, Florida Atlantic University, ¹³Lukuru Wildlife Research Foundation, Quartier de Kingabois, Commune de la Gombe, Kinshasa, Democratic Republic of Congo

In 1932, Schwarz described the skin and skull of a juvenile male guenon as *Cercopithecus dryas*. Decades later, a partial adult skin from central Congo Basin was described as another new species, *C. salongo*. Osteological specimens later confirmed the distinctiveness of *C. salongo*, but subsequent research proposed that *C. salongo* simply represents adult *C. dryas*. Thus, many researchers accept *C. dryas* as the only valid name for these mysterious monkeys, whereas others recognize *C. dryas* and *C. salongo* as separate species. Unfortunately, the single juvenile *C. dryas* type specimen makes it difficult to accurately predict adult *C. dryas* morphology. In 2014, a rare guenon was discovered in the TL2 region of central Congo Basin matching the descriptions of both *C. dryas* and *C. salongo*. Adult specimens of the TL2 guenon share distinctive dental features with *C. salongo*, inspiring statistical comparison between all known *C. salongo*/TL2 specimens and the partially erupted adult dentition of *C. dryas* for the first time. Results demonstrate that *C. dryas* incisors are distinctively small, plotting

ABSTRACTS

closest to *C. salongo* among all available guenon specimens ($n=215$). Furthermore, a discriminant functions analysis ($n=102$) based on four dental variables clearly separates *C. salongo* specimens from other guenons and classifies *C. dryas* as a member of the *C. salongo* group. Our observations on the holotype *C. dryas* and *C. salongo* skins also confirm they are extremely similar. Therefore, direct morphological evidence strongly suggests these populations are conspecific and *C. dryas* is the only valid name for these highly endangered monkeys.

This study was generously funded by the AAPA Professional Development Grant Program, the PSC-CUNY Faculty Award Program, and Hunter College.

Human reproductive hormone measures: Methodological considerations and anthropological importance

THERESA E. GILDNER

Department of Anthropology, Dartmouth College

Energetic investment in reproduction has long been recognized as very costly, influencing developmental, physiological, and behavioral patterns in men and women. These effects are largely coordinated through the actions of reproductive hormones (e.g., testosterone, estrogen, and progesterone). Here, the utility and limitations of minimally-invasive reproductive hormone measurement techniques are explored, providing a novel perspective on how these measurements can enhance reproductive endocrinology research. Salivary steroid measures are most commonly used, although several dried blood spot (DBS) assays are also available, and researchers continue to explore the efficacy of other sample types. These relatively inexpensive, simple measures have facilitated the collection of multiple samples from a single participant, allowing researchers to more accurately track the diurnal and cyclical variation exhibited by many reproductive hormones. Ultimately, the ability to collect fine-grained participant data allows biological anthropologists to better test questions central to human evolutionary biology, life history theory, and public health. For example, fieldwork using these techniques among several groups (e.g., Shuar, Ache, Tsimane, and Filipino men) has demonstrated that testosterone levels vary across populations. This variation has been linked with differences in activity levels, disease exposure, and nutrition, with implications for male health. Additionally, this research indicates that key life events (e.g., fatherhood or aging) alter testosterone profiles in certain contexts. These findings highlight how minimally-invasive collection techniques can be implemented to evaluate hormone profiles across diverse social and

ecological conditions. Still, more work is needed to standardize collection and laboratory analysis procedures, thereby enabling more direct data comparisons between researchers.

The American Philosophical Society Lewis and Clark Fund; National Science Foundation (#BCS-1650674, BCS-1341165, BCS-0824602, BCS-0925910, GRF-2011109300); Ryoichi Sasakawa Young Leaders Fellowship Fund; University of Oregon; Wenner-Gren Foundation for Anthropological Research.

Observation of visitors at a chimpanzee ecotourism site reveals opportunity for multiple modes of pathogen transmission

DARCEY B. GLASSER¹, TONY L. GOLDBERG² and JESSICA M. ROTHMAN³

¹Psychology, Hunter College of The City University of New York, ²Pathobiological Sciences, School of Veterinary Medicine, University of Wisconsin-Madison, ³Anthropology, Hunter College of The City University of New York

Chimpanzee (*Pan troglodytes*) tracking is a popular ecotourism activity across Sub-Saharan Africa, offering visitors a personal wildlife experience and providing governments a source of much needed foreign income. However, chimpanzee ecotourism may increase the risk of disease transmission to and from the apes. Previous risk assessments have primarily focused on aerosol transmission, while other modes, such as environmental features and fomites, may also be important. This study assessed how tourist behaviors might facilitate cross-species disease transmission at a popular tourist site in Kibale National Park, Uganda. We collected observational data during 100 chimpanzee tracking excursions ($n=235$ hours). We recorded behaviors of over 500 tourists, guides, and student interns. Common behaviors included spitting, sneezing, and coughing. Per excursion, instances of individuals touching their faces averaged 125.84 ($SD=34.45$), and instances of people touching large tree trunks or branches while near chimpanzees averaged 230.14 ($SD=108.66$). Uncommon behaviors included urinating, defecating, discarding waste, and applying aerosol bug sprays. Initial tourist group sizes and durations of group merging were also calculated. Multiple tourist groups merged over 30% of the time, increasing group size to a mean of 17 tourists instead of the recommended 6. Overall, high rates of merging, coupled with frequent unsanitary behaviors, may increase the risk of cross-species disease transmission. Regulations to minimize the impact of ecotourism on chimpanzee and human infection risk should consider the realities of tourist behavior and the full range of modes by which pathogen transmission between species might occur.

Department of Psychology, Hunter College of The City University of New York, Graduate Women in Science, Hunter College of The City University of New York.

Variation in the trabecular structure of the proximal tibia between obese and non-obese individuals

DEVORA S. GLEIBER, DEBORAH L. CUNNINGHAM and DANIEL J. WESCOTT

Anthropology, Texas State University

Obesity adds a biomechanical burden to the human knee joint that should be reflected in the trabecular structure of that joint. We assess the differences in trabecular architecture of the proximal tibia in obese and non-obese individuals. Tibiae of ten obese and ten non-obese, age-matched females and males were scanned using high-resolution computed tomography. A cubic volume of interest (VOI) was extracted from below the center of the medial and lateral condyles and bone volume fraction, connectivity density, degree of anisotropy, and trabecular thickness and separation were calculated for each VOI. Two-tailed t-tests show that only females have significant differences in the trabecular architecture of obese and non-obese individuals. Obese females have significantly lower trabecular separation and greater connectivity density in the medial condyle. There is a nearly significant difference in anisotropy in the medial condyle, with obese females having less directionally oriented trabecular structures than non-obese females. The results of this study suggest that the biomechanical burden of obesity is reflected in the proximal tibia trabecular structure of females, but not of males. The differences between obese and non-obese females are more pronounced in the medial condyle and are due to the addition of trabeculae in obese females rather than an increase in the trabecular thickness. This signal of obesity may differ in males and females due to differences in body fat distribution. This study further contributes to our understanding of how obesity affects the skeleton, and more broadly how bone reacts to mechanical usage.

This research is supported in part through instrumentation funded by the National Science Foundation under Grant NSF/MRI 133804.

The evolution of gape and bite force potential in primates

HALSZKA GLOWACKA¹ and GARY T. SCHWARTZ²

¹Department of Basic Medical Sciences, University of Arizona College of Medicine-Phoenix, ²Institute of Human Origins, School of Human Evolution and Social Change, Arizona State University

Selection for high bite-force magnitude and large canines have seemingly opposite effects on the bony morphology of the masticatory system. All things being equal, increased proximity of molars to the adductor muscle resultant should increase bite-force magnitude, while an increase in canine size (with a concomitant increase in gape) should increase the distance between the last molar and the resultant to allow an anterior migration of the resultant during posterior biting. We investigated

ABSTRACTS

whether jaw gape (measured as canine overlap and jaw length) and food toughness influence the proximity of the last molar to the adductor muscle resultant (termed Resultant-Molar), while controlling for skull size. We collected 3D coordinate data from samples of adult primate skulls ($n=21$ species) and used PGLS and AICc to determine the best-fit model(s) and predictor variables(s) that explained interspecific variation in Resultant-Molar. Results showed no support for the notion that larger gapes increase Resultant-Molar; skull size was the only variable that significantly (positively) influenced Resultant-Molar ($R^2=0.79$, $\Lambda=1.0$). We performed a second set of analyses on a subset of species ($n=7$) for which data on dietary toughness were available. These results indicated that jaw length and maximum food toughness both had positive effects on Resultant-Molar ($R^2=0.98$, $\Lambda=0$). We suggest that selection pressures for increased bite force and large canines do not have opposing effects on masticatory morphology and that the evolution of large canines did not come at a cost to bite-force production.

Funding provided by NSF-DDIG 1540338, Wenner-Gren Foundation Doctoral Fieldwork Grant, Leakey Foundation Research Grant, James F. Nacey Fellowship, Elizabeth H. Harmon Research Endowment, and Donald C. Johanson Paleoanthropological Research Endowment.

Multi-Isotopic Investigation to Determine the Provenance of an Unidentified Female

GENNIFER GOAD¹, KIRSTEN VEROSTICK¹, ERIN KIMMERLE¹ and GEORGE KAMENOV²

¹Anthropology, University of South Florida,
²Geological Sciences, University of Florida

Forensic anthropologists increasingly use chemical isotope analysis in the investigation of unidentified human remains, as biochemical georeferencing continually improves with the development of modern reference data of known origins. In March of 2018, the skeletal remains of a 20 to 30 year-old female of Hispanic and African-American ancestry were discovered in a wooded area of Central Florida and submitted to the FL Institute of Forensic Anthropology and Applied Sciences (IFAAS) for anthropological and isotopic analyses. This study presents and applies the high-precision lead isotope data of 63 modern human teeth with known origin, which were previously analyzed for strontium isotopes, to the multi-isotopic investigation of these unidentified remains. This dataset contains isotopic information of individuals from the United States ($n=34$), Colombia ($n=9$), Haiti ($n=5$), Cape Verde ($n=3$), Morocco ($n=2$), El Salvador ($n=2$), Guatemala ($n=2$), Honduras ($n=2$), Jamaica ($n=1$), Dominican Republic ($n=1$), Albania ($n=1$), and United Kingdom ($n=1$). The results found that, independently, the oxygen, strontium, and lead isotopes of the young woman fall within the normal range of an individual born

and living in the USA. However, a multi-variate approach using strontium and lead isotopes offer an alternative interpretation - she may have been born and resided outside of the USA, likely in the Caribbean. The decedent's carbon isotope values also demonstrate a diet typical of the Caribbean, corroborating an origin outside of the USA. Independently of IFAAS, investigators have made a presumptive identification with an individual from Haiti, validating the results of the multi-isotopic approach.

The utility of geographic information systems (GIS) software for the spatial analysis of bone microstructure

TIMOTHY P. GOCHA

Forensic Division, Clark County Office of the Coroner/Medical Examiner, Department of Anthropology, University of Nevada Las Vegas

Histological analyses of bone microstructure can reveal information regarding health and disease, biomechanical forces acting on tissues, or even help in the identification of an individual through estimation of their age-at-death. Historically, however, histological analyses have used very small regions of interest (ROIs). Recently, geographic information systems (GIS) software, combined with improved imaging and computing capabilities, has allowed for more thorough analyses of complete bone cross-sections than previously possible. This presentation will survey examples of these advances from a series of studies examining the femoral midshaft.

Thirty complete cross-sections from modern cadaveric donors were examined, 15 of each sex, ranging from 21-97 years old. Seamless cross-sectional images were imported into ArcGIS for analysis, where polygon features were used to segment the cortex into ROIs, and point features were used to mark histological variables, such as remodeling events. Spatial imaging and analysis of histological variables revealed significant spatial patterning of remodeling density, elucidating that the anterolateral region of the femur is more subject to tensile loading than the anteromedial region. Further analyses revealed that ROI size has a direct impact on estimating age-at-death, and that small ROIs are not recommended. Lastly, new models for estimating age, informed by the spatial analysis in GIS, demonstrate that histological analysis of the femoral midshaft can estimate age-at-death into the tenth decade of life with an average error of less than six years. The use of GIS for spatial analysis of bone microstructure is still a novel one, but demonstrates much promise.

Night and day: Subfossil faunal representation in neighboring Malagasy caves illustrates interaction and exclusion by predator and prey

LAURIE R. GODFREY¹, ZACHARY S. KLUKKERT², MARGARET E. LEWIS³, NOROMAMY J. RAHANTAHARIVAO⁴, LOVASOA RANIVOHARIMANANA⁴, PETERSON FAINA⁴, NICK SCROXTON^{5,6} and STEPHEN J. BURNS⁵

¹Anthropology, University of Massachusetts, Amherst, ²Anthropology, City University of New York Graduate Center, New York Consortium in Evolutionary Primatology (NYCEP), ³Biology Program, Stockton University, ⁴Sedimentary Basins, Evolution, Conservation (BEC), University of Antananarivo, ⁵Geosciences, University of Massachusetts, Amherst, ⁶Earth, Atmospheric and Planetary Sciences, Massachusetts Institute of Technology

The flooded caves of Tsimanampesotse National Park are magnificent graveyards of extinct lemurs and their associated fauna – windows into Madagascar's past prior to human arrival and through the human period. The diverse assemblage includes extinct, locally extirpated, extant, and introduced species. Preliminary excavation has yielded over 1000 fossils and a series of stalagmites that recorded regional climate and vegetation over the past 50,000 years. A fluctuating record of wet and dry periods has emerged; some taxa found today only in the eastern rainforest were once distributed across the island. Most surprising is the extent to which neighboring caves differ in faunal representation. Mitoho Cave has yielded many bones of the giant extinct fosa, *Cryptoprocta spelea*, and a distal humerus of a newly-discovered congener that was even larger – the largest mammalian carnivore known from Madagascar. Vintany Cave has yielded a trove of giant lemur bones, particularly *Pachylemur*, as well as horned crocodiles, elephant birds, hippos, raptors, giant extinct couas, and primates that persist in the area today, but almost no *Cryptoprocta*. We show how differences in taxonomic representation relate to differences in the structure of the caves, which, in turn, reveal how the sites were used by now-extinct species. Evidence of mammalian carnivoran predation has been found on bones of lemurs as large as gorillas or orangutans, including *Megaladapis edwardsi*, which has also been found at Tsimanampesotse. The newly-discovered carnivore and the caves themselves enrich our understanding of the ecosystem and primate niches in southwest Madagascar.

Funded by NSF BCS-1750598 (to LRG and SJB) and NSF AGS-1702891 (to SJB).

Beyond race: Functional consequences of human genetic variation within the human population

OMER GOKCUMEN

Biological Sciences, University at Buffalo

ABSTRACTS

Our view of humans has changed in the last decade. Beginning with humble insights from reading short sentences of the genetic code, we now come to read entire chapters of human history and nature. Traditional racial categorizations, still the stuff of much political and cultural reality, lost their meaning in our understanding of human genetic variation. Instead, we have discovered millions of variants in our genomes that contribute to our biological variation. Every aspect of our being, from our tendency towards mental illness to our preference in cereals, is now interrogated by titanic genetic association studies. Some of these functionally relevant variants are common and are not necessarily specific to any population. They are our inheritance from a now lost population of ancestors that we all share. Indeed, our own research has identified dozens of such ancient genomic structural variations (i.e., deletions, duplications, inversions, and translocations of large segments of DNA) that shape our biology in small but observable ways. They have been maintained in our genomes through adaptive forces over millions of years, affecting organismal functions ranging from growth and epidermal differentiation to digestion and the immune system. They underlie important traits that vary among humans- height, longevity, susceptibility to myriad diseases and resistance to pathogens that plagued us for millions of years. At this exciting junction where we now can "write" our own genetic code, it is crucial to recognize that genetic variation within human populations is real and has implications in how we shape our future.

National Science Foundation (Grant No. 1714867)

Chimpanzee reverse zoonoses: unfortunate natural experiments in great ape comparative medicine and demography

TONY L. GOLDBERG¹, SARMI BASNET², MELISSA EMERY-THOMPSON³, JAMES E. GERN², KRISTINE A. GRINDLE², KEVIN E. LANGENGRABER⁴, ZARIN MACHANDA⁵, JOHN C. MITANI⁶, MARTIN M. MULLER³, JACOB D. NEGREY⁷, EMILY OTALI⁸, LEAH OWENS¹, ANN C. PALMENBERG⁹, TRESSA E. PAPPAS², SARAH PHILLIPS-GARCIA³, RACHNA B. REDDY⁶, ERIK J. SCULLY¹⁰ and RICHARD W. WRANGHAM¹⁰

¹School of Veterinary Medicine, University of Wisconsin-Madison, ²Department of Pediatrics, University of Wisconsin-Madison, ³Department of Anthropology, University of New Mexico, ⁴Department of Anthropology, Arizona State University, ⁵Department of Anthropology, Tufts University, ⁶Department of Anthropology, University of Michigan, ⁷Department of Anthropology, Boston University, ⁸Makerere University Biological Field Station, Makerere University, ⁹Department of Biochemistry, University of Wisconsin-Madison, ¹⁰Department of Human Evolutionary Biology, Harvard University

Over 31 years, 27% of deaths in the Kanyawara chimpanzee community of Kibale National Park, Uganda, were attributable to respiratory disease – a pattern mirrored at other long-term research sites – and evidence points to human origins for most infections. Here, we report comparative data on viral respiratory disease in the chimpanzees of Ngogo and Kanyawara communities in Kibale. Epidemiological modeling estimated the basic reproduction number (R_0 , a measure of transmissibility) of three recent outbreaks as ranging from 1.27 to 1.83, which are similar to values for the "common cold" in humans. Affected chimpanzees showed age-related patterns of morbidity similar to those in humans, with infants and older adults most severely affected. Gross pathology resembled that in humans suffering severe infections (e.g. deep lung consolidation, pericardial effusions, persistent wheezing likely due to emphysema). For one pathogen, rhinovirus C, genotyping of the CDHR3 locus (the viral receptor) showed chimpanzees from Kibale and across Africa to be universally susceptible, similar to Neanderthals and Denisovans, but different from modern humans, who possess a recently evolved protective allele. This observation may explain similarities between chimpanzee infections and infections of asthmatic human children. Overall, our analyses show that infected chimpanzees in Kibale recapitulate the most severe forms of human disease, and that demographic correlates of infection are similar between chimpanzees and humans. If so, human infection of, for example, asthmatic children, the elderly, and the immunocompromised may serve as the best models for understanding chimpanzee infection with respiratory viruses of human origin.

Comparative analyses of human and chimpanzee demography, aging and health were supported by NIH Award 5R01AG049395 through the National Institute for Aging and the Office of Research on Women's Health.

An epigenetic measure of biological aging in rhesus macaques

ELISABETH A. GOLDMAN¹, KENNETH L. CHIOU², LAUREN J.N. BRENT³, MICHAEL J. MONTAGUE⁴, MICHAEL L. PLATT^{4,5}, JULIE E. HORVATH^{6,7,8}, SIERRA SAMS², KIRSTIN N. STERNER¹ and NOAH SNYDER-MACKLER²

¹Anthropology, University of Oregon, ²Psychology, University of Washington, ³Centre for Research in Animal Behaviour, University of Exeter, ⁴Neuroscience, University of Pennsylvania, ⁵Psychology, University of Pennsylvania, ⁶Biological and Biomedical Sciences, North Carolina Central University, ⁷Genomics & Microbiology Research Lab, NC Museum of Natural Sciences, ⁸Evolutionary Anthropology, Duke University

DNA methylation is an epigenetic modification to the genome that primarily affects CG dinucleotides ("CpG sites") and can influence gene expression. The epigenetic clock is a robust quantitative model that uses age-dependent

changes in DNA methylation to produce a highly accurate age estimate referred to as epigenetic age. Epigenetic age is a measure of biological aging that can be used to detect if an individual is aging at an accelerated or decelerated rate. While chronological age increases at a constant rate, measures of biological age reflect genetic and environmentally-driven heterogeneity in the pace of aging. Accelerated epigenetic aging, where biological age exceeds chronological age, is associated with increased disease and mortality risk. While epigenetic clock models have been developed in mice, humans, and dogs, no robust age prediction model currently exists for a nonhuman primate. Here, we developed an epigenetic clock for rhesus macaques (*Macaca mulatta*). We measured genome-wide CpG methylation in blood samples from 105 rhesus macaques aged 5 to 28 years (roughly equivalent to 15 to 84 years in humans) living on the island of Cayo Santiago off the coast of Puerto Rico. We measured methylation at 2,846,027 CpG sites across the genome and employed a machine learning approach (elastic net regression) to identify sets of sites that together robustly predict chronological age. In addition to describing the clock, we will present preliminary data that use this age predictor model to investigate the effect of the environment and genetics on aging and age-related diseases in the Cayo macaques.

Funding for this study was provided by NIH R00-AG051764.

Until They All Come Home: The Recovery and Identification of America's Prisoner of War/Missing in Action Personnel

JESSE R. GOLIATH
Scientific Analysis, Defense POW/MIA Accounting Agency

More than 82,000 U.S. military service members and personnel remain missing from past conflicts such as World War II, Korean War, Vietnam War, Cold War, and Gulf Wars. The Defense POW/MIA Accounting Agency's (DPAA) mission is to provide the fullest possible accounting for missing U.S. personnel from these past conflicts and return their remains to U.S. soil. DPAA deploys hundreds of active duty service members, civilians, and contractors across Europe and the Indo-Pacific region to investigate and recover Americans who went missing in action and exhume remains of individuals who were interred as unknowns. Analysts in the DPAA Laboratory, the only forensic skeletal identification lab accredited by the American Society of Crime Laboratory Directors/Laboratory Accreditation Board (ASCLD/LAB), utilize established population-specific forensic anthropological methods, as well as multiple lines of evidence to identify unaccounted-for individuals. These lines of evidence include field operations (archaeological recoveries and cemetery disinterments), historical records,

ABSTRACTS

material evidence, dental records, chest radiograph comparisons, histology, and mitochondrial and nuclear DNA testing. Each line of evidence is examined and correlated to create potential short-lists and recommendations for identifications. All lines of evidence are evaluated by the agency's medical examiners to determine an individual identification. Using these multifaceted lines of evidence, DPAA has identified approximately 645 missing individuals since 2015, ultimately bringing closure to the families of these fallen service members.

Optical staining of bone mineral in human osteons reveals a fiber texture of mineral grains

SANTIAGO GOMEZ¹, BIN HU² and TIMOTHY BROMAGE²

¹Anatomia Patologica, Universidad de Cadiz, ²Biomaterials, New York University College of Dentistry

Bone tissue is an inorganic-organic composite made of hydroxyapatite mineral, collagen fibers, and cement (non-collagenous proteins). Although the mineral component hydroxyapatite is negatively birefringent and represents over 65% of bone weight, undecalcified bone sections imaged by polarization microscopy show a predominant positive birefringence. The analysis of bone mineral thus relies on other methods, such as electron microscopy or imaging methods based on X-rays that have shown the hydroxyapatite phase to consist of nanometric-sized platelets arranged parallel to the collagen fibers. In this study we attempt to visualize the mineral phase using polarization microscopy. Samples from human cortical bone were rendered anorganic by: i) heating the samples at 200°C for 24 hours, or ii) treating with (0.5%) NaOCl solution at 50°C for 3 days. Samples were then prepared for and observed by polarization microscopy, which demonstrated a birefringence specific for the mineral phase. To better characterize the mineral, we focused on osteonal lamellae of very thin sections (< 10µm-thick) using polarization microscopy configured with several compensators ($\frac{1}{4} -\lambda$, $\frac{3}{4} -\lambda$, $1 -\lambda$, $1 \frac{1}{4} \lambda$). The high spatial resolution images identified mineral grains of micrometric size ($0.43 \pm 0.07 \mu\text{m}$ diameter). As a result of small changes in the relative retardation of the O- and E-rays, these grains were optically stained, exhibiting different interference colors. These grains are interpreted as mineral-packets in which the crystals present the same orientation of their optic axis. They exhibited the original fibrous texture and were arranged in an orderly fashion relating to the lamellar microarchitecture.

Assessing the status of *Homo heidelbergensis* through dental morphology and ancestral state reconstruction approaches

AIDA GOMEZ-ROBLES

Department of Anthropology, University College London, Department of Genetics, Evolution and Environment, University College London, Department of Life Sciences, Natural History Museum

Because it is often claimed that *Homo heidelbergensis* was the ancestral species to Neanderthals and modern humans, ancestral state reconstruction approaches are particularly apt to assess its status. Combining geometric morphometric analysis of dental variation and ancestral reconstruction approaches yields two fundamental results. Firstly, *H. heidelbergensis* does not show the expected dental morphology of the last common ancestor (LCA) of Neanderthals and modern humans. On the contrary, European specimens ascribed to *H. heidelbergensis* show Neanderthal dental affinities. Secondly, fossil specimens predating 700 ka are unlikely candidates to represent the Neanderthal-modern human LCA because they would have had to experience an extremely fast dental evolution to give rise to early Neanderthals. Together, these results imply that European specimens classically ascribed to *H. heidelbergensis* cannot be part of the Neanderthal-modern human last common ancestral species. Rather, those European specimens have to be either phylogenetically related to Neanderthals or part of a dead evolutionary lineage that is not related to Neanderthals or to modern humans. These results have two possible implications for the status of *H. heidelbergensis*. First and most likely, they can imply that *H. heidelbergensis* is not a valid taxon because it includes early representatives of the Neanderthal lineage in Europe (and, probably, of the modern human lineage in Africa). Second, they can imply that *H. heidelbergensis* is a distinct species if excluding from its hypodigm specimens with Neanderthal affinities, but that it had no further evolutionary continuity into Neanderthals or modern humans.

Research is funded by the UCL-Excellence program

Population-specific trabecular variation patterns drive heterogeneity in modern human phenotypic covariance matrices of trabecular and cortical bone properties

ADAM D. GORDON¹, KRISTIAN J. CARLSON^{2,3}, LILY J. DOERSHUK⁴, TEA JASHASHVILI^{5,6}, JAAP P. P. SAERS⁷, NICHOLAS B. STEPHENS⁴, JAY T. STOCK^{7,8} and TIMOTHY M. RYAN⁴

¹Department of Anthropology, University at Albany (SUNY), ²Department of Integrative Anatomical Sciences, Keck School of Medicine, University of Southern California, ³Evolutionary Studies Institute, University of the Witwatersrand, ⁴Department of Anthropology, Pennsylvania State University, ⁵Molecular Imaging Center, Department of Radiology, Keck School of Medicine, University

of Southern California, ⁶Department of Geology and Paleontology, Georgian National Museum, ⁷Department of Archaeology, Cambridge University, ⁸Department of Anthropology, Western University

Phenotypic covariance matrices (P) are often assumed to be proportional to additive genetic covariance matrices (G) in evolutionary studies where direct estimation of G is impossible (e.g., extinct populations), and population P matrices often stand in for species G matrices. We investigate whether P matrices incorporating three classes of skeletal variables (element size, cortical properties, and trabecular properties) are similar across four archaeological populations that varied in subsistence strategy. Each individual contributed 22 femoral and humeral variables. P matrices were compared for all populations simultaneously and for all pairwise combinations using the Flury hierarchy common principal components (CPC) approach: models were evaluated assuming ever-increasing similarity among matrices (i.e., heterogeneity, one or more shared CPCs but different eigenvalues, proportionality, and equality).

Results for population P matrix pairs ranged from heterogeneity to equality. Subsets of P matrices were then generated for each class of skeletal variable and compared among populations. For size and cortical variables, equality between matrices was supported for all population pairwise comparisons. However, trabecular P matrix results indicated heterogeneity or few shared CPCs among populations. Phenotypic covariation patterns are apparently stable across human populations for element size and cortical variables, but not trabecular variables. Given developmental plasticity in cortical and trabecular properties, we caution that P matrix similarity may not indicate G matrix similarity if phenotypes are primarily the outcome of environmental responses, and P matrix dissimilarity may not indicate G matrix dissimilarity if plastic traits in different populations have similar genetic patterning but are exposed to different environments.

Funding: NSF BCS-1719187, NSF BCS-1719140, NRF-DST (South Africa), European Research Council under the European Union's Seventh Framework Programme (FP/2007–2013)/ERC Grant Agreement n.617627 and RCUK/BBSRC grant BB/R01292X/1.

Muscle synergy based-locomotor control in bipedal and quadrupedal walking: *Macaca fuscata* and *Pan troglodytes*

RYOSUKE GOTO¹, TETSUYA SHITARA¹, SUSAN LARSON² and YOSHIHIKO NAKANO¹

¹Human Sciences, Osaka University, ²Medicine, Stony Brook University

Hominoids more frequently use bipedal walking than non-hominoids. We hypothesize that hominoids have locomotor pattern generating systems that could adapt the quadrupedal locomotor

ABSTRACTS

pattern to bipedal walking. To test the hypothesis, we collected a dozen of electromyograms of hindlimb muscles in *Macaca fuscata* and *Pan tryglodytes*. Based on the muscle synergy model, we quantified activations and compositions of several muscle synergies (i.e. muscle groups consisting of co-activating muscles during motor behaviors) during bipedal and quadrupedal locomotor bouts. Using non-negative matrix factorization, we extracted the activation phases and compositions of four muscle synergies, and compared the synergies between bipedal and quadrupedal walking.

The bipedal and quadrupedal locomotor patterns differed intraspecifically, but Japanese macaques and chimpanzees showed similar pattern changes between locomotor modes. This suggests both chimpanzees and macaques have similar flexible pattern generating systems, thus our hypothesis is rejected. During quadrupedal walking, two of the four muscle synergies activated in the first and second half of stance phase (MS2 and MS3, respectively). MS2 included hip, knee, and ankle extensors and MS3 involved hip flexors. In bipedal walking, the MS3, instead of MS2, included the ankle extensors. These results suggest that during bipedal walking loading response (MS2) and push off (MS3) are clearly separated, but the MS2 functions in both during quadrupedal walking. The locomotor transition could change the sensory input and, hence, the compositions of the MS2 and 3 are adjusted accordingly.

Testing least cost path (LCP) models for travel time and kilocalorie expenditure: implications for landscape genomics

KYLE M. GOWEN^{1,2}, TIMOTHY S. DE SMET^{1,3,4}, RALPH M. GARRUTO^{1,5,6} and JEFFREY K. LUM^{1,2,5}

¹Anthropology, Binghamton University, ²Laboratory of Evolutionary Anthropology and Health, Binghamton University, ³Geophysics and Remote Sensing Laboratory, Binghamton University, ⁴Geological Sciences and Environmental Studies, Binghamton University, ⁵Biology, Binghamton University, ⁶Laboratory of Biomedical Anthropology and Neurosciences, Binghamton University

Least Cost Path (LCP) analysis allows a user to define a cost parameter through which cost of movement can be assessed using Geographical Information Systems (GIS). These analyses are commonly used to construct theoretical movement through a landscape, which has been useful for creating hypotheses concerning prehistoric archaeology and landscape genomics. However, LCP analysis is commonly employed without testing the generated LCP(s), complicating its validity.

This paper proposes a model for analyzing movement in ArcGIS by using topography data to calculate slope. This slope data is then used to calculate LCPs based on travel

time and kilocalorie expenditure through modified equations. For proof of concept, LCPs were constructed in the Nature Preserve at Binghamton University, a 182-acre area that consists of wetland and mountainous terrain and a Fitbit® Charge activity monitor was used to test the accuracy of the model's predictions.

Paired sample t-tests show a lack of significant difference between calculated and walked time (27:44 vs. 28:06, $p = .420$), indicating that our model can accurately predict travel time. Paired sample t-tests also show a lack of significant difference between calculated and observed kilocalorie expenditure for two paths (68 vs. 72 and 122 vs. 133, $p = .278$), indicating accuracy in predicting kilocalorie expenditure. Although not significantly different, straight line distances vs. walked distances (1.347 vs. 2.08, $p = .068$) suggest that straight lines do not reflect real movement. Our model can predict travel time and kilocalorie expenditure accurately and future iterations will focus on calculating cost associated with crossing waterways.

This research was made possible through start-up funds from Binghamton University's Laboratory of Evolutionary Anthropology and Health and Provost's Doctoral Fellowship Program.

Sociality and diet drove selection for shifts in primate brain size

MARK GRABOWSKI^{1,2,3}, BJØRN T. KOPPERUD⁴, MASAHITO TSUBOI² and THOMAS F. HANSEN²

¹Research Centre in Evolutionary Anthropology and Palaeoecology, Liverpool John Moores University, ²Centre for Ecological and Evolutionary Synthesis, Department of Biosciences, University of Oslo, ³Center for the Advanced Study of Human Paleobiology, The George Washington University, ⁴Natural History Museum, University of Oslo

Increased brain size in humans and other mammals is hypothesized to confer benefits in terms of cognition but bring new energetic costs associated with growing and maintaining energetically expensive neural tissue. Previous studies have argued that changes in diet, rather than metrics of sociality, led to shifts in brain size, but results have been equivocal. Here we use a newly compiled dataset and Ornstein-Uhlenbeck models of evolution to test for an adaptive relationship between endocranial volume and major diet components (percentage feeding time) and metrics of sociality (average group size, social structure, mating size). We also account for measurement error, which has not been addressed in previous analyses and can have a large effect on parameter estimates. Our results show that, contrary to previous studies, there is a strong relationship between brain size and all measures of sociality when body size and measurement error are taken into account, but this relationship is nonlinear for average group size. Dietary components were also shown to have

an effect on relative brain size but to a far lesser extent. Overall, our results suggest that more complex evolutionary hypotheses and models are needed to uncover the factors that drove primate brain evolution.

Funding for this research was provided the U.S. Fulbright Foundation to MG.

Work minimization and toppling concerns predict limb phasing in wild primates

MICHAEL C. GRANATOSKY¹, CALLUM F. ROSS¹, MYRA F. LAIRD¹, ADAM VAN CASTEREN², JANINE CHALK-WILAYTO³, MARIANA DUTRA FOGAÇA^{4,5}, JUSTIN A. LEDOGAR⁶, DAVID S. STRAIT², BARTH W. WRIGHT⁷ and JAMES R. USHERWOOD⁸

¹Organismal Biology and Anatomy, University of Chicago, ²Department of Anthropology, Washington University in St. Louis, ³Department of Biomedical Sciences, Mercer University Medical School, ⁴Department of Biodiversity and Conservation, Federal University of Maranhão, ⁵Research Department, Neotropical Primates Research Group, ⁶Department of Evolutionary Anthropology, Duke University, ⁷Department of Anatomy, Kansas City University of Medicine and Biosciences, ⁸Structure and Motion Laboratory, The Royal Veterinary College

Numerous studies have documented variation in limb phases across quadrupeds. Recent models have accounted for this variation by relating limb phasing to mechanical work requirements and energetic minimization, but primate gait patterns do not match predictions of global energetic minimization. This is thought to be a constraint placed on primates to prevent toppling on thin arboreal supports where forefoot placement is essential for testing the substrate prior to committing body weight. However, on large substrates, where rapid pitching at the instant of forefoot placement is likely inconsequential, primates should use limb phasing that prioritizes energetic minimization. Using video-recordings of five arboreal primate species (*Alouatta seniculus*, *Ateles paniscus*, *Chiropotes satanas*, *Pithecia pithecia*, and *Sapajus apella*) collected from Brownsberg Nature Park in Suriname, we test the capabilities of wild primates to modify limb phasing patterns based on substrate diameter. In all species, except *Pithecia*, animals adopt varying phase patterns that minimize energetic expenditure while moving on large diameter supports. However, on medium and narrow supports, animals exclusively utilize gait patterns that sacrifice some energetic costs in order to decrease the risk of toppling at the moment of forefoot placement. These findings suggest an inherent flexibility associated with primate gaits, while also stressing that energetic minimization may not always be the primary optimality criterion during locomotion. These data highlight the constraints that a fine-branch arboreal environment has placed on primate locomotor behavior.

ABSTRACTS

Comparative morphology of the hominoid subscapularis enthesis

DAVID J. GREEN

Department of Anatomy, Campbell University
School of Osteopathic Medicine

Subscapularis is active during vertical climbing in hominoids, whereas other rotator cuff muscles are mostly silent. Previous work highlighted three-dimensional differences in subscapular fossa shape, but these investigations did not consider attributes of subscapularis muscle size and force potential, nor the shape of its insertion site along the lesser tubercle of the humerus. This study evaluates the correspondence of subscapularis origin and insertion shape with published investigations of muscle size and physiological cross-sectional area (PCSA) to further interrogate subscapularis' role during hominoid locomotion.

African ape subscapular fossae are superoinferiorly broad with prominent superior angles and mediolaterally constricted blades, while orangutans and gibbons have mediolaterally elongated fossae with lower superior angles – reminiscent of the pattern seen in monkeys. In contrast, African ape and gibbon lesser tubercles are superoinferiorly taller than those of monkeys. This shape may be associated with functional differentiation of subscapularis and the importance of shoulder mobility in hominoid locomotion, but the orangutan lesser tubercle was shorter and more like those of monkeys. Finally, the subscapularis muscle comprises a significantly greater percentage of total rotator cuff PCSA in orangutans, gibbons, and monkeys than in African apes, despite the latter having broader subscapular fossae. Though general patterns of congruence emerge, it is clear that one may draw only limited behavioral inferences from individual characterizations of hard or soft tissue traits. Moreover, variation in soft tissue configurations suggests that modifications in mass and/or PCSA may contravene phylogenetic constraints and enable functional equivalence in the absence of hard tissue correspondence.

I gratefully acknowledge the National Science Foundation (BCS-0824552) and Wenner-Gren Foundation.

Interpreting intra-population variability from dental morphology and tooth dimensions of a modern Seminole Native American sample

MADELYN K. GREEN¹ and SEAN D. TALLMAN^{1,2}

¹Anatomy and Neurobiology, Boston University,
²Anthropology, Boston University

Native American and Asian populations are typically grouped together in a single broad ancestry category despite their distinct population histories. Examining intra-population variation and developing population-specific methods of Asian and Native American groups aid in redefining

ancestry organization to better reflect the population diversity. Past research by the authors in a modern Japanese population reflect homogeneity within the sample, validating the utilization dental methods in ancestry discussions. Dentitions are ideally suited to measure intra-population variability due to heritabilities of both their tooth size and dental morphological characteristics within populations. Continued dental observations of Asian and Native American groups provide evidence that support the elimination of umbrella grouping of the aforementioned ancestries. Individual casts from a modern Seminole population housed at Ohio State University reflect a relatively unbiased sample, as demographics range from juveniles to adults, with both sexes being equally represented. Dental morphology and tooth dimensions were recorded on dental casts for 79 individuals (f=41; m=38) using the Arizona State University Dental Anthropology System (ASUDAS) and mesiodistal and buccolingual measurements. Dental morphology and tooth dimension data were compared between individuals using univariate and ANOVA statistical testing. The results indicate that Seminole tooth sizes and dental morphological traits exhibit limited variability within the sample. This dental homogeneity is likely due to the geographic and culturally isolated population history of the Seminole. The similarities in population-wide uniform dental trait expression and measurements between the Seminole of this study and the previously investigated Japanese population corroborate the need for continued ancestry category refinement.

Stable Isotope Measures of Weaning Age and Early Childhood Diet in the Ancient Andes: Variation in Early Life Experiences and Health Outcomes across Status and Sex in Tiwanaku-Affiliated Sites in Peru and Bolivia

ALEXANDRA M. GREENWALD^{1,2}, DEBORAH BLOM³,
NATALYA ZOLOTOVA⁴ and KELLY KNUDSON²

¹Center for Evolution and Medicine, Arizona State University, ²School of Human Evolution and Social Change, Arizona State University, ³Department of Anthropology, University of Vermont, ⁴Keck Foundation Laboratory for Environmental Biogeochemistry, Arizona State University

We employ stable isotope measures ($\delta^{15}\text{N}$ and $\delta^{13}\text{C}$) of weaning age and early childhood diet derived from serial micro-samples of first molar dentin from 21 individuals dating to the Middle Horizon (Tiwanaku V) (A.D. 500-1100) interred at both Chen Chen in the Moquegua Valley, and Tiwanaku, in the Titicaca Basin, to examine interpersonal variation in breastfeeding behavior and diet across ecological zones, status, and biological sex. We find that average weaning ages between Chen Chen and Tiwanaku are comparable – at 32.6 and 34.7 months, respectively. However, modal weaning patterns differ between

regions. A higher proportion of Tiwanaku individuals are breastfed for longer durations than are the individuals interred at Chen Chen. Irrespective of region, females' mean weaning age is older than males'. Individuals who died during childhood exhibit younger weaning ages than those who survived to adulthood, adding to growing clinical and archaeological evidence that prolonged breastmilk consumption reduces morbidity and mortality across the lifespan. Childhood diets at Tiwanaku include greater quantities of animal protein and maize than those at Chen Chen ($10.7\text{‰} \pm 0.8 \delta^{15}\text{N}$, $-12.6\text{‰} \pm 2.6 \delta^{13}\text{C}$ versus $6.7\text{‰} \pm 1.96 \delta^{15}\text{N}$, $-13.2\text{‰} \pm 1.4 \delta^{13}\text{C}$), despite the later serving as an important maize-growing region in the Tiwanaku empire. These data suggest that children raised in the higher-status sectors of Tiwanaku are receiving comparatively greater levels of parental investment, in the form of prolonged breastfeeding and parental provisioning of nutritious food in early childhood, than those raised in the outlying settlement of Chen Chen in the Moquegua Valley.

Funding provided to A.G. by a postdoctoral research fellowship from ASU CEM, and by NSF to D.B. and K.K. (BCS-1317237 to D.B. and BCS-1317184 to K.K.)

A Biogeochemical Assessment of Treponemal Disease: Diagnosis, Host Mobility, & Mercury Treatment

LESLEY A. GREGORICKA

Department of Sociology, Anthropology, & Social Work, University of South Alabama

With few exceptions, bioarchaeologists are only just beginning to consider the complex relationship between pathological conditions and the incorporation of isotopes into skeletal tissues. Here, the current application of stable isotope and trace elemental analyses toward understanding the origins and spread of treponemal disease among past populations is assessed, and best practices and limitations for such biogeochemical techniques evaluated. First, hypotheses surrounding the impact of pathological conditions on isotope values as a means of improving differential diagnoses are explored. While chronic conditions such as untreated syphilis may exhibit distinctive values, particularly in newly-formed bone lesions, modification of isotope values detected for other pathological conditions has been minor, calling into question whether treponematoses would affect isotope fractionation in detectable ways. Secondly, the temporal and geographic spread of infectious disease was interconnected with patterns of mobility and interaction. Subsequently, establishing the origins and movements of past individuals using isotopes (including multi-tissue and serial sampling) impacts the interpretation of disease prevalence by revealing underlying social forces and exchange networks that contributed to its transmission. Finally, detection of mercury

ABSTRACTS

treatments in skeletal tissues offers the potential to identify individuals in primary/secondary stages of syphilis when pathological changes to bone have not yet occurred. Various analytical techniques have been applied to tackle this issue, although more experimental studies appear necessary to develop standardized methods and to enhance our understanding of mercury uptake into the skeleton relative to soft tissue. Together, these promising techniques represent an important step toward bioarchaeologically assessing disease, movement, and treatment.

Head and neck range of motion and its relation to cervical vertebral morphology in primates

NEYSA GRIDER-POTTER¹, THIERRA K. NALLEY², NATHAN E. THOMPSON³, RYOSUKE GOTO⁴ and YOSHIHIKO NAKANO⁴

¹School of Human Evolution and Social Change, Arizona State University, ²Department of Medical and Anatomical Sciences, Western University of Health Sciences, ³Department of Anatomy, New York Institute of Technology College of Osteopathic Medicine, ⁴Department of Human Sciences, Osaka University

The neck provides stable, yet mobile platform for the head. Head mobility is particularly important during locomotion, grooming behaviors, and predator vigilance. The anatomy that underlies head mobility, however, is poorly understood. We hypothesize that cervical vertebral morphology influences head and neck ranges of motion (ROM). We predict that: 1) longer spinous and transverse processes physically constrain extension and lateral flexion respectively and 2) craniocaudally taller articular facets facilitate greater ranges of flexion. To test these predictions, we collected ROM data from 7 species of primate (n=16) and 5 additional species from the literature. Under anesthetization, individuals were gently, but firmly manipulated into their maximum ranges of flexion, extension, and lateral flexion. Radiographs were taken in these positions, as well as a neutral position. Intervertebral ranges of motion were then calculated using ImageJ. Morphological data were measured from skeletal material using Rhinoceros software.

Phylogenetic generalized least squares regressions were used to test relationships between intervertebral ROM and cervical features. In accord with predictions, articular facet height is positively correlated with range of flexion at three mid-cervical joints. Spinous process length is negatively correlated with extension in two lower cervical joints. Contrary to the predictions, transverse process length is positively correlated with lateral flexion in two lower cervical joints. Overall, the weak association between morphology and ROM suggest that the limits on ROM are more

likely dictated by soft tissue rather than bony morphology. As such, our results do not support using these vertebral features to estimate ROM in fossil species.

This research was supported through the National Science Foundation's Dissertation Improvement Grant (BCS-1731142) and East Asia and Pacific Summer Institute's program (1515271) to NGP.

Exploring pathways to skeletal phenotypes: Biomarkers of skeletal health and bone mineral density in NHANES 2003-2004

JACOB GRIFFIN, STEPHANIE BERGER and SOPHIA DENT

Anthropology, UNC Chapel Hill

Due to osseous tissue plasticity and sensitivity to environmental influences, bioarchaeologists and human biologists often use skeletal phenotypes as important indicators of individual and population lifestyles. With widespread prevalence across the globe, osteoporosis remains a leading cause of bone fracture and morbidity in adults. Although osteoporosis is an aging phenotype of clinical significance, limited research examines how lifestyle factors impact the physiological pathways leading to bone turnover dysregulation and low bone mineral density (BMD). Previous studies have shown that inflammatory proteins are associated with the inhibition of collagen and osteocalcin, leading to reduced matrix and bone formation. Inflammation thereby provides a mechanism for lifestyle and social factors to contribute to low BMD. The pathway between biocultural factors, inflammation, and bone mineral density was tested using 7656 individuals from the US National Health and Nutrition Examination Survey (NHANES, 2003-2004). Ordinary least squares found a strong, statistically significant association ($p < 0.01$; denoted with *) between total BMD (g/cm²) and education level [0.056*(0.002)], BMI [0.009*(0.000)], CRP [0.010*(0.002)], age [0.001*(0.000)], physical activity [0.023*(0.002)], BAP [-0.002*(0.000)], and total cholesterol [1.452^-04*(0.000)]. Mediation analysis found that CRP mediated the relationship between biocultural factors and bone turnover dysregulation. Inflammation provides an explanatory model through which lifestyle factors can impact the biological aging process, resulting in osteoporosis and frailty, and this model can be applied to past populations by bioarchaeologists.

Discriminant function analysis of cervical diameters of permanent teeth to estimate sex of subadult skeletal remains

MAURA K. GRIFFITH and SIMON HILLSON

Institute of Archaeology, University College London

Full biological profiles cannot be constructed for most subadult remains because sex cannot reliably be estimated using skeletal elements. The

limited biological profile for subadult remains in turn limits the analysis that can be performed on those remains. To address this problem, odontometric analysis of permanent teeth was conducted using post-medieval assemblage. Skeletal material was excavated by Archaeology South East from the Litten Site (ESC11) in Chichester, Sussex, England. Approximately 400 individuals from the excavation were retained and housed at the University College London Institute of Archaeology. The cervical diameters of the permanent teeth of 40 adults (20 female, 20 male) were used to establish a baseline for discriminant function analysis. 22 of 26 cervical diameters were significantly different between males and females ($p < 0.05$). 52 subadults and one indeterminate sex adult had discriminant scores calculated based on the cervical diameters of permanent teeth to estimate sex. After a jack-knife procedure, five functions classified more than 75% of both males and females correctly. Using these five functions, 32 individuals (61.54%) had their sex estimated. 19 individuals were identified as female or probable female; 13 individuals were identified as male or probable male. Due to the dimensions needed to calculate discriminant scores for this assemblage, the minimum age that can be included is approximately 7 years old at death. Further research should investigate if the cervical dimensions of deciduous dentition in this assemblage is sufficiently dimorphic to estimate sex via discriminant function analysis.

Variability of saw blades and saw marks measured from nonhuman bone: Implications for the evaluation of accuracy of microscopic saw mark analysis

ALICIA R. GROSSO, SHARON A. TOTH and DEBORAH L. NEIDICH

Anthropology, University of Pittsburgh

Forensic cases with postmortem saw dismemberment provide a challenge for forensic anthropologists to identify the blade used. Since the Daubert ruling (1993), it's necessary to critically reevaluate examination methods. In resulting validation studies, animal models are frequently used. The present study shows the need to evaluate the significance of nonhuman cutting material on variability of blade measurements from bone.

Two saws (6 TPI rip and 8 TPI crosscut) were used to cut deer and human long bones (n cuts = 32 human crosscut, 32 human rip, 62 deer crosscut, and 55 deer rip). All noted tooth hops (TH) were measured. Thirty measurements were randomly taken between blade teeth to compare variability of distance between teeth (DBT) to TH measured from bone. Welch Two Sample T-tests were performed to check for significant differences ($p < 0.05$) between all TH (DBT) measurements.

ABSTRACTS

Mean TH (DBT) and standard deviation for each group was 3.09 ± 0.03 mm for deer crosscut, 4.03 ± 0.04 mm for deer rip, 3.31 ± 0.19 mm for human crosscut, 3.93 ± 0.15 mm for human rip. 3.06 ± 0.04 mm for the crosscut blade, and 4.12 ± 0.04 mm for the rip blade.

Differences were found between type of cutting material when comparing the variance in TH measurements, with nonhuman tissue resulting in narrower confidence intervals than human tissue. Our confidence interval for TPI as presented to investigators should include at least ± 2 TPI to reflect not only variability of the saw, but also variability of human tissue.

Assessing the impacts of natural disaster on primate habitat in Sulawesi, Indonesia

NANDA B. GROW-BLONG

Department of Sociology, Social Work, and Anthropology, Utah State University

On September 28, 2018, a magnitude 7.5 earthquake struck the island of Sulawesi just 78 km north of the city of Palu. This major earthquake triggered a tsunami, major liquefaction, aftershocks, and landslides in the region. While these geologic and climatic events devastated the urban infrastructure of Palu and resulted in thousands of human casualties, the environmental effects of the disaster on the borders of the affected region are less clear. Palu is located at the northern border of Lore Lindu National Park, and four species of endemic primates reside in and around the park boundaries. The national park experienced a 4.4 magnitude primary earthquake that caused soil disruption and mud flows. To assess the extent of ecological disturbance in primate habitat areas, this study compared a time series of Landsat 8 data consisting of satellite images of Central Sulawesi taken between September and October 2018. Comparison of images of forested land prior to and following the earthquake indicates there was an increase in the proportion of exposed substrates and surface litter. A spectral mixture analysis found a higher proportion of soil and non-photosynthetic vegetation compared to green vegetation. While human subsistence activity is a primary cause of deforestation in Central Sulawesi, this study indicates that increasingly frequent natural disasters cause a decrease in forest canopy cover in primate habitat. Field surveys on the ground are necessary to obtain data on the specific changes that occurred.

Testing the Effectiveness of Permanent Canine Tooth Metrics for Sex Estimation in a Medieval Prussian Sample

ARIEL GRUENTHAL-RANKIN^{1,2}, KATHERINE GADDIS², ARKADIUSZ KOPERKIEWICZ³, MAREK POLCYN⁴ and MARISSA RAMSIER²

¹Anthropology, Binghamton University,

²Anthropology, Humboldt State University,

³Archaeology, University of Gdansk, ⁴Anthropology, Lakehead University

Odontometric methods of assessing sexual dimorphism in human skeletal remains show promise when attempting to estimate sex in subadult, fragmentary, or commingled remains. However, previous studies testing such methods and their level of accuracy have produced mixed results. This study applies one such methodology, utilizing permanent canine teeth, to a sample of Prussian adults from the medieval (mid-14th to mid-15th century) cemetery at Beżławki, Poland. Sex was estimated osteologically for all individuals in the sample, and only those estimated consistently as male or female by multiple methodologies were included. Bucco-lingual (BL) and mesio-distal (MD) measurements were taken at the canine cervix along the cemento-enamel junction (CEJ) of every healthy canine for individuals in the sample. This resulted in three variables for each measurement: dimension (BL or MD), position (left or right), and jaw (maxillary or mandibular). Sample size fluctuated depending on these variables (range: $n=12-18$), with limitations due to missing teeth, presence of calculus, or unclear CEJ. Results from t-tests indicated that the male and female mean scores differed significantly for all canines in the mesio-distal dimension ($p<0.05$). However, there was substantial overlap between male and female measurements, which affected the probability of accurate sex estimation in subadult and indeterminate remains based on various sectioning points. The results of this study demonstrate that, whereas odontometric methods of sex estimation hold promise when individuals lie at the extremes, the spectrum of sexual dimorphism in humans may not allow for discrete sectioning of males and females in all cases.

Another look at canine variation in Neanderthals

DEBBIE GUATELLI-STEINBERG, GRACE V. CALHOUN and MARK HUBBE

Anthropology, The Ohio State University

According to previous studies, Neanderthal canines may have been more sexually dimorphic than those of modern humans. In primates, canine dimensions appear to be affected by levels of prenatal testosterone. Greater sexual dimorphism in Neanderthal canines would therefore seem consistent with a recent study of hominin second-to-fourth digit ratios suggesting that Neanderthals had elevated levels of prenatal

testosterone relative to modern humans. Here, we compare variation in canine bucco-lingual (BL) measurements of Sima-de-los-Huesos hominins (15 upper canines, 17 lower canines) as well as Krapina Neanderthals (7 upper canines, 7 lower canines), to two population samples of modern humans (one of Gullah ($N=31$) and one of Seminole ($N=39$) origin). We predicted that if Sima and Krapina canines were more sexually dimorphic in the BL dimension than those of modern humans, then these fossil hominins' canine BL measurements would exhibit greater variance and/or coefficients of variation than those of modern humans. Variance and coefficients of variation for Sima and Krapina samples were compared to the distribution of values for modern humans generated through bootstrapping. The results do not support our prediction, with both the variance and coefficient of variation falling within modern human ranges. Thus, for the BL dimension at least, Neanderthal canines are not more variable than those of our modern human samples, suggesting that Neanderthal canines were not more sexually dimorphic. We conclude that whether Neanderthal canine sexual dimorphism is greater than that of modern humans may depend on the modern human samples to which Neanderthals are compared.

Male mutation bias is pervasive across primates

LUCAS HENRIQUES VISCARDI¹, VANESSA RODRIGUES PAIXÃO-CÔRTEZ², GUILLERMO REALES¹, TIMOTHY H. WEBSTER^{3,4}, MARIA CÁTIRA BORTOLINI¹ and C. EDUARDO GUERRA AMORIM⁵

¹Departamento de Genética, Universidade Federal do Rio Grande do Sul, Brazil, ²Instituto de Biologia, Universidade Federal da Bahia, Brazil, ³School of Life Sciences, Arizona State University, ⁴Department of Anthropology, University of Utah, ⁵Department of Ecology and Evolutionary Biology, University of California, Los Angeles

Primates exhibit marked variation in substitution rates. This is commonly attributed to differences in life history across species and sexes, but its exact causes remain elusive. To hone our understanding of the factors shaping the primate molecular clocks, we leveraged neutral genetic variation in 16 primate reference genomes to infer substitution rates on the autosomes and sex chromosomes, and compiled information on 19 life history traits. We confirm previous observations of substantial variation in neutral substitution rates in primates, but fail to replicate previously identified associations between substitution rates and life history traits. We observed relatively more neutral substitutions on the autosomes (~25% more than in the X-chromosome on average), consistent with male mutation bias in all studied species and their ancestors. The same pattern is observed for the Y-chromosome relative to the autosomes for a subset of five species for which we had Y-chromosome data.

ABSTRACTS

Moreover, we found that male mutation bias is strongest among Cercopithecidae and weaker in Strepsirrhines and Platyrrhini. Within great apes, we find a puzzling pattern where humans exhibit evidence of stronger male mutation bias than chimpanzees, contrasting extant ape reproductive biology. These results are replicated when we correct for differences in the strength of background selection between the X and the autosomes, reference sequence alignment bias, and variable error estimates across chromosomes. We discuss these results in the light of differences in mating strategies, intensity of sperm competition, and changes in the life history of these species across time.

CNPq (Brazil), CAPES Foundation (Brazil)

Age-Associated Epigenetic Changes in Chimpanzees and Humans

ELAINE E. GUEVARA^{1,2}, RICHARD R. LAWLER³, NICKY STAES^{1,4,5}, CASSANDRA M. WHITE¹, CHET C. SHERWOOD¹, JOHN J. ELY⁶, WILLIAM D. HOPKINS^{7,8} and BRENDA J. BRADLEY¹

¹Center for the Advanced Study of Human Paleobiology, Department of Anthropology, The George Washington University, ²Department of Anthropology, Yale University, ³Department of Sociology and Anthropology, James Madison University, ⁴Behavioural Ecology and Ecophysiology Group, Department of Biology, University of Antwerp, ⁵Centre for Research and Conservation, Royal Zoological Society of Antwerp, ⁶MAEBIOS, Alamogordo, ⁷Keeling Center for Comparative Medicine and Research, University of Texas MD Anderson Cancer Center, ⁸Division of Developmental and Cognitive Neuroscience, Yerkes National Primate Research Center

Recent studies have demonstrated a consistent pattern of change with age in methylation levels at sites across the genome in humans. Comparing the pattern of epigenetic change with known age among species can offer insights into lineage-specific differences in life history schedules and patterns of physiological deterioration. Although chimpanzees are humans' closest living phylogenetic relatives, they appear to show a faster increase in mortality rate with age. Here we examined how the pattern of epigenetic aging in chimpanzees differs from that in humans. We profiled genome-wide blood methylation levels using the Illumina Infinium EPIC array for 99 samples from 75 chimpanzees aged 1-53 years (22 chimpanzees were sampled at multiple ages during their lifespan). More than a third (184,405) of the assayed sites showed significant change (5% false discovery rate) in methylation with age, ~28% of which also show significant age-related change in humans. Enrichment analysis revealed sites uniquely linked with aging in chimpanzees were disproportionately associated with genes involved in metabolic processes, whereas sites uniquely linked with aging in humans were associated with genes involved in nervous system

development, ion transport, and signaling. Nearly 80% of between-species shared aging-associated sites showed a significantly faster rate of change in chimpanzees. Thus, although chimpanzees and humans show considerable overlap in epigenetic aging patterns, they also show substantial divergence in the rate and landscape of epigenetic aging. These differences offer potential clues to the physiological pathways underlying differences in aging between the two species.

The Leakey Foundation, National Science Foundation (BCS-1733896), Yale MacMillan Center for International Studies, Yale Institute for Biospheric Studies, and Yale and The George Washington University anthropology departments funded this research.

Ancient DNA study of M21 Excavated from Lingkou site, Lintong, Shaan Xi Province

YAQI GUO, DAWEI CAI, NAIFAN ZHANG, SIQI ZHU, CHANG LI, XINYUE SHAO, YONGDI WANG and QIYAO LIANG

School of Archaeology, Jilin University

In this study, we extracted ancient DNA of M21 excavated from Lingkou site, Lintong, Shaan Xi Province. The DNA fragments of the hypervariable region of the mitochondrial DNA (16017-16409, including primer length) were amplified using two sets of overlapping primers, and a pair of primers were used to amplify the AMG gene for gender identification. After multiple extraction, amplification and sequencing, we finally obtained a 354bp mitochondrial sequence which is true and reliable. Molecular sex determination showed that M21 was a woman, which was consistent with the physical anthropology identification, suggesting the reliability and accuracy of genetic testing. In addition, we use the blast program to search the GenBank nucleic acid database, and the sequence of M21 was not found in modern populations, suggesting that M21 maternal line has extinct. M21 belonged to the ancient haplogroup M. Phylogenetic analysis showed that M21 had a close affinity to 2 individuals from Shaan Xi Province, and 1 individual from Lajia site, Qinghai Province. Combining physical anthropological analysis, our result suggested that M21 is likely to be the local indigenous people. In addition, M21 also has a very close genetic relationship with some people in Gan-Qing area, suggesting a certain link between that the Yellow River upstream and midstream residents.

A preliminary study of Pleistocene bovid mortality profiles in East Turkana, Kenya

KAITA N. GURIAN¹, ELEANOR CORDINER², ASHLEY S. HAMMOND^{3,4} and FRANCES L. FORREST^{4,5}

¹Department of Anthropology and Sociology, James Madison University, ²Department of Archaeology, Durham University, ³Division of Anthropology, American Museum of Natural History, ⁴New York Consortium in Evolutionary Primatology, (NYCEP), ⁵Sackler Educational

Laboratory for Comparative Genomics and Human Origins, American Museum of Natural History

Age-at-death distributions of bovids have been previously used to reconstruct site formation processes at hominin localities, and can provide clues about the agents (i.e., hominins, carnivores) that helped form the site. Previous studies have concluded that modern hunter-gatherer populations produce a prime-dominated mortality profile when hunting size 3 or larger bovids, and inferences of hominin hunting have been made for sites like FLK Zinjanthropus (Olduvai Gorge, Tanzania) based on this idea.

In this study, we used bovid mortality profiles to analyze site formation in Koobi Fora, Kenya. During the 2018 field season of the Koobi Fora Field School, 43 lower bovid molars were recovered from three different geological members, the Okote (1.33-1.61 Ma), KBS (1.61-1.79 Ma), and Upper Burgi (1.79-2.02 Ma). Bovid size classes were established, and analysis of infundibulum loss was used to age the molars into juvenile, prime adult, and old adult categories. The mortality profile was generated using triangular graphing software and was compared to mortality profiles from modern lion-killed bovids, hyena-killed bovids, and mortality data from FLK Zinjanthropus.

Although the results are preliminary, several interesting patterns emerge. The data collected from Koobi Fora was highly prime-dominated and was found to be statistically significantly different from the modern predator-killed bovids. The Koobi Fora mortality profile overlaps with the profile from FLK Zinjanthropus, and becomes more prime-dominated through time. This result indicates that East Turkana assemblages could be forming in part due to hominin hunting, which perhaps increases over time.

Funding Statement: This research was supported by the National Science Foundation (IRES-OISE 1358178) and would not be possible without the support of the National Museums of Kenya

Intraspecific variability in early *Australopithecus afarensis* mandibular morphology: new insights from 3.6 Million-year-old hominin juvenile mandibles from Woranso-Mille, Ethiopia

YOHANNES HAILE-SELASSIE¹ and TIMOTHY M. RYAN²

¹Physical Anthropology, Cleveland Museum of Natural History, ²Anthropology, Pennsylvania State University

Mandibular morphology of *Australopithecus afarensis* is relatively well-known due to the presence of abundant fossil mandibles representing this taxon. However, only a few juvenile mandibles of the species are known. Here, we describe two recently discovered hominin juvenile mandibles from Woranso-Mille, Ethiopia (KSD-VP-1/39

ABSTRACTS

and MKM-VP-1/626), radioisotopically dated to 3.6 million years ago. We assign these mandibles to *Australopithecus afarensis* based on metric and morphological similarities with juvenile mandibles of the species from Hadar and Laetoli. These specimens increase the sample size of juvenile mandibles of *Australopithecus afarensis* from poorly known time period and yield new insights on the degree of variability in juvenile mandibular morphology in the earliest members of the species. MKM-VP-1/626 has symphyseal morphology similar to the contemporaneous adult L.H.-4 and juvenile L.H.-2 from Laetoli, whereas KSD-VP-1/39 is more like adult individuals from Hadar (A.L. 400-1a) and Middle Awash (MAK-VP-1/12). Our analysis further indicates that given the documented inter- and intra-species variability in hominin symphyseal morphology, inclination of the mandibular symphysis by itself may not have taxonomic or biological significance (for example, the symphyseal base of L.H.-4 and L.H.-2 being “cut-away”), unless it is supplemented by other lines of evidence. However, the fact that the new 3.6 million-year-old juvenile mandibles from Woranso-Mille generally have a more receding symphysis than any of the juvenile and most adult mandibles of *Australopithecus afarensis* from the younger Hadar sequence lends support to the observed trend in symphyseal morphological change in the *Australopithecus anamensis*–*Australopithecus afarensis* chronospecies lineage.

This research was financially supported by grants from the National Science Foundation (BCS-1124705, BCS-1124713) and the Cleveland Museum of Natural History.

The fetus in bioarchaeology: new approaches to unlocking the maternal-infant nexus

SIÂN HALCROW¹, ANNE MARIE SNODDY¹, CHARLOTTE KING¹, ALISHA ADAMS¹, BERNARDO ARRIAZA², VIVIEN STANDEN³ and MARC OXENHAM⁴

¹Department of Anatomy, University of Otago, ²Instituto de Alta Investigación, Universidad de Tarapacá, ³Departamento de Antropología, Universidad de Tarapacá, ⁴School of Archaeology and Anthropology, Australian National University

Until relatively recently, fetuses, along with infants and children, were largely overlooked in bioarchaeological research. Over the past 20 years there has been increasing recognition of the importance of research on infants and children in the archaeological context. However, although fetuses are now sometimes included in the analysis of population health and isotopic studies of weaning and diet in the past, most research focuses on postnatal individuals. The neglect of fetuses is a problem because we are missing a crucial part of the skeletal sample that is informative for understanding past population demography, stress and adaptation, and social

organization factors. In fact, it could be argued that the gestational period is the most informative way to assess environmental stress where both the mother and child are more susceptible to malnutrition and infectious disease. This paper reviews bioarchaeological research that has been undertaken in this area and starts to build a theoretical framework to conceptualize fetuses from an archaeological context. We present case examples of our bioarchaeological research that use the methods of incremental isotope analyses of deciduous teeth to look retrospectively at the fetal period, paleopathology of perinates, and microscopic deciduous dental enamel defect analyses to assess fetal health and the maternal-infant relationship. We outline how these approaches can aid in extending our understanding of the epidemiology of disease, maternal and infant stress experience, and the consequences of early stress on later life experience.

Marsden Fund; University of Otago

Get an eyeful of this: Gross anatomy and morphometrics of the squirrel monkey (*Saimiri*) interorbital region

LAUREN B. HALENAR-PRICE^{1,2}, BRIAN SHEARER^{2,3,4}, CLAIRE E. TERHUNE⁵, CAITLIN YOAKUM⁵ and SIOBHÁN B. COOKE^{2,4,6}

¹Department of Biology, Farmingdale State College, SUNY, ²NYCEP Morphometrics Group, New York, NY, ³Department of Cell Biology, New York University School of Medicine, ⁴Department of Anthropology, The Graduate Center, CUNY, ⁵Department of Anthropology, University of Arkansas, ⁶Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine

Saimiri and *Cebus* have a narrow interorbital region compared to other platyrrhines. The extreme nature of this trait in *Saimiri* leads to the development of an interorbital fenestra in adults. This feature has played a role in the phylogenetic interpretation of the fossil *Dolichocebus gaimanensis*, but as we know little about variation in the growth and development of the fenestra, its shape, or surrounding anatomical structures in extant taxa, our ability to make additional inferences is limited. Here we attempt to fill some of those gaps in our knowledge.

Interorbital fenestra outline and 3D cranial shape were captured from CT scans ($n > 30$) of *S. boliviensis*, *S. oerstedii*, and *S. sciureus*. While there is a relatively clear separation between the three species in shape space for both variables, the two landmark sets do not covary strongly. Within *S. sciureus*, however, males seem to share a dorsoventrally short but anteroposteriorly long fenestra and a more dolichocephalic cranium, while females and juvenile males share a rounder fenestra and more globular neurocranium.

Volumetric analyses of diffusible iodine-based contrast-enhanced CT (diceCT) scans were conducted on the extraocular muscles and periorbital membrane in *Saimiri* and *Cebus* to demonstrate the soft tissue correlates for this unique fenestra. Despite hard tissue differences between the two genera, the soft tissues present little variation, with similar arrangements of the extraocular muscles observed in both. These results shed light on a unique morphological feature that has not been extensively evaluated, and has implications for our understanding of platyrrhine evolution.

The evolution of the primate forelimb and neocortical areas involved in manual dexterity

ANDREW C. HALLEY¹, MARY K.L. BALDWIN¹ and LEAH KRUBITZER^{1,2}

¹Center for Neuroscience, University of California, Davis, ²Department of Psychology, University of California, Davis

One of the distinguishing features of primates are their unique capacity for dexterous control of the hands when compared with other mammals. This specialization for forelimb control, particularly the fine manipulation of objects using individual digits, is associated with novel features of the primate neocortex. It is well understood that primates' unique capacity for manual dexterity relies on specializations in both motor and posterior parietal cortex (PPC), yet relatively little is known about how cortical areas that control the forelimb have evolved from simpler networks. Recent work in our laboratory examines the diversity across mammals of movement representations in the neocortex using long-train intracortical microstimulation (LT-ICMS) techniques. Here we examine the reorganization of primate posterior parietal cortex (PPC) relative to other mammalian radiations, drawing on recent LT-ICMS studies in both New and Old world monkeys, rodents, bats, and tree shrews. Compared with other species, both strepsirrhine and haplorrhine primates exhibit an expanded PPC containing representations of complex forelimb movements, particularly of the digits and hand. While some features of movement maps are similar across primate species, we also see unique forelimb representations associated with differences in anatomy and behavior (e.g. precision grip in primates with opposable thumbs) and substantial variation between individuals of the same species. This suggests that movement maps in PPC may not be strictly specified during development, but rather reflect patterns of use over an individual lifetime generating species-typical movements.

ABSTRACTS

What factors influence nest reuse among chimpanzees (*Pan troglodytes verus*)?

ANDREW R. HALLORAN^{1,3,4} and CATHERINE E. BOLTEN²

¹Chimpanzee Care, Save The Chimps,

²Anthropology, University of Notre Dame,

³Research, Conservation Society of Sierra Leone,

⁴Anthropology, Florida Atlantic University

A high frequency of nest reuse, with chimpanzees placing new nesting material atop old nests, occurs at the Tonkolili Site in Sierra Leone, and indicates chimpanzees reacting to locally specific external factors. Nest reuse is thought to increase when there is a lack of preferred nesting trees, and may represent niche construction. The Tonkolili Site presents a highly fragmented mosaic landscape where optimal nesting sites are sparse. Additionally, because chimpanzees have been historically hunted at this site, avoidance of humans is presumably a factor in nesting site selection. In a survey of 86 nests at the Tonkolili Site, 69% had new material on top of decayed material. Examining subsets of this survey reveals key differences in where nest reuse primarily occurs. In a long riverine forest bordering several crop fields, 58% of the nests showed evidence of reuse. These nests give the chimpanzees easy proximity to crops and allow them to move seasonally based on the cycle of cultivation. This is compared with 84% of nests that have been reused in a forest that is avoided by humans due to a historical cultural taboo, where chimpanzees are afforded year-round protection from humans. Considering the influence of labor schedules and cultural taboos on preferred nesting spaces, the factors influencing nest reuse at the Tonkolili Site appear to be more associated to the specifics of the neighboring human community, rather than availability of nesting trees. This suggests that factors influencing nest reuse can be variable and site specific.

This research was funded by a grant from the Eck Institute for Global Health at the University of Notre Dame.

Evaluating Life History Trade-Offs Through the Presence of Linear Enamel Hypoplasia at Pueblo Bonito and Hawikku: A Biocultural Study of Early Life Stress and Survival in the Ancestral Pueblo Southwest

ALLISON HAM¹, DANIEL TEMPLE¹, HAAGEN KLAUS¹ and DAVID HUNT²

¹Anthropology, George Mason University,

²Anthropology, Smithsonian Institution

Due to the indelible nature of enamel, bioarchaeologists commonly use linear enamel hypoplasia (LEH) to detect early investments in survival, and have identified an association between the presence of LEH and constraints in growth and maintenance, as well as an increased susceptibility to future stress events. This study evaluates the relationship between early life stress and

survivorship in the Ancestral Pueblo Southwest by examining the presence of LEH in two skeletal samples from Pueblo Bonito (A.D. 800-1200) and Hawikku (A.D. 1300-1680). The study hypothesizes that in both samples the presence of LEH will be associated with decreased survivorship and an increased likelihood of mortality when compared to individuals with no LEH observed.

Kaplan-Meier survival analysis reveals statistically significant differences in the mean survival time between people with and without LEH for the Hawikku sample, but no significant differences for the Pueblo Bonito sample. These findings suggest that individuals at Hawikku who experienced early life stress, as indicated by LEH presence, had a higher level of frailty than those who showed no signs of the defect. Hence, it is likely that the metabolic event that led to LEH formation caused a physiological trade-off early in life that effected the ability to mitigate future stressors, increasing susceptibility to death. By applying a life history framework and engaging with evolutionary biological concepts, this work seeks to provide a deeper understanding of the relationships between indicators of early life stress, such as LEH, and mortality and survivorship in the Ancestral Pueblo Southwest.

Differentiating between frugivory and folivory in primates using non-destructive XRF measurements of strontium/calcium ratios: A case study from Kibale National Park

MARIAN I. HAMILTON^{1,2}, B. LEE DRAKE² and SHERRY V. NELSON²

¹Anthropology, University of Northern Colorado,

²Anthropology, University of New Mexico

Numerous studies employ ratios of strontium to calcium to differentiate between faunal dietary categories, primarily to identify differences in trophic levels (for example, carnivores versus herbivores) or generalized dietary groupings, such as browsers and grazers. While these studies have included representative species from numerous African fauna, none have examined full primate communities. These previous studies have also relied on traditional destructive analyses (such as acid digestion and ICP-MS assays), making them difficult, costly, and often prohibitive to replicate in fossil contexts. In this study, we present tooth enamel strontium/calcium ratios collected via non-destructive handheld XRF analysis from six species of primate from Kibale National Park, Uganda, representing frugivorous and folivorous diets. We also include matched pairs of fruit and leaves. Strontium/calcium ratios significantly differ between frugivores (redtail monkeys, *Cercopithecus ascanius*; blue monkeys, *Cercopithecus mitis*; olive baboons, *Papio anubis*; and chimpanzees, *Pan troglodytes schweinfurthii*) and folivores (red colobus monkeys, *Procolobus badius*; black and white colobus monkeys,

Colobus guereza) ($P < 0.05$, Wilcoxon Mann-Whitney U-test). Paired plant measurements show significantly higher concentrations of strontium in leaves compared to fruit, which is consistent with previous studies and current results. This demonstrates that strontium/calcium ratios can be used to more granularly differentiate both modern and fossil primate dietary preference into frugivory and folivory, and such analysis can be done entirely through nondestructive means. This methodology holds great promise for paleo-primateology and paleo-anthropology research, particularly for species in which fossils are too rare for large samples to be destructively analyzed.

This work was supported in part by the National Science Foundation Grant #DGE-0903444, the Wenner-Gren Foundation, and the Leakey Foundation.

The *Oreopithecus bambolii* (IGF 11778) lumbar region: Revised anatomy

ASHLEY S. HAMMOND^{1,2}, LORENZO ROOK³, SALVADOR MOYÀ-SOLÀ⁴ and SERGIO ALMÉCJA^{1,2,4}

¹Division of Anthropology, American Museum of Natural History, ²New York Consortium of Evolutionary Primatology (NYCEP), ³Dipartimento di Scienze della Terra, Università di Firenze, ⁴Institut Català de Paleontologia Miquel Crusafont, Universitat Autònoma de Barcelona

The IGF 11778 *Oreopithecus* skeleton was found by a coal-miner in 1958 (Baccinello). Although being nearly complete, most of the morphology was flattened and imbedded in a lignite slab, limiting interpretations of its morphology. Recently, the pelvic and vertebral elements were prepared, exposing key aspects of IGF 11778 trunk. The newly-prepared anatomical portions confirm that the last thoracic and L1-L3 vertebrae are in articulation but displaced. The vertebral elements found in contact with the pelvis require revision to original descriptions, however. The proximal vertebra found with the pelvis was originally reported as the L5. However, the small portion of bone that was thought to be an L4 fragment is actually the offset pedicle region of the vertebra below, and so the cranial vertebra preserved with the pelvis is likely the L4 rather than L5. Additionally, what was previously assumed to be the cranial portion of the sacrum can now be recognized as a lumbar vertebra. These revised element identifications require that IGF 11778 had at least 5 lumbar vertebrae. Finally, the two vertebrae preserved with the pelvis are displaced, which has previously given the impression that there was substantial lumbar vertebral entrapment. The new preparations of IGF 11778 show that only the most distal vertebra (presumed L5) would have actually been entrapped, as inferred from upper ilium proportions and transverse process morphology. The

ABSTRACTS

newly visible morphology argues that the lumbar region in *Oreopithecus* lacked the extreme adaptations seen in extant great apes that relate to stiffness of the lower back.

Funding from: Wenner-Gren Foundation, Leakey Foundation, Spanish AEI/FEDER EU, Generalitat de Catalunya CERCA Programme, MINECO, The University of Florence, National Science Foundation

Are we overestimating commensal species densities? A case study of the long-tailed macaque (*Macaca fascicularis fascicularis*)

MALENE F. HANSEN^{1,2}, VENTIE A. NAWANGSARI¹, SIGNE ELLEGAARD², MARIA M. MOELLER², FLORIS M. VAN BEEST³, NIELS M. SCHMIDT³, MIKKEL STELVIG¹, CARL TRAEHOLT¹ and TORBEN DABELSTEEN²

¹Research and Conservation, Copenhagen Zoo, ²Behavioural Ecology Group, University of Copenhagen, ³Department of Biosciences, Aarhus University

Species density and abundance data is crucial for ecosystem management. However, such information is often lacking or anecdotal, especially for seemingly abundant species. Long-tailed macaques (*Macaca fascicularis fascicularis*) are distributed across Southeast Asia, and classified as "widespread, yet rapidly declining", yet no precise local density and abundance data exists. To provide density and abundance estimates for a long-tailed macaque population we conducted line transect distance sampling throughout Baluran National Park, East Java, Indonesia covering all habitats. Long-tailed macaque density is 41.40 ± 12.31 ind/km², and abundance 10350 ± 3077.8 individuals (Distance 7.1). We also conducted a non-random point distance sampling survey on roads and trails, where macaques are provisioned indicating the perceived density and abundance; density 1449 ± 465.85 ind/km², abundance 362260 ± 116460 ind. Line transect sampling results prove that macaque density is low, equalling non-provisioned population densities, yet perceived density is much higher underlining that we cannot assess an entire population from non-random road and trail surveys. Habitat suitability analysis (R SDM ensemble map AUC>0.7) shows a preference for secondary forest and open savannah indicating that long-tailed macaques also inhabit dry areas, and are not only edge species. Our results provide much needed baseline data for this species, and we recommend conducting scientific surveys of long-tailed macaques throughout their range, and possibly reassessing conservation status and measures for long-tailed macaques. We also advise exercising extreme caution regarding estimating density of seemingly abundant species from anecdotal evidence.

Bovoid Tribe Abundance as an Indicator of Spatial and Temporal Heterogeneity in the Omo-Turkana Basin from 2.0-1.38 Ma

ANNALYS HANSON¹, MARYSE D. BIERNAT², KAEDAN O'BRIEN³, ALYSSA ENNY⁴, JOSHUA PORTER⁵, DAVID R. BRAUN^{5,6,7} and W. ANDREW BARR⁵

¹Department of Anthropology, Emory University, ²Department of Anthropology and Institute of Human Origins, School of Human Evolution and Social Change, Arizona State University, ³Department of Anthropology and Natural History Museum of Utah, University of Utah, ⁴Department of Biology, Stockton University, ⁵Department of Anthropology and Center for the Advanced Study of Human Paleobiology, The George Washington University, ⁶Archaeology Department, University of Cape Town, ⁷Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology

Fluctuations of paleolake Lorenyang and volcanic activity in the Turkana Basin from 2.0-1.38 Ma caused environmental shifts during a crucial period of hominin evolution. To examine spatial variability in habitats within the Turkana basin, we studied faunal abundance data compiled from the Koobi Fora (KF), Nachukui, and Shungura Formations of the Omo Group. KF was further divided into two sub-regions: those proximal to the depositional center of the basin (axial) and those distal (marginal). We predicted that areas marginal to the basin axis would show expanding xeric (dry, open) environments, while areas axial to the basin axis would experience less change.

Alcelaphin, reducin, and tragelaphin (n=4122) bovids have specialized locomotor and dietary morphology. Alcelaphini are cursorial grazers in xeric grasslands, while reducinci are fresh-grass grazers in edaphic grasslands near permanent water. Tragelaphini occupy diverse habitats but are predominantly browsers/mixed-feeders.

Results indicate that the axial and marginal regions of KF had similar mesic environments until 1.87 Ma when the margin experienced an increased abundance of xerophilic alcelaphini. The Nachukui Fm. underwent a similar transition from mesic to xeric habitats in this time frame. The Shungura Fm. was mesic throughout but became dominated by reducinci at 1.87-1.56 Ma due to transgression of the lake. Overall, our results show that these three formations experienced ecological change differently in response to changing basin hydrology. Turkana Basin environments were not homogeneous between 2.0-1.38 Ma, and hominins would have experienced distinct environmental pressures in various portions of the basin.

Interneurons of the anthropoid striatum: reorganization and computational considerations

KARI L. HANSON^{1,2}, CAROLINE H. LEW², BRANKA HRVOJ-MIHIC², ERIC HALGREN^{1,3}, MARY ANN RAGHANTI⁴ and KATERINA SEMENDEFER^{1,2,3}

¹Institute for Neural Computation, University of California San Diego, ²Department of Anthropology, University of California San Diego, ³Neurosciences Graduate Program, University of California San Diego, ⁴Department of Anthropology, Kent State University

The striatum, comprised of structures critically involved in social and reward-based learning, inhibitory control of behavior, and language production, represents a site of significant modification in mammalian evolution in both macro- and microstructure. In particular, the computational demands of the expanding cerebral cortex are supported by an increase in the percent of specialized cell types, known as interneurons, from some 5% of total neuronal populations in the rodent to more than 20% in the primate striatum. This may represent a significant shift in local processing capacities derived in the primate order. Utilizing a sample of 8 anthropoid primate species (including humans), we analyzed the distribution of interneurons expressing choline acetyltransferase, parvalbumin, and calretinin in the dorsal and medial caudate nucleus, putamen, and nucleus accumbens regions. Overall differences in interneuron distributions seem to suggest that modifications in neural circuitry in the striatum may be shared at the hominoid level, with evidence for species-level differences in the densities of interneuron subtypes. Interestingly, our previous research has shown that the human striatum scales much smaller than expected for a primate brain of its size. We consider the implications of reorganization at the gross level and its relationship to intrinsic microstructure and density of total neurons, as well as interneuronal subtypes among mammalian species.

This research was supported by a Wenner Gren Dissertation Fieldwork Grant.

Relationships between individual level variables and fracture characteristics in human ribs subjected to anterior-posterior loading

ANGELA L. HARDEN¹, VICTORIA M. DOMINGUEZ¹ and AMANDA M. AGNEW^{1,2}

¹Skeletal Biology Research Laboratory, The Ohio State University, ²Department of Anthropology, The Ohio State University

Thoracic injuries, specifically rib fractures, are associated with high levels of mortality, and a deeper understanding of rib fractures is prudent to accurate trauma analyses. This research investigates the predictability of rib fracture patterns, locations, or number of fractures from individual level variables (age, sex, stature, weight, and

ABSTRACTS

BMI). Previous research modified a fracture classification system and applied it to human ribs subjected to dynamic anterior-posterior loading, and no trends were observed for rib level. Fracture characteristics were analyzed in 346 human ribs; eight different fracture patterns were observed (n=394), fracture locations ranged from 0–99%, and the number of fractures per rib ranged from 0–3. No significant correlations were found between fracture location and age, stature, weight, or BMI (all $r < 0.04$) and no trends were observed when fracture patterns or number of fractures were included as categorical subgroups. No trends were found between number of fractures, fracture patterns, age, sex, and BMI. The large amount of fracture pattern variation in ribs subjected to the same loading condition suggests that mechanism may not be able to be determined from fracture pattern. Additionally, these findings demonstrate that individual level variables should not be used as predictors of fracture patterns, locations, or number of fractures. This research contributes an interdisciplinary approach to the analysis of fracture characteristics and their mechanisms. Future research will examine relationships between fracture characteristics and global rib geometry, cross-sectional rib geometry, and rib structural properties derived from experimental testing.

Interspecific variation of calcaneal morphology in gorillas

CHRISTINE M. HARPER, CHRISTOPHER B. RUFF and ADAM D. SYLVESTER

Center for Functional Anatomy and Evolution, The Johns Hopkins University School of Medicine

The foot plays a prominent role in weight-bearing suggesting it may reflect locomotor variation. Despite the immense amount of foot research, the calcaneus has been relatively understudied. Here we analyzed the entire calcaneal shape of *Gorilla gorilla gorilla* (n=41), *Gorilla beringei graueri* (n=17) and *Gorilla beringei beringei* (n=8) to understand how morphology relates to locomotor behavior.

Calcanei were surface scanned and external shape analyzed using a three-dimensional geometric morphometric sliding semilandmark analysis. Semilandmarks were slid to minimize the bending energy of the thin plate spline interpolation function relative to the updated Procrustes average. Generalized Procrustes Analysis was used to align landmark configurations and shape variation was summarized using a principal components analysis. Procrustes distances between species were calculated and resampling statistics were run to test for group differences.

All subspecies demonstrate statistically different morphologies ($p < 0.005$ for pairwise comparisons). *G. b. graueri* separates from other

subspecies based on posterolateral morphology, with *G. b. graueri* demonstrating an elongated peroneal trochlea, and thus more bone superiorly than *G. g. gorilla*. Compared to *G. b. beringei*, *G. b. graueri* has less bone inferiorly near the tuberosity. Cuboid and posterior talar facet shapes correlate with arboreality. *G. b. beringei* (most terrestrial) has a flatter cuboid facet and a more transversely oriented/relatively smaller posterior talar facet than *G. g. gorilla* (most arboreal) and *G. b. graueri* represents an intermediate morphology. These differences demonstrate a relationship between calcaneal shape and locomotor behavior and suggest that *G. b. graueri* may load its foot differently from the other subspecies.

This project was supported by NSF grant # BCS - 1824630.

Scaling of whole brain blood flow rate in marsupials and euarchontans

ARIANNA R. HARRINGTON¹, LEONIE LANGE-HODGSON², VERA WEISBECKER² and DOUG M. BOYER¹

¹Department of Evolutionary Anthropology, Duke University, ²School of Biological Sciences, University of Queensland

Metabolic costs are often thought to limit the evolution of large, complex brains. Compared to the largest marsupial brains, similarly sized primate brains tend to have greater neuronal density. Therefore, if the metabolic rate of brain tissue is primarily dependent on neuron numbers, we would expect primate whole brain metabolic costs to increase more rapidly with brain mass than marsupial whole brain costs. Here, the relationship between brain cost and neuronal density is tested using predictions of brain blood flow rate, which are isometrically correlated with brain metabolism. Flow rate (Q) was predicted in n=43 marsupial and n=38 euarchontan (primates, dermopterans, and scandentians) species using the radii of osteological foramina that transmit the internal carotid (ICA) and vertebral (VA) arteries to the brain. After log transformation of variables, phylogenetic regression of Total Q (Q of ICA + Q of VA) against endocranial volume (ECV) recovered a slope of 0.88 in euarchontans, similar to previously observed values of the scaling of brain glucose use rates to whole brain mass in placentals. However, phylogenetic ANCOVA shows that the slope ($=1.05$) of the marsupial regression is significantly higher. Furthermore, marsupial residuals are significantly larger than those of euarchontans using phylogenetic ANOVA, indicating that marsupial brains have a higher blood flow rate and hence higher tissue specific metabolic cost for a given brain mass compared to euarchontans. This may suggest

that euarchontans have faced differing selective pressures for reducing the mass specific metabolic costs of relatively larger, more neuronally dense brains compared to marsupials.

This research was funded by Australian Research Council Discovery Grant DP170103227, NSF BCS 1552848, NSF DBI 1701714, and NSF BCS 1825129.

Temporal Rift: Gene Flow or Genetic Drift? A case study of Korean Joseon Dynasty (1392-1910) and Modern (post-1910) Populations

KATHERINE I. HARRINGTON¹, CHRISTOPHER J. BAE¹, U-YOUNG LEE², EUN JIN WOO³, SHINWON AHN⁴ and KYUNG-SEOK HU⁵

¹Department of Anthropology, University of Hawaii at Manoa, ²Catholic Institute for Applied Anatomy, Department of Anatomy, The Catholic University of Korea, ³Department of History, Sejong University, ⁴Department of Cultural Anthropology, Hanyang University, ⁵Department of Oral Biology, Yonsei University College of Dentistry

Using 3D geometric morphometric (GM) methods, landmark coordinate data ($p \sim 43$) were collected on adult cranial samples from the Korean Joseon Dynasty (1392-1910; $n \sim 45$) and Modern Koreans (post-1910; $n \sim 93$) to test the hypothesis that they are a continuous population with little to no gene flow. This hypothesis rests upon the microevolutionary concept of the neutral model. The 3D GM data were analyzed using generalized Procrustes analysis, principal component analysis, and discriminate function analysis. Three sets of analyses were completed: entire cranium; facial region; and cranial vault region (n and p varied with each analysis due to the varying condition of individual remains). The results of the analyses show that there are differences, best seen in the facial landmarks, between the two temporal populations with < 0.01 p-values, but that this difference is small such that they are indistinguishable on scatter plot graphs. While it is difficult to distinguish them on the scatter plot graphs, the Modern sample displays a greater range of variation than the Joseon Dynasty sample. These results could indicate that admixture from other populations has resulted in greater variation in the Modern population. Alternatively, the greater degree of variation in the Modern sample may be a reflection of greater sample size (i.e., greater chance for more variability to appear). Nevertheless, the noticeable overlap in the scatterplots could suggest that a few centuries are not enough to evaluate microevolutionary processes at work in these Korean samples in a way that is easily observed in the human cranium.

Funding was provided by the Center for Korean Studies, University of Hawai'i at Mānoa and the Department of Anthropology, University of Hawai'i at Mānoa.

Body temperature estimates for Bornean orangutans (*Pongo pygmaeus wurmbii*) from internal fecal temperature measurements

FAYE S. HARWELL^{1,2}, RINALDI GOTAMA^{2,3},
KATHERINE S. SCOTT^{2,4}, BRODIE PHILP² and
CHERYL D. KNOTT^{1,2}

¹Anthropology, Boston University, ²Research, Gunung Palung Orangutan Project, ³Anthropology, Hong Kong University of Science and Technology, ⁴Anthropology, Oxford Brookes University

Monitoring health status is a critical aspect of primate conservation, yet can be difficult to non-invasively investigate in the wild. Because mammals are endothermic, body temperature can be used as a health marker for primates. Using a method previously tested on chimpanzees and humans, we estimated body temperature of wild Bornean orangutans by measuring the internal temperature of fecal sample. Upon quickly collecting a fecal sample after defecation, we recorded internal temperature of the sample at 20-sec intervals for six minutes. Data included a series of temperatures for each sample that we fitted to a sigmoid curve, which was used to estimate body temperature. Estimated body temperature was not affected by sex ($F(2,92) = 0.431$, $P = 0.651$), weather ($F(2,92) = 1.175$, $P = 0.313$), or collection time ($r = -0.074$, $N = 95$, $P = 0.468$). Estimated body temperature was higher for fecal samples that fell from lower estimated heights ($r = -0.23$, $N = 95$, $P = 0.0004$) and were heavier ($r = 0.23$, $N = 75$, $P = 0.0475$). We compare these results from the field to captive fecal samples, taking place on the ground, to determine the accuracy of this field method. From our field samples ($N = 95$), orangutans appear to have a lower internal body temperature (33.44 ± 1.74 °C) on average than either chimpanzees or humans. Previous studies have demonstrated that orangutans have a lower metabolic rate than other great apes. Lower body temperature may serve as a metabolic adaptation of orangutans to survive extended periods of low food availability when energy needs to be conserved.

Funding provided by NSF grant BCS-163882, Leakey Foundation, Disney Wildlife Conservation Fund, US Fish and Wildlife Great Ape Conservation Fund #F15AP00812.

Deforming feet, deforming substrates: 3D dynamics of the human foot during footprint formation revealed through biplanar X-ray methods

KEVIN G. HATALA^{1,2}, SABREEN MEGHERHI¹, DAVID A. PERRY³ and STEPHEN M. GATESY³

¹Department of Biology, Chatham University, ²CASHP, The George Washington University, ³Department of Ecology and Evolutionary Biology, Brown University

Fossil hominin footprints record unique data on foot anatomy and biomechanics that can provide critical insights into the evolution of human

bipedalism. Accurately interpreting these data, however, requires parsing complex mechanical processes through which a final footprint arises. Neither the substrate nor the foot is rigid, hence they continually respond to each other's changing shapes, motions and forces, resulting in a final footprint that is not a simple, linear representation of foot anatomy or kinematics.

Here, we apply new biplanar X-ray and 3D animation methods to study dynamic foot-substrate interactions during human track formation. Seven subjects walked across four substrates (three deformable muds and solid carbon fiber) with radiopaque markers adhered to the external surfaces of their feet. Marker 3D motions were used to visualize and quantify continuous interactions at the foot-substrate interface. We found that soft tissue deformation, and the motions that define standard gait phases, differ markedly across substrates. For example, heel strike is a discrete impact event that causes significantly greater vertical compression of the heel pad on rigid substrates. However, the heel deforms significantly less and sinks for significantly longer, often into midstance, on compliant muds. These and other differences in 3D foot dynamics across substrates encourage us to reconsider the interpretive frameworks commonly used to analyze fossil footprints. We suggest that process-based analyses (e.g., computer simulation to understand how footprint shapes form) may be more fruitful than exclusively product-based analyses that only compare final footprints to each other.

We are grateful for funding support from the National Science Foundation (SMA-1409612, DBI-1262156, BCS-1825403, BCS-1824821), Chatham University, and the Brown Undergraduate Teaching and Research Awards program.

Interobserver Agreement in Scoring Dental Morphology using ASUDAS in South Australian Whites

SAVANNAH HAY, LAURA E. CIRILLO, TATIANA VLEMING-MENDIETA, DORI KENESSEY, ROSE L. PERASH, STEPHANIE J. COLE, KRISTEN A. BROEHL and G. RICHARD SCOTT

Department of Anthropology, University of Nevada, Reno

Despite standards for scoring dental morphological trait expression, accuracy varies based on an observer's level of experience. Previous studies show the application of each trait for assessing ancestry in various populations, but they have yet to identify which traits multiple observers more accurately record. This research focuses on scoring traits from photographs of dental casts from South Australian whites ($n = 224$). Each cast had a series of photographs that allowed for observations on shoveling on the upper incisors, tuberculum dentale (TD) on the upper canines, distal accessory ridge (DAR) on upper and lower canines, hypocone on

upper M1 and M2, Carabelli's cusp on upper M1 and M2, and lingual cusp number on the lower premolars. Eight observers with varying levels of experience (ranging from little experience to expert) were randomly assigned dental traits to score the entire sample, resulting in between three and five observers per trait. All scores were based on the Turner-Scott Dental Anthropology System (ASUDAS). Agreement was calculated by reporting the greatest to the least variance between any two observers, when a difference in scores within one ASUDAS grade was considered to be in agreement. Shoveling ranged from 95-100% agreement between observers; TD from 80-94%; DAR from 72-92%; hypocone from 85-99%; Carabelli's from 68-96%; premolar cusp number from 71-88%. This study demonstrates traits vary in observer agreement. Traits observed by multiple levels of experience resulted in the largest ranges. Results suggest certain traits can be assessed with high accuracy, but variation in observer experience affects interobserver agreement.

Temporal clustering of sexual contacts can maintain endemic sexually transmitted virus in mobile subsistence populations

ASHLEY HAZEL and JAMES HOLLAND JONES

Earth System Science, Stanford University

Parameterizing contact patterns that drive pathogen transmission is critically important for building useful predictive models, but contact behavior is highly complex, especially sexual contact. Most sexual contact rates for epidemiologic modeling are based on partner exchange rates only, assuming that per-partner rates of sexual contact are equal and that sexual contact is evenly dispersed in time. These assumptions are broadly unrealistic, especially when subsistence mobility has a strong influence on the spatial and temporal distribution of people and their sex partners. Our fieldwork among semi-nomadic pastoralists in Kaokoveld, Namibia showed that seasonal subsistence mobility influences access to sexual partners and sexually transmitted infection (STI) exposure. In Kaokoveld, mild partner concurrency is culturally normative, contact rates vary within and between partnerships, and per-partner contact is highly temporally clustered.

Motivated by these observations, we hypothesized that temporal variability and clustering in sexual contact has significant impacts on STI dynamics, particularly for viruses with low transmission probabilities, like herpes simplex virus. We built an agent-based model of sexual mixing based on our detailed sexual network data from Kaokoveld (2015-2016), and we incorporated epidemic processes of common viral STIs to compare epidemic outcomes with and without temporal clustering of per-partner contact. We found that, even during high-dispersal periods,

ABSTRACTS

when partner access was relatively low, virus transmission was sustained when per-partner contacts were highly clustered because clustering increased exposure opportunity and risk per exposure. Thus, human-obligate STIs with low transmissibility can be endemically sustained, even when partner exchange rates are relatively low.

This research was funded by a postdoctoral grant from the Wenner-Gren Foundation and departmental funds from Stanford University.

Diachronic changes in craniofacial morphology among the Middle-Late Holocene populations from Hehuang region, Northwest China

LETIAN HE^{1,2}, DANIEL H. TEMPLE², MINGHUI WANG³, QUANCHAO ZHANG⁴, WU LIU¹ and NOREEN VON. CRAMON-TAUBADEL⁵

¹paleoanthropology, Institute of Vertebrate Paleontology and Paleoanthropology, Chinese Academy of Sciences, ²Sociology and Anthropology, George Mason University, ³Physical anthropology, Institute of Archaeology, Chinese Academy of Social Sciences, ⁴Archeaology, Jilin University, ⁵Anthropology, University at Buffalo

Objectives: This study analyzes craniofacial shape variation in the Hehuang region of Northwest China within a population genetic framework, and takes a diachronic approach to explore the factors influencing morphological transformation during the middle to late Holocene.

Materials and methods: The sample comprises 76 adult skulls from five archeological sites, ranging from 4,500BP to 1,530BP. 3D geometric morphometrics, multivariate statistics, quantitative evolutionary genetic and biodistance analyses were performed to study the diachronic variation in craniofacial morphology. Analyses were performed on two cranial modules: the face and the cranial vault, across three major diachronic groups representing the late Neolithic (LNA), the Bronze Age (BA), and the Han-Jin dynasty (HD).

Results: Average regional F_{ST} for both cranial modules was low, indicating relatively greater variation within diachronic groups than among them. While LNA and BA groups did not show any significant differences in facial and vault shape, significant craniofacial shape changes were detected between BA and the HD groups. Moreover, among-group distances based on the face and vault were significantly correlated, indicating that these two modules reveal the same evolutionary pattern.

Discussion: The consistent craniofacial morphology during the LNA and the BA, and the shift in morphology between the BA and the HD indicates that cranial modules are predominantly correlated with the neutral population history in this area. The Hehuang population evolved *in situ*

with few changes, despite cultural and dietary changes, until the Han-Jin dynasty when migrations from the Central Plains is associated with extra-local gene flow to the area.

Strategic Priority Research Program, National Natural Science Foundation of China, and China Scholarship Council.

Population Variation in Dental Development and Its Effect on Forensic Age Estimation

KELLY N. HEIM¹, MARIN A. PILLOUD², HASSEM GEHA³ and YING WU⁴

¹Anthropology, University of South Florida, ²Anthropology, University of Nevada, Reno, ³School of Dentistry, University of Texas Health Science Center at San Antonio, ⁴School of Dentistry, Oregon Health Sciences University

The process of dental development is more stable than skeletal development and is often considered the most accurate method of age estimation in subadults. However, dental development can be affected by secular change, socioeconomic status, sex, and ancestry. Therefore, it is problematic that the established methods for subadult dental age estimation in the United States do not accurately reflect the populations to which they are being applied. The goal of this presentation is to analyze sex and/or ancestry differences in dental development based on a modern U.S. sample and to evaluate the effect these differences may have on age estimation.

Dental development was evaluated on 1,757 orthopantomograms of individuals ages 5-20 taken between 1972 and 2017, using the Demirjian et al. (1973) scoring system. Age estimation methods that do and do not account for sex and/or ancestry were created from a training subset, to evaluate whether group-specific methods perform significantly better than general methods.

Overall, no significant differences in developmental scores exist between sexes and/or ancestry groups. When there are significant differences, females are more developmentally advanced than males, and dental development in Hispanic individuals is more advanced than that of European Americans.

Using confidence intervals and linear models for age estimation, methods based on all individuals exhibit comparable accuracy and precision when compared to sex- and/or ancestry-specific methods. Therefore, although significant developmental differences do exist between sexes and ancestry groups, the magnitude of these differences may be minimal enough that age estimation from dental development is unaffected.

Midline Shifts in Modern Populations: Comparison of Migrants and a Donated Skeletal Collection

KARI E. HELGESON, COURTNEY C. SIEGERT, CHLOE P. MCDANELD, NICHOLAS P. HERRMANN, M. KATE SPRADLEY and MICHELLE D. HAMILTON

Anthropology, Texas State University

This research seeks to identify if the presence of vertebral border shifts occurs at a higher rate in individuals presumed to be migrants. The etiology of border shifts is believed to be genetic, but environmental stress may also contribute. Cranial and caudal vertebral border shifting occurs when vertebral elements adopt characteristics of adjacent vertebral types. Border shifts can occur at the occipitocervical, cervicothoracic, thoracolumbar, lumbosacral, or sacrocaudal regions and are represented by numerous traits including cervical ribs and sacralization. The sample populations consist of seventy-eight individuals from the Texas State University Donated Skeletal Collection (TSDSC) and sixty-two individuals that represent Central American and Mexican migrants who died crossing the Texas/Mexico border. The TSDSC consists mostly of individuals who identify as white, with some identifying as black and Hispanic. Major and minor shifts in either the cranial or caudal direction were considered and scored as present or absent for each border. The chi-square test of independence indicates significantly higher frequencies of vertebral shifting at the lumbosacral region in the migrant individuals. When ancestry is controlled for, migrant individuals still differ in the lumbosacral region from self-identified Hispanics in the TSDSC. Additionally, migrant individuals exhibit a higher frequency of linear enamel hypoplasia on the maxillary incisors suggesting structural inequality and long-term stress. Although lumbosacral border shifts occur at a higher frequency in the migrant group, the results will be discussed in the context of quantifying this population variation to better understand whether these differences are due to genetics or environmental stress.

An initial examination of biological affinities of northeastern Indian populations relative to other South Asians. A dental morphology investigation

BRIAN E. HEMPHILL¹, TSIAPISA POJAR² and BANRIDA LANGSTIEGH²

¹Anthropology, University of Alaska, Fairbanks, ²Anthropology, North East Hill University, Shillong

Biological affinities of the numerous Tibeto-Burman-speaking ethnic groups of northeastern India remain largely unknown due to cultural taboos against submission of bodily fluids for DNA analysis. Historically, oral traditions and anthropomorphic observations have suggested little affinity between these ethnic groups of northeast India and other ethnic groups of South Asia.

ABSTRACTS

This study employs 17 tooth-trait combinations of the Arizona State University Dental Morphology System among 616 individuals of three ethnic groups (Paites, Sema Nagas, Tankhul Nagas) from Manipur and Nagaland. These data were contrasted with 12 samples encompassing 2,090 living individuals of ethnic groups from south-eastern peninsular India, west-central peninsular India, and northern Pakistan based upon pairwise MMD values examined with correspondence analysis (CA) neighbor-joining cluster analysis (NJ) and multidimensional scaling (MDS).

CA indicates that, with the exception of *tuberculum dentale*, traits scored on separate teeth within dental field yield unique biodistance information. Results are consistent across NJ and MDS as both identify a fundamental and profound division between members of north-eastern ethnic groups and all other South Asians. Secondary divisions distinguish Indic-speaking ethnic groups of west-central peninsular India from Dravidian-speaking ethnic groups of southeastern peninsular India. Ethnic groups of northern Pakistan show no affinities to peninsular Indians or to Tibeto-Burman-speaking ethnic groups of northeast India. These results are consistent with oral traditions that maintain that northeastern Indians, as well as northern Pakistanis, are recent émigrés to South Asia.

This work was supported by a Fulbright Senior Research Fellowship to BEH.

Silent evidence of Pre-Columbian treponemal infection in the Western half of the Old World

MACIEJ HENNEBERG^{1,2} and RENATA J. HENNEBERG¹

¹Biological Anthropology and Comparative Anatomy Unit, The University of Adelaide, ²The Institute of Evolutionary Medicine, University of Zurich

Learning about diseases in the past relies on physical evidence of human remains (classical paleopathology) and human creations including written documents and art (paleopathography). When English became the dominant language of scientific communication, experimental disciplines benefitted from easier collaboration while knowledge based on historical sources and multilingual skills became rare. The importance of American and British scientific journals and the peer review system, often leads to self-censorship of less established authors for whom English is not their first language, adding to the difficulty of publishing contributions to debated subjects, such as the history of syphilis. This review of published literature, conference presentations, on-line theses/dissertations in several languages including Croatian, Turkish, Russian, and Spanish, and discussion of paleopathographic evidence, was conducted to evaluate treponemal disease

reported from Europe and the Mediterranean with secure dates before 1492 that fit standard diagnostic criteria and/or effects of treatment with mercury.

At least ten cases/sites dated between the 6th century B.C. and 13th century A.D. are discussed, including 7 congenital cases: Costebelle and Hamage, France; Medinaceli, Spain; Iznik, Turkey; Metaponto and Oplontis, Italy; and Chersonesos, Crimea. Paleopathographic contributions from medical writings and art evidencing treponemal disease in the Old World are also presented including transcription of fragments of "Causes" in Chapter XXII of the *Lilium Medicinae* written by Bernard de Gordon in 1303 and faces of congenital syphilis individuals sculpted by Veit Stoss before 1489. There is no doubt that treponematoses fitting standard characteristics of syphilis, was present in the Old World before 1492.

Effects of mean annual precipitation and temperature on carbon and nitrogen isotopes in neighboring chimpanzee sites within Gombe and Ugalla National Parks

ISABEL HERMSMEYER¹, ANDREW SOMERVILLE², JAMES MOORE¹, ANDREW FROEHLE³ and MARGARET SCHOENINGER¹

¹Anthropology, University of California San Diego, ²World Languages and Cultures, Iowa State University, ³Orthopaedic Surgery, Wright State University

Diet influences carbon and nitrogen stable isotope ratios ($\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values) in animal tissues; and here we explore the influences of the local ecology on those values in six separate troops of chimpanzees (*Pan troglodytes*). In this study we build upon Schoeninger et al.'s 2016 paper by exploring the influence of environmental factors by comparing three separate chimpanzee sites within Gombe Park to another three separate sites in neighboring Ugalla Park. We present new $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values by using hairs collected from night nests in the 90's and early 2000's from Gombe and Ugalla. We then compare these new chimpanzee $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values to local Mean Annual Precipitation (MAP), Mean Annual Temperature (MAT), and the relationship between MAP and MAT. We used these comparisons to test hypotheses based on known effects of these variables on the $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values in plant tissues that may be consumed by the chimpanzees. The comparisons show that hair from chimpanzees living in sites with lower MAP have higher $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values than do chimpanzees living in sites with higher MAP. Neither $\delta^{13}\text{C}$ or $\delta^{15}\text{N}$ were significantly related to MAT, however, the relationship between MAP and MAT was seen to be significant. These results suggest the potential of using $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values in primate tissues to infer attributes

of their local ecology in circumstances where ecology may be unknown, such as samples collected in the last few hundred years or fossil hominins.

Anthropology outreach initiatives: How to get involved in the local community as a graduate student

MARGARITA HERNANDEZ, TINA LASISI, CHLOE MCGUIRE, EMILY KATE and GINA BUCKLEY

Department of Anthropology, Penn State University

The fall of 2017 marked the formation of the Anthropology Graduate Student Association: Outreach Committee at Penn State University. The goal of this committee is to create an environment for graduate students to develop anthropological outreach activities to reach all age groups (elementary, middle school, high school, and families) that generally do not have exposure to this topic. Since its inception, the Outreach Committee, run entirely by graduate students, continues to participate in various outreach initiatives within the university and local communities. These activities, centered on all subfields of anthropology, range from tabling at elementary school science fairs to creating weekly lessons for CEEL - an after-school program for elementary school students. Lesson and curriculum topics include a criminal forensic investigation, recreating the structure of DNA using candy models, exploring different cultures by writing letters to students from around the world, and an interactive archaeological dig for ancient human remains. Here, we present some of our successful implementations and provide access to resources for applications in other settings. We hope to normalize and encourage graduate student participation in outreach and education activities within their universities and the broader communities. We also hope to show the value of participating in these activities, both from a broader impacts perspective and a professional development perspective, to encourage and facilitate the widespread dissemination of our research, and its implications, with the general public.

This material is based upon work supported by the National Science Foundation Graduate Research Fellowship Program under Grant No. DGE1255832 to M.H.

A new interpretation of the anomalous dental modifications of Olduvai Hominid 1 (OH1), Tanzania

RAQUEL HERNANDO^{1,2}, JOHN C. WILLMAN^{1,2}, MARIE MATU³ and ISABELLE CREVECOEUR³

¹Paleoanthropology, IPHES, Institut Català de Paleoeologia Humana i Evolució Social, ²Àrea de Prehistòria, Universitat Rovira i Virgili (URV), ³UMR 5199 PACEA, Université de Bordeaux

ABSTRACTS

The partial skeleton of Olduvai Hominid 1 (OH1) from Tanzania is associated with Later Stone Age material culture and exhibits morphological affinities with other Late Pleistocene African humans. Despite the paucity of human fossils from Late Pleistocene East Africa, few analyses of OH1 are published. Thus, we present a new investigation of the anomalous non-dietary dental wear of OH1 originally attributed to plant processing behaviors. Methods include macroscopic and microscopic (ESEM) observations of all labial and buccal tooth surfaces. Results confirm the presence of large, concave facets exposing dentin on the labial surfaces of all three preserved mandibular incisors. Facets are also present on the labial/buccal surfaces of all *in situ* maxillary and mandibular canines and premolars, most first molars, and some second molars. The newly discovered facets on canines and the posterior dentition are more pronounced in the maxilla than in the mandible and most marked in premolars compared to molars and canines. Contrary to an earlier analysis, the concave facets on the mandibular incisors are unlikely to relate to manipulative behaviors; instead, they closely resemble wear caused by adornments worn in lower-lip piercings ("labrets" or "lip plugs") known from bioarchaeological and ethnographic contexts. The wear suggests that the OH1 wore three facial piercings – two buccal and one in the lower lip. Our findings suggest that the expression of social identities through intentional body modification is more diverse than previously documented elsewhere in Africa during the Late Pleistocene (e.g., ablation) and early Holocene (e.g., ablation, chipping, and filing).

Marie Skłodowska-Curie Actions (H2020-MSCA-IF-2016 No. 749188); AGAUR (Ref. 2017SGR1040 and 2017PFR-URV-B2-91); and MINECO/FEDER (Ref. CGL2015-65387-C3-1-P).

Correlations between Cranial Morphometric Variation and Climate in western South America

BRIANNE HERRERA¹ and MARK HUBBE^{1,2}

¹Anthropology, The Ohio State University, ²Instituto de Arqueología y Antropología, Universidad Católica del Norte, Chile

Microevolutionary processes have affected modern human cranial variation in ways that are not well understood, with different studies reporting contradictory results concerning the extent to which natural selection and climate shaped the cranium. While a consensus exists that cranial shape can be used to reconstruct phylogenetic relationships among modern human populations, it is important to ascertain the individual contribution from both climate and diet on cranial morphology since they are confounding factors when using crania to assess population affinity. Here, we compare functional anatomical modules of the cranium to climatic

variables in order to explore how each module responds to neutral evolutionary processes or natural selection. 204 3D-scanned crania from six sites (three countries) covering the Andes were analyzed, with 78 landmarks divided into 10 functional regions of the cranium. Cluster analyses, multidimensional scaling, and Fst calculations were performed on each region of the skull to explore congruence between cranial regions. Mantel and Partial Mantel tests were also run to compare the morphological distances with climatic distances. Our results demonstrate that several regions of the cranium show a significant correlation with temperature. However, these correlations are all negative. Additionally, our Fst values were higher than most previously obtained Fst estimates, including for world-wide samples (0.3634 vs 0.2760). These results are likely due to the fact that we used 3D data rather than the standard linear cranial measurements. Overall, our results indicate that the local environment likely has only a small effect on cranial morphology for populations living in the Andes.

Coevolution and coextinction of primates and their parasites

JAMES P. HERRERA¹ and CHARLES L. NUNN^{1,2}

¹Evolutionary Anthropology, Duke University, ²Duke Global Health Institute, Duke University

Coevolution occurs in a complex ecological setting involving predators and their prey, plants and pollinators, and hosts and parasites. Extinction threatens the integrity of these ecological relationships, affecting ecosystems more broadly. With approximately 60% of primates threatened with extinction, the loss of threatened species will impact the coevolved relationships with their parasites. We hypothesize that primate host extinctions will lead to parasite extinctions and destabilization of host-parasite ecological networks. We tested this hypothesis in a network analysis, modeling the factors predicted to influence both parasitism and threat status. We analyzed bipartite networks of connections between 198 primates and 750 parasites using exponential random graph models, a network regression that incorporates all pairwise interactions. We found that large-bodied species, and those with larger geographic extents have more parasites than smaller, geographically restricted species, and closely related species have more parasites in common than distant relatives. If the 97 threatened species in our dataset go extinct, 251 parasite species could also go extinct. Despite these losses, network structure would remain stable. Key network measures would be similar before and after extinction: specifically, modularity, a measure of subdivision, is 0.28 and would be 0.23 if hosts go extinct. Eigenvector centralization, a measure of density, is 0.62 and would be 0.57 after extinction. These results identify the phenotypes related to risk of

infection, and point to high specialization in the parasite communities of threatened primates. We conclude that primate species extinction will result in parasite extinction, with potentially cascading impacts on ecosystem function.

The Neanderthals before the Neanderthals: The Levantine scenario

ISRAEL HERSHKOVITZ

Anatomy and Anthropology, Tel Aviv University

Pooling new data from fossil hominins uncovered in a number of prehistoric sites (Qesem, Zuttiyeh, Tabun, Misliya, Neshar-Ramla) suggests the presence of Neanderthal-like hominins in the Levant prior to the Skhul and Qafzeh hominins (ca. 120,000-90,000 years). The present study discusses the taxonomical status of these hominins and the implications to the evolution of *Homo sapiens* and Neanderthals. The study examines the potential relationships of these hominins with the later Levantine Neanderthal group from Amud, Kebara and Ein Qashish. Our results dismiss the notion that Neanderthals are a one-time late episode in the human history of the Levant (seeking refuge from the expanding glaciers in Europe), and raise the possibility of Neanderthal migration from the Levant to Eurasia. In addition, our morphological analysis offers a new taxonomical status for the Skhul and Qafzeh hominins (that are long time considered to be anatomically modern humans).

This research was supported by the Dan David Foundation, The Leakey Foundation, National Geographic, Wenner Gren Foundation, Israel Science Foundation, Binational Science Foundation

Bonobo (*Pan paniscus*) dietary diversity: testing fallback food models

ALEXANA J. HICKMOTT¹, MONICA L. WAKEFIELD², MICHEL T. WALLER^{1,3}, COLIN M. BRAND¹ and FRANCES J. WHITE¹

¹Department of Anthropology, University of Oregon, ²Sociology, Anthropology, and Philosophy Department, Northern Kentucky University, ³Department of World Languages and Cultures, Central Oregon Community College

Although several different frameworks for understanding primate feeding preferences and the importance of fallback foods have been proposed, the fit of bonobos (*Pan paniscus*) to these models is unclear. Marshall & Wrangham's (2007) staple and filler foods continuum groups bonobos with gorillas by deemphasizing frugivory whereas Lambert's (2007) continuum of quality focuses more on adaptations to utilizing non-preferred resources during seasonal shortages. Previous results show seasonal differences in fruit availability for bonobos in the Lomako Forest, Democratic Republic of Congo, suggesting the potential importance of non-fruit fallback foods during periods of low

ABSTRACTS

dietary diversity. We examined the availability of three dietary categories (ripe fruit, leaves, and flowers) in the diets of the Lomako Forest, bonobos to identify candidate fallback resources. Food availability was assessed from phenology data collected between May - October 2017 and regressed against monthly dietary diversity scores (Shannon's Diversity Index). Linear regressions showed that monthly dietary diversity did not vary significantly with ripe fruit availability [$R^2_{adj} = -0.3272$, $df = 1, 3$, $P = 0.9135$], flower availability [$R^2_{adj} = -0.2323$, $df = 1, 3$, $P = 0.654$], or leaf availability [$R^2_{adj} = 0.5262$, $df = 1, 3$, $P = 0.1019$]. These results highlight the lack of fit of bonobos to simple fallback food paradigms. Further investigation is necessary to test how bonobos adapt to seasonal variation and whether factors including small scale seasonal shifts, fruit patch size, party size, nutritional quality, and resources like insects and meat, obscure possible fit to current fallback food paradigms.

Differences in grooming behaviors in mantled howler monkeys (*Alouatta palliata*) based on weather conditions

HEATHER N. HICKS

Anthropology, University of Illinois at Urbana-Champaign, Anthropology, James Madison University, Anthropology, Maderas Rainforest Conservancy

As group living primates, mantled howler monkeys (*Alouatta palliata*) can provide insight into the functions of both auto- and allo-grooming behaviors. The purpose of this study is to determine if grooming behaviors in mantled howler monkeys differ based on weather conditions (rain vs. non-rain) at La Suerte Biological Field Station in Costa Rica. Twenty-five hours of data on grooming behavior were collected in July 2018 using one-zero sampling of focal animals. I predicted that mantled howler monkeys would spend more time grooming in non-rainy weather conditions than in rainy weather. I also predicted that they would participate in more auto-grooming behaviors than allo-grooming behaviors across all weather conditions. I found that mantled howler monkeys spent more time participating in grooming behaviors in non-rainy weather conditions (12.3% of time auto-grooming and 0.2% of time allo-grooming) than in rainy weather (8.7% of time auto-grooming and 0.3% allo-grooming). Although mantled howler monkeys are a group-living primate species, they are not as gregarious as other social primates. I found that mantled howler monkeys spent relatively little time participating in allo-grooming across weather conditions. Allo-grooming is often regarded as a key social-bonding mechanism which solidifies relationships among groupmates. Thus it is likely that mantled howler monkeys are not

characterized by strong social bonds within their groups. It is likely that they most often resort to auto-grooming for more practical means such as combating parasites.

Assessing the determinants of primate gait kinematics in an ecological and phylogenetic framework, Part I: Phylogenetic methods for biomechanics

TOBIN L. HIERONYMUS¹, LIZA J. SHAPIRO², NOAH T. DUNHAM¹, ALLISON MCNAMARA² and JESSE W. YOUNG¹

¹Anatomy & Neurobiology, Northeast Ohio Medical University, ²Anthropology, University of Texas at Austin

Interspecific comparisons of primate locomotor profiles and gait kinematics are commonly used by physical anthropologists for insight into primate locomotor adaptations and evolution. The use of phylogenetic comparative approaches in locomotor biomechanics has lagged behind other aspects of organismal biology, in part because kinematic variables do not fit well with the mechanics of standard approaches. We propose a multivariate approach that uses a direct representation of phylogenetic structure via phylogenetic eigenvector maps (PEM), which decomposes tree shape into a set of orthogonal linear contrasts. This study uses a set of kinematic and substrate variables for 11 platyrrhine species, gathered at field sites in Ecuador and Costa Rica. In contrast to most applications of phylogenetic comparative methods, in which taxa are the unit of analysis, our focus in this analysis was on individual strides (total $n = 1,233$). The inclusion of several strides per taxon (minimum n per taxon = 57) allows the use of a complete phylogenetic model (10 terms) without exhausting the degrees of freedom available for analysis of other variables. To assess the relationships between gait, substrate, and phylogeny, we used a combination of variation partitioning and redundancy analysis. Phylogeny and substrate explain 58% and 21% of kinematic variance, respectively, with a marked overlap (20%), indicating that both substrate use and kinematics are divergent with phylogeny. PEM loadings point to local "hotspots" of kinematic divergence in callitrichine and pitheciid taxa. This study highlights the utility of multivariate phylogenetic comparative approaches for understanding determinants of primate locomotor kinematics.

Research supported by NSF BCS-1640552 and BCS-1640453

Age estimates for hominin fossils and the onset of the Upper Palaeolithic at Denisova Cave

THOMAS HIGHAM¹, KATERINA DOUKA², VIVIANE SLON², ZENOBIA JACOBS³, CHRISTOPHER RAMSEY¹, FABRIZIO MAFESSONI⁴, MAXIM

KOZLIKIN⁷, BO LI⁵, DANIEL COMESKEY¹, THIBAUT DEVIESE¹, SAMANTHA BROWN², BENICE VIOLA⁶, MICHAEL BUCKLEY⁵, MATTHIAS MEYER³, RICHARD ROBERTS⁴, SVANTE PAABO³, ANATOLY DEREVIANKO⁷, MICHAEL SHUNKOV⁷ and JANET KELSO³

¹Oxford Radiocarbon Accelerator Unit, Oxford University, ²Department of Archaeology, Max Planck Institute for the Science of Human History, ³Department of Evolutionary Genetics, Max Planck Institute for Evolutionary Anthropology, ⁴Centre for Archaeological Science, School of Earth and Environmental Sciences, University of Wollongong, ⁵Manchester Institute of Biotechnology, University of Manchester, ⁶Department of Anthropology, University of Toronto, ⁷Institute of Archaeology and Ethnography, Russian Academy of Sciences, Siberian Branch, Novosibirsk

Denisova Cave is a key site in understanding the complex relationships between hominin groups inhabiting Eurasia over the last 300,000 years. DNA evidence has shown the presence of a hitherto unknown hominin: the "Denisovans". High coverage genomes from Neanderthal and Denisovan fossils found at the cave provide evidence for mixture between the two groups. Determining the age of these fossils is important if we are to understand the nature of hominin interaction, as well as aspects of their cultural and subsistence adaptation. We obtained 50 new radiocarbon dates from the site covering the end of the Middle and start of the Upper Palaeolithic periods.

We used a Bayesian age modelling approach combining chronometric (radiocarbon and optical ages), stratigraphic and genetic (separation times estimated from deeply-sequenced genomes) data. Our age estimates provide robust estimates for fossils in the site. Between ~140–110,000 years ago both Neanderthals and Denisovans overlapped. *Denisova 11*, the direct offspring of a Denisovan and a Neanderthal, falls just after this interval, ~110–90,000 years ago. The *Denisova 3* phalanx predates the radiocarbon limit at 56,400–67,600 years ago. Dates of pierced tooth ornaments and bone points from the upper layers yielded the earliest evidence for the production of such artefacts in Eurasia, at c. 48–45,000 years ago. Based on present archaeological evidence, these artefacts may have been produced by Denisovan people. Whether anatomically modern humans (AMH) were involved is not possible to determine at present because their remains have not yet been identified in the Altai region.

This research was funded by the European Research Council, The Max Planck Society, the Russian Science Foundation and the Royal Society.

ABSTRACTS

Mortality and skeletal lesion profiles among Prehispanic Lower Pecos foragers of southwest Texas

CHARLES E. HILTON^{1,2} and MARSHA D. OGILVIE²

¹Anthropology, University of North Carolina, Chapel Hill, ²Texas Archeological Research Laboratory, University of Texas at Austin

For several decades, researchers examining health within living hunter-gatherers describe them as exhibiting lower levels of morbidity and chronic disease relative to those in small-scale agriculturalists and post-industrial populations. Low forager morbidity levels are noted to result from lifestyles combining strenuous habitual physical activities with diets low in obesogenic foods. Such morbidity characteristics have been extended to prehistoric and fossil human foragers, thereby suggesting that earlier foragers lived healthy disease-free lives. Our paper addresses health, morbidity, and mortality by examining paleopathological lesions and mortality profiles for Prehispanic Archaic Period (2300-1300 YBP) Lower Pecos (LP) foragers of southwest Texas. The LP cultural region encompasses canyonlands near the confluences of the Devils, Pecos, and Grande Rivers. Our bioarchaeological investigation examines most of the archaeologically-derived human skeletal remains from 37 rockshelters near these rivers. The LP foragers are represented by approximately 204 skeletons (80 immature and 124 adult individuals). Each skeleton was assessed for morbidity evidence including infections, fractures, periodontal disease, and joint degeneration. Like other bioarchaeological assemblages, the LP skeletal 'population' exhibits a paleodemographic profile with a high percentage of neonates/infants and a low percentage of elderly adults. While LP foragers exhibit few lesions indicative of chronic dietary deficiencies nor infectious diseases, the high number of perinatal and infant remains are suggestive of high infant mortality and low life expectancy at birth. These health, morbidity, and paleodemographic analyses are contextualized with respect to understanding human forager health and resiliency in the Chihuahuan Desert landscape.

Are we what we eat? A 3D Geometric morphometric analysis of human mandibular variation over time in Britain in relation to dietary changes

CARA S. HIRST

Institute of Archaeology, University College London

Previous studies have reported significant changes in mandible morphology associated with major dietary transitions, such as the advent of agriculture and the industrial revolution. Changes in food processing technology are thought to have resulted in a softer diet, resulting in lower levels of masticatory stress, which in turn

influences mandible morphology through alterations in bone remodelling. These studies however have typically focussed on the comparison of two periods, and as such it is not known if reported changes in mandible morphology represent a consistent reduction in mandibular robusticity, or if mandible morphology fluctuates between periods associated with diet. Furthermore, by only focussing on major dietary transitions it is not known how susceptible the mandible is to minor changes in diet.

The aim of this study is to fill the current gaps in the literature by analysing how mandible morphology has changed in Britain from the Neolithic through to the Post-Medieval period.

Approximately 1000 mandibles were 3D scanned and landmark based geometric morphometric analysis was conducted with Canonical Variate Analysis utilised to determine how mandible morphology varied between the six time periods analysed in this study.

Results determined that in general mandible morphology became increasingly gracile over time, with more pronounced changes occurring between the Neolithic and Iron and Bronze Age thought to be associated with the intensification of arable agriculture. In addition, significant increases in gracilisation occurred between the Anglo-Saxon and Medieval and also the Medieval and Post-Medieval periods likely related to modernisation and industrialisation of food processing technologies.

World-wide variation in incisor shoveling reveals evidence of selection in the Beringian Standstill population

LESLEA J. HLUSKO^{1,2}, JOSHUA P. CARLSON², GEORGE CHAPLIN³, SCOTT A. ELIAS⁴, JOHN F. HOFFECKER⁴, MICHAELA HUFFMAN^{1,2}, NINA G. JABLONSKI³, TESLA A. MONSON⁵, DENNIS H. O'ROURKE⁶, MARIN A. PILLOUD⁷, CATHERINE TAYLOR^{1,2} and GEORGE R. SCOTT⁷

¹Integrative Biology, University of California Berkeley, ²Human Evolution Research Center, University of California Berkeley, ³Anthropology, Penn State University, ⁴Institute of Arctic and Alpine Research, University of Colorado Boulder, ⁵Anthropology Institute, University of Zurich, ⁶Anthropology, University of Kansas Lawrence, ⁷Anthropology, University of Nevada Reno

Several genome-wide association studies reveal that a variant of the *Ectodysplasin A Receptor* (*EDAR*) has an additive effect on human incisor shoveling, such that the presence of one or two alleles of *V370A* corresponds to a moderate or strong degree of shoveling. We analyzed shoveling for 5,333 individuals from 54 archaeological populations across Eurasia and the Western Hemisphere. We use an evolutionary quantitative approach to test the hypothesis that genetic drift alone can account for the shift in phenotypic mean between Asian and Western Hemisphere

populations, as the latter demonstrate much higher frequencies and degrees of shoveling. We employ a range of theoretical extremes for heritability estimates (0.05 to 1), a range of possible phenotypic variances (0.86 to 1.23), and a generation time of 25 years across 100 to 400 generations. We find that all combinations of parameter values within published ranges reject the neutral hypothesis with 95% confidence, suggesting that the increase in incisor shoveling observed in Native American populations is the result of selection. This finding accords with the genomic evidence that reveals strong selection for the *EDAR V370A* allele. This concurrence of dental and genomic data places the selection event on *V370A* within the Beringian refugium during the Last Glacial Maximum, a region that is environmentally extreme due its very low levels of ultraviolet radiation exposure. We hypothesize that the phenotypic target of selection was likely the pleiotropically related ductal branching of the mammary gland rather than incisor shoveling.

Paternal activity budgets of San Martin titi monkeys (*Plecturocebus oenanthe*) in response to habitat destruction, daily temperature range, and infant age

SHANNON HODGES

Anthropology, Texas A&M University

The critically endangered San Martin titi monkey (*Plecturocebus oenanthe*) is endemic to Peru and occupies primarily degraded habitat. To determine whether *P. oenanthe* fathers, the primary infant caregivers, employ specific strategies to cope with the energetic demands of parenting given different environmental stressors, I tracked activity budgets of fathers while they provided infant care. I predicted that resting would be 1) positively correlated with habitat destruction, 2) positively correlated with daily temperature range, and 3) negatively correlated with infant age. I expected the opposite outcomes for traveling and feeding. I used instantaneous sampling to collect approximately 200 hours of data over the course of 14 months for two groups living at two distinct sites in the San Martin Region of Peru. I used chi-squared tests and correlation tests ($\alpha=0.05$) to compare activity budgets of two fathers by relative level of habitat destruction, daily temperature range categorized as either Low (<10 degrees Celsius) or High (≥ 10 degrees Celsius), and infant age (1-5 months of age). Neither habitat destruction nor temperature ($p>0.05$) affected overall activity budget. However, habitat destruction significantly impacted activity budget when infants were 3-5 months of age ($p<0.05$) and temperature significantly altered activity budget at the high destruction site ($p<0.05$). As predicted infant age significantly altered overall activity budget in the expected manner ($p<0.001$), and these differences were also shown within each level of

ABSTRACTS

habitat destruction ($p < 0.001$). Results indicate that *P. oenanthe* fathers employ an energy-minimizing strategy to cope with environmental stressors while caring for offspring.

Funding: Fulbright, International Primatological Society, Primate Conservation, Inc., Mohamed bin Zayed Species Conservation Fund, Explorers Club, Sigma Xi, L.T. Jordan Foundation, Texas A&M University.

Native American origins: An interdisciplinary critique of current models

JOHN F. HOFFECKER¹, G R. SCOTT², DENNIS H. O'ROURKE³, MARK A. SICOLI⁴ and LESLEA J. HLUSKO⁵

¹INSTAAR, University of Colorado, ²Anthropology, University of Nevada, ³Anthropology, University of Kansas, ⁴Anthropology, University of Virginia, ⁵Human Evolution Research Center, University of California

Most archaeologists currently entertain one of two models for the origin of the Native American population. These models postulate a source for Native Americans in Northeast Asia after the Last Glacial Maximum (LGM) or <18,000 years ago, either in the interior (i.e., Lena Basin) or the maritime zone (Hokkaido/Sakhalin/Primor'e). The pertinent archaeological data exhibit massive gaps, however, and accommodate a variety of alternative scenarios.

Most of the pertinent analyses in other disciplines cannot be reconciled with either of the current models in archaeology. Linguists observed decades ago that a post-LGM origin in NE Asia could not account for the diversity in Native American languages, and more recently, the same observation has been applied to the exceptionally high number of language isolates in the Americas. Working initially with mtDNA data, many human geneticists concluded that Native American lineages diverged from their Asian parent lineages before the LGM, and most whole-genome analyses (including aDNA) now indicate a similar pattern. The presence of traits found in SE Asian/Australian groups among South Americans can be reconciled with a post-LGM source in NE Asia only by postulating an early dispersal in the Americas ("Population Y") for which there is little corroborating evidence.

Dental anthropology also provides support for pre-LGM divergence of all Native American groups from their Asian parent population. Analysis of a large sample of teeth for 24 morphological traits indicates a deep split between living Native American groups and their Asian source population, indicating a pre-LGM divergence.

DMTA of Muchik sacrifice victims from Cerro Cerillos

MEGAN R. HOFFMAN¹, MACKENZIE C. VERMILLION¹, CHRISTOPHER W. SCHMIDT¹ and HAAGEN D. KLAUS²

¹Anthropology, University of Indianapolis, ²Anthropology, George Mason University

Dental microwear texture analysis (DMTA) is used to interpret microscopic dental wear, usually in the context of diet. DMTA focuses on microsurface relief at the finest scales via profilometry with submicron resolution and scale-sensitive fractal analysis software. The current study employs DMTA in order to contextualize microwear signatures of Muchik subadults ($n = 8$) from the site of Cerro Cerillos, who were sacrificed between roughly A.D. 900 and 1375. They are compared to a sample of non-sacrificed contemporaneous Muchik people from Huaca Sialupe ($n = 7$). The study employed standard DMTA procedures for the analysis. Dental replicas were studied with a white-light confocal profiler at 100X. Texture variables included complexity, anisotropy, and textural fill volume. Statistical comparisons were made via ANOVA. Data were normally distributed but heteroscedastic. Thus Welch's test was incorporated into the analyses. The results indicate no significant differences between the sacrificed children and the people of Huaca Sialupe. The heteroscedasticity is of interest as it suggests the sacrificed subadults' diet was modest compared to that of the non-sacrificed people, particularly for complexity. That is, each sacrifice victim consumed similar foods for a period of several days or weeks before they died. In summary, the diet data indicate the sacrificed children came from the local Muchik population, but each child ate a very particular range of foods leading up to their being sacrificed. This may echo practices known in other Andean cultures, where sacrifice victims were fêted and provided distinctive ritual diets as part of the pre-sacrificial program.

Seeing the flowers for the trees: trichromacy provides food detection advantages for white-faced capuchins

JEREMY D. HOGAN¹, LINDA M. FEDIGAN¹, CHIHIRO HIRAMATSU², SHOJI KAWAMURA^{3,4} and AMANDA D. MELIN^{1,5,6}

¹Anthropology and Archaeology, University of Calgary, ²Human Science, Kyushu University, ³Integrated Biosciences, University of Tokyo, ⁴Graduate School of Frontier Sciences, University of Tokyo, ⁵Medical Genetics, University of Calgary, ⁶Alberta Children's Hospital Research Institute, University of Calgary

Trichromatic (red-green) color vision is found in many primate species and may offer advantages for detecting reddish food sources including fruits and flowers. However, other cues are often available and foraging differences based on color vision phenotype are difficult to evaluate in wild

primate populations. Costa Rican white-faced capuchins (*Cebus capucinus imitator*) possess a polymorphic color vision system, offering the opportunity to directly compare foraging patterns among conspecific individuals. Floral resources are seasonally important to capuchins, and we ask: 1) are flowers that are consumed by monkeys more visible to trichromats than to dichromats? and 2) do trichromatic capuchins consume flowers more often than do dichromats? We determined the colour vision phenotype of 83 capuchins based on amino acid variation of the L/M opsin gene from fecal DNA. We collected spectroscopic data from 14 dietary flower species and modeled their conspicuity in the color space of capuchins. Finally, using behavioural data collected over 22 months we compared foraging behaviours of dichromats and trichromats using generalized linear mixed models. A large majority of flowers were more conspicuous to trichromats, and trichromats foraged in small flower patches significantly more often than dichromats did (Estimate=0.6882, SE=0.2449, $z=2.754$, $p=0.006$). These data demonstrate a difference in wild primate foraging patterns based on colour vision type, supporting the hypothesis that trichromacy enhances long-distance detection of small, ephemeral resources. This advantage, which probably also extends to fruits, likely contributes to the maintenance of colour vision polymorphism in Neotropical monkeys.

Natural Sciences and Engineering Research Council of Canada, The Canada Research Chairs Program, the University of Calgary, and the Japan Society for the Promotion of Science 16K14818 and 15H02421.

Surface area and volume of the body in Late Pleistocene *Homo*

TRENTON W. HOLLIDAY^{1,2} and BORYANA M. KASABOVA¹

¹Anthropology, Tulane University, ²Evolutionary Studies Institute, University of the Witwatersrand

Using nine osteometric measurements to estimate anthropometric data, and modeling the human body as a series of cylinders and frusta, body surface area (SA) and volume (V) were calculated for a sample of Late Pleistocene fossil hominins (3 Neandertals, 2 Skhul-Qafzeh, 3 European Early Upper Paleolithic [EUP], and 12 terminal Pleistocene specimens from Europe, the Levant, and North Africa). The fossils were compared to SA and V estimates for a large sample of high latitude/cold-adapted ($n=266$) and low latitude/heat-adapted ($n=384$) recent human skeletons. ANCOVA for the recent human samples indicates that the slopes of the body volume to surface area regression relationship are not significantly different between the geographic groups ($P=0.94$), but the intercepts are ($P < 0.01$), with the cold-adapted group having

ABSTRACTS

a significantly higher intercept. Thus, high latitude groups tend to have greater body V for any given SA than low latitude groups – much of this due to their wider bi-iliac breadths.

The fossils show the following pattern: Neandertals fall at or above the line for recent high-latitude groups (i.e., look even more “cold-adapted”), while the Skhul-Qafzeh and European EUP samples fall about or below the line for the recent low latitude groups (i.e., look more “heat-adapted”). The terminal Pleistocene specimens from Europe and the Near East show greater variation, with some looking more cold-adapted, while others look more heat-adapted. These results are consistent with Neandertals and the earliest moderns showing different climatic adaptations; gene flow between these groups may be evident in the terminal Pleistocene.

This research was funded in part by NSF (#SBR-9321339), the L.S.B. Leakey Foundation, and Tulane University.

A Phylogenetic Analysis of European Pliopithecoids

ANDREW C. HOLMES and DAVID R. BEGUN
Anthropology, University of Toronto

The Pliopithecoidae is a clade of extinct catarrhine primates that inhabited Eurasia from 18 to 7 million years ago. Known primarily from fossilized dental remains, pliopithecoids have remained a poorly understood taxonomic group since their discovery by Édouard Lartet in 1837. We present a systematic phylogenetic analysis of over one hundred metric and non-metric dental and mandibular characters from 12 European pliopithecoid species. Character states were collected using CT scans, 3D surface scans, linear measurements, and observations made on the original fossil specimens. Characters were polarized using extinct anthropoid taxa from Egypt (Parapithecoidae, Propithecoidae) and extant Platyrrhines as outgroups. We used both maximum parsimony and maximum likelihood analysis to reconstruction pliopithecoid phylogeny. Our results support the validity of the Pliopithecoidae as a distinct anthropoid clade. All European taxa are grouped into two families, Pliopithecidae and Crouzeliidae. Contrary to previous studies, we find that fossil material from Priay, France, which has been assigned to both *Pliopithecus* and *Anapithecus*, better fits with the *Plesiopithecus* hypodigm. Our analyses also support the recognition of *Epiplioptithecus vindobonensis* as distinct genus, the sister taxon to *Pliopithecus*.

Funded by Ontario School of Graduate Studies, Natural Sciences and Engineering Research Council of Canada, and Department of Anthropology, University of Toronto.

Design and function of the chewing muscles in papionins: fiber phenotype and fiber architecture

MEGAN A. HOLMES¹, KIERA LUNN² and ANDREA B. TAYLOR³

¹Department of Community and Family Medicine, Duke University School of Medicine, ²Evolutionary Anthropology Department, Duke University, ³Department of Basic Science, Touro University

Sooty mangabeys (*Cercocebus atys*) present a form-function paradox: they routinely feed on hard seeds suggesting frequent forceful muscle activation, yet they do not exhibit architectural features of the jaw-adductors that are advantageous for producing relatively large bite forces. Fiber phenotype is also an important determinant of muscle function and may fine-tune jaw muscles to improve feeding performance. Non-primate mammals that spend a significant portion of their day chewing express a slow, fatigue-resistant fiber type. Here we test the hypothesis that *C. atys* (n=4) possess a slower, more fatigue-resistant masseter compared to closely related papionins with less obdurate diets (*Macaca mulatta*, n=3; *M. fascicularis*, n=3; *Papio anubis*, n=4). We used IHC to quantify the distribution and proportion of type 1 (slow; MyHC-1, MyHC α -cardiac) and type 2 (fast; MyHC-2, MyHC-M) fibers. Muscle sections were photographed and saved as digital images. Fibers were counted and scored for intensity as dark, intermediate, light or unstained. Hybrid fibers (single fibers expressing multiple MyHC isoforms) were ubiquitous throughout the sample. Fiber-type phenotype was significantly dependent on species (loglinear regression, p=0.001), largely driven by a greater proportion of MyHC-1/ α -cardiac/MyHC-2 hybrid type in *C. atys* (87%) and *Panubis* (71%). However, MyHC-1/ α -cardiac fibers predominantly stained intermediate-dark while much of MyHC-2 fibers (50-90% across species) stained lightly. Initial results indicate the papionin masseter is characterized by a slow/fatigue-resistant fiber phenotype, potentially more extreme in *C. atys*. The prevalence of hybrid fibers complicates functional interpretations and suggests a more complex picture than can be accounted for by feeding behavior alone.

This work was supported by NSF BCS 1719743.

Walking before footwear: plantar calluses protect the foot without trading-off tactile sensitivity

NICHOLAS B. HOLOWKA¹, BERT WYNANDS², TINA DRECHSEL², DIRESBACHEW W. HAILE³, ROBERT OJIAMBO MANG'ENI³, PAUL OKUTOYI⁴, TIMOTHY K. SIGE⁵, VICTORIA A. TOBOLSKY¹, ANDREW K. YEGIAN¹, CLAUDIO ZIPPENFENNIG², THOMAS L. MILANI² and DANIEL E. LIEBERMAN¹

¹Department of Human Evolutionary Biology, Harvard University, ²Department of Human Locomotion, Technische Universität Chemnitz,

³Department of Physiology, Moi University Medical School, ⁴Department of Orthopedics, Moi University Medical School, ⁵Department of Statistics and Computer Science, Moi University

Habitually barefoot humans possess thick plantar calluses that develop in response to frictional stresses during walking and running. Because all humans were barefoot until relatively recently, plantar calluses should be viewed as a normal feature of human anatomy, yet we know surprisingly little about them. In this study we tested the common assumption that thick calluses trade-off protection with a loss of tactile sensitivity. We collected data from a large sample of adults from a Kalenjin-speaking population in western Kenya, including 35 usually barefoot individuals and 46 usually shod individuals. We used ultrasound to measure callus thickness at the heel and first metatarsal head and found that usually barefoot individuals have thicker calluses than usually shod individuals at both locations (p<0.001). We also measured skin hardness using a Shore durometer and found that hardness correlates with epidermal thickness across subjects at both the heel (r=0.64, p<0.001) and metatarsal head (r=0.56, p<0.001), with usually barefoot individuals having harder skin (p<0.001). Finally, we tested the sensitivity of fast-adapting mechanoreceptors at these locations using a standard vibration stimulus protocol. We found no relationship between plantar sensitivity and callus thickness at either location, even after controlling for the effects of age, sex and footwear use. This finding indicates that unlike footwear, calluses provide protection without loss of dynamic plantar sensitivity, making them a remarkable example of evolutionary engineering that allows humans to walk and run barefoot safely.

Funded by the American School of Prehistoric Research (Harvard University).

Lower mechanization levels are associated with increased age-related limb bone strength in European skeletal samples

BRIGITTE HOLT

Anthropology, University of Massachusetts

Age-related declines in bone mass are well documented in modern and recent populations for both men and women. Previous research suggests, however, that while pre-industrial populations also undergo endosteal resorption with age, both sexes also exhibit compensatory periosteal apposition, possibly related to high physical activity levels (PALs) characteristic of prehistoric populations. This project tests the hypothesis that, relative to the pre-Medieval period, decreased PALs and increased mechanization in Medieval Europe resulted in increased age-related cortical bone loss and reduced bone strength. While both groups are expected to exhibit age-related declines in percent cortical thickness, the less mechanized and less sedentary pre-Medieval

ABSTRACTS

group should also show age-related increases in compensatory periosteal apposition (increased total area or TA). Bone areas and thickness (CA, TA, %CA) and bending strength (Zp) for upper and lower limb bones are quantified for a large European skeletal sample, divided into pre-Medieval group (Neolithic-Iron Age, 7300-1650BP, N=868) and Medieval groups (550-1350AD, N=864). Pre-Medieval and Medieval men and women show marked declines in age-related %CA. In both periods, both sexes experience declines in limb bone CA with age. However, while there are also declines in TA and bending strength in the older Medievals, the loss of cortical area in pre-Medieval males and females is compensated by significant increases in age-related TA, resulting in either increases or maintenance of bending strength. These results suggest that the higher physical demands associated with more limited transport and mechanized farming means in pre-Medieval periods contributed to maintenance of bone strength in older adults.

A candidate gene approach to assessing phenotype/genotype correlations in the nasal complex

NATHAN E. HOLTON^{1,3}, THOMAS WELK¹, LINA MORENO-URIBE¹, TODD R. YOKLEY² and ROBERT G. FRANCISCUS³

¹Orthodontics, The University of Iowa, ²Sociology and Anthropology, Metropolitan State University, Denver, ³Anthropology, The University of Iowa

Variation in the modern human nasal complex has largely been assessed within the context of climatic adaptation. While patterns of morphological variation and their functional implications are reasonably well understood, we lack information regarding the mechanisms that generate the morphological variation that evolution acts upon. An important step toward understanding this dynamic is to identify the genetic architecture that underlies nasal phenotypic variation. To address this, we used a candidate gene approach to provide the first phenotype/genotype analysis of the combined external and internal nasal complex using a sample of n=120 subjects predominantly of European ancestry. Nasal complex morphology was characterized using 3D coordinate landmarks obtained from cone beam CT scans, while DNA was obtained from saliva samples. Phenotypic variation in the nasal complex was quantified using PCA of Procrustes superimposed landmarks. We assessed the correlations between PC scores and single nucleotide polymorphisms (SNPs) in 21 genes/loci previously shown to influence skeletal and cartilage development or known to influence facial morphogenesis more broadly. Significant correlations were found between SNPs and PC scores describing variation in internal and external length (e.g., *SHH*, *LATS1*), nasal complex width and external nasal projection (e.g., *SATB2*, *MANT2*,

LMO4), and external nasal shape (*PAX7*, *SATB2*). Our results underscore the highly polygenic nature of nasal shape and provide an important first step toward understanding the developmental mechanisms that underlie variation in nasal complex morphology.

Survivorship and urbanization in medieval England

EMMA S.L. HOOK¹, BRITTANY S. WALTER² and SHARON N. DEWITTE³

¹Department of Archaeology, University of Sheffield, ²Defense POW/MIA Accounting Agency Laboratory, Department of Defense, ³Department of Anthropology, University of South Carolina

Medieval England experienced intensive urbanization, exposing increasing numbers of people to urban environmental factors often associated with poor health, such as high population density, unsanitary living conditions, elevated risk of infection and precarious food supplies. Previous research revealed elevated risks of dying and reduced survival for adults in medieval London compared to rural adults, but did not address patterns among nonadults. We expand on this previous work by assessing risks of mortality and survival as proxies for health among nonadults. Our combined sample (urban n=2230 rural n=328) was drawn from seven medieval cemetery assemblages: the London cemeteries of St Mary Spital, St Mary Grace, East Smithfield, St Nicholas Shambles, and Guildhall Yard; and the rural cemeteries of Barton on Humber, Lincolnshire and Thornton Abbey, Lincolnshire. Attritional burials and catastrophic (associated with famine and plague) burials are included in the sample. Adult ages were estimated using transition analysis, and demographic patterns were assessed using Kaplan-Meier survival analysis and Cox proportional hazards analysis. Analyses including catastrophic burials indicate that rural adults experienced reduced mortality and elevated survivorship compared to their urban counterparts, but that urban nonadults experienced reduced mortality and elevated survivorship compared to rural nonadults. Analyses excluding catastrophic burials reveal no differences between urban and rural adults, but reduced mortality and elevated survivorship for urban nonadults compared to rural nonadults. These results suggest that urban environments were not detrimental to children but may have been detrimental to adults, and that rural environments may have negatively affected the health of children.

Funding provided by the NSF (BCS-0406252, BCS-1261682, BCS-1539502, BCS-1722491), Wenner-Gren Foundation (#7142, #8247), American Association of Physical Anthropologists, the Walker Institution, and University of South Carolina Department of Anthropology.

Persistence hunting in Levant: Both Neandertals and modern humans could run down a horse

MARTIN HORA^{1,2}, HERMAN PONTZER² and VLADIMÍR SLÁDEK¹

¹Department of Anthropology and Human Genetics, Charles University, ²Department of Evolutionary Anthropology, Duke University

Persistence hunting is generally associated with African environments and the origins of the genus *Homo*. However, persistence hunting could be feasible also in other locations and for later *Homo* who lacked sophisticated weaponry. Here, we examine the capacity of Neandertals and Middle Paleolithic modern humans (MPMH) to employ persistence hunting to various-sized horses in Levant by comparing their aerobic endurance (i.e., maximal duration of locomotion at given aerobic velocity).

We modeled three Neandertals, four MPMHs, and four variants (body mass: 110, 250, 500, and 800 kg) of a horse. We used a previously described heat exchange model parametrized to humans and horses to estimate body temperature and water loss during locomotion in hot (35–40 °C) and dry (35%–65% relative humidity) conditions. Endurance was delimited by body temperature threshold (40 °C) and water loss threshold (human: 10% of body mass, horse: 20% of body mass).

Our results suggest that Neandertals and MPMH would be able to run down a large horse (500 and 800 kg) even at jogging velocities (2–3 m/s) at most of the simulated conditions. For both taxa, it should be possible to run down smaller horses (250 kg) using running velocities (3–5 m/s) in less humid conditions. Small pony-sized horses (110 kg) could not be caught using persistence hunting as they attain heat balance even at velocities exceeding the human aerobic range. We conclude that the *Equus* remains in the Neandertal and MPMH sites in Levant could be a product of persistence hunting.

This work was supported by the Czech Science Foundation (grant number 18-16287S).

The influence of occupation, habitual activity, and SES on osteometric variation in modern humans

HALEY E. HORBALY¹ and MARK HUBBE^{2,3}

¹Department of Anthropology, University of Tennessee, Knoxville, ²Department of Anthropology, The Ohio State University, ³Instituto de Arqueología y Antropología, Universidad Católica del Norte, Chile

Previous research has shown that intensity and frequency of repeated loading patterns throughout the life of an individual can affect cross-sectional properties of bone, but few studies have explored whether this affects other bone dimensions. Repeated loading

ABSTRACTS

patterns are capable of significantly changing bone morphology, even after adolescence, and socioeconomic status (SES) is known to correlate with growth outcomes at all stages of life. Thus, the present study analyzes occupation, habitual activity (HA), and socioeconomic status (SES) data as potential environmental factors influencing bone dimensions in a sample of 585 modern adult skeletons from the Bass Collection. Occupation, HA, and SES were scored on an ordinal scale based on data provided by the donors (1-5 for occupation and SES; 1-3 for habitual activity), with lower scores representing low activity levels or SES group, and vice-versa. Sex-specific Kruskal-Wallis tests explored the associations between environmental factors and 44 metric dimensions of postcranial long bones. Males show more significant differences in osteometrics between scores of lifelong occupation (12 of 44 tests returning $p < 0.05$) and SES (7 of 44 tests returning $p < 0.05$); female tests return limited significant results. Most of the differences are the result of the most extreme values of occupation and SES being different from the rest. No significant associations were detected among HA scores for either sex. Overall, the results show that occupation plays a role in promoting differences in skeletal dimensions, especially for males, while showing that HA does not seem to be a meaningful source of variance.

Diversity and distribution patterns of a primate community in the Peruvian Amazon

ROSE M. HORES and SUSAN M. FORD

Department of Anthropology, Southern Illinois University

Knowledge of the range of taxa that co-occur in heterogeneous landscapes and their patterns of distribution provide insight on the spatio-temporal relationships between communities of species and their habitats. However, investigations of large primate communities co-occurring across a single mosaic landscape site remain scarce. The goal of this study is to investigate the diversity and distribution patterns of a primate community of 12 co-occurring species inhabiting a mosaic landscape in the Peruvian Amazon.

The study was conducted at the Tahuayo River Amazon Research Center (TRARC) in northeastern Peru (September 2012-February 2014). The site includes four types of flooded forests plus non-flooded forests. We tested the hypothesis that primate distribution in a mosaic landscape is dependent on forest structure (habitat type).

Line-transect and reconnaissance sampling were used to calculate the encounter rates of each primate species per habitat. Mean encounter rates per 100 km were compared across the habitats using ANOVA and Tukey's method. The standard alpha level of 0.05 was used.

A total of 2345.93 km was surveyed, and 714 primate encounters were recorded. Primates overall were least encountered in the most flooded habitat as were *Pithecia* spp. and *Sapajus macrocephalus*. *Lagothrix lagotricha poeppigii* were only encountered in the non-flooded forests. Most primates were ecological generalists.

These data provide a basis for understanding the diversity and distribution patterns of a primate community occurring in a mosaic landscape. Understanding spatio-temporal relationships can further assist in conservation efforts geared towards the promotion and maintenance of tropical forest regeneration and diversity.

Funding for this project was provided by Idea Wild, Amazonia Expeditions, and Southern Illinois University's Uakari Research Fund.

The skin microbiome of the Cayo Santiago rhesus macaques

CHRISTINA ROCHE¹, LAUREN BRENT², JENNY WANG³, MICHAEL MONTAGUE³, KARLI WATSON⁴, ANGELIA RUIZ LAMBIDES⁵, MICHAEL PLATT^{3,6,7} and JULIE HORVATH^{1,8,9}

¹Research and Collections, North Carolina Museum of Natural Sciences, ²Centre for Research in Animal Behaviour, University of Exeter, ³Department of Neuroscience, University of Pennsylvania, ⁴Institute of Cognitive Science, University of Colorado Boulder, ⁵Cayo Santiago Field Station, Caribbean Primate Research Center, University of Puerto Rico, ⁶Marketing Department, University of Pennsylvania, ⁷Department of Psychology, University of Pennsylvania, ⁸Department of Biological and Biomedical Sciences, North Carolina Central University, ⁹Department of Evolutionary Anthropology, Duke University

Primate skin is rich with microscopic organisms including bacteria and Archaea, which contribute to the overall health of animals including impacts on wound healing and body odor. We collected behavioral data and axillary skin microbial swabs from free-ranging Indian origin rhesus macaques (*Macaca mulatta*) living on Cayo Santiago in Puerto Rico. These animals are highly social and can provide insight into how host behaviors influence skin microbes, and how the skin microbes may impact overall health. Here we assess skin microbiota from more than 80 animals from four different social groups to illustrate the power of an integrative behavioral and microbiome dataset to elucidate information about behavioral influences on microbiome composition. We amplified the V4 region of the 16S rRNA from all samples with high throughput sequencing on an Illumina MiSeq. Data were analyzed with QIIME2. The

bacterial and Archaeal composition of macaque skin was very diverse with 25 known Phyla including those commonly found on primate skin (Firmicutes) as well as less common Nitrospirae. We found significantly differentially abundant taxa between the social groups, such as a species of Rhodospirillaceae. Animals with higher levels of self-grooming show more Myxococcales, an order of bacteria found in clay skin treatments in India used for healing. We also found taxa differential between age groups, such as *Blautia*. Our study sheds light on the ecology and evolution of microbiota community structure in these free-ranging monkeys and these findings are directly relevant to understanding connections between behavior, ecology and the skin microbiome.

Recent regulatory changes shaped human vocal and facial anatomy

GENEVIEVE HOUSMAN¹, DAVID GOKHMAN² and LIRAN CARMEL²

¹Section of Genetic Medicine, University of Chicago, ²Department of Genetics, The Hebrew University of Jerusalem

Changes in gene regulation are broadly accepted as key drivers of phenotypic differences between closely related species. However, it is largely unknown what regulatory changes occurred during our recent evolution and which of these modifications have shaped human-specific traits. By harnessing the natural degradation processes of methylated and unmethylated cytosines in ancient DNA, we developed a method to reconstruct full DNA methylation maps from ancient individuals. Further, we have assayed methylation patterns in skeletal tissues from several extant nonhuman primate species to determine variation present across the larger primate phylogeny. Here, we use >60 DNA methylation maps of ancient and present-day human groups, as well as six chimpanzee maps, to detect regulatory changes that emerged in modern humans after the split from Neanderthals and Denisovans. We found ~800 differentially methylated regions that emerged along our lineage after the split from archaic humans. We show that genes affecting vocalization and facial features went through particularly extensive methylation changes. Specifically, we identify silencing patterns in a network of genes (*SOX9*, *ACAN*, *COL2A1* and *NFIX*), and show that the knockout of *NFIX* in mice results in vocal tract alterations that mimic the modern human configuration which is optimal for speech. Our results provide insights into the molecular mechanisms that may have shaped the modern human face and voice and suggest that they arose after the split from Neanderthals and Denisovans.

<https://doi.org/10.1101/106955> for a list of all contributing authors.

ABSTRACTS

The Environment Beyond Points of Directional Change

ALLISON HOWARD¹, ELIE GURARIE², ELISABETTA VISALBERGHI³, PATRICIA IZAR⁴, DOROTHY FRAGASZY¹ and WILLIAM FAGAN²

¹Psychology, University of Georgia, ²Biology, University of Maryland, College Park, ³ISTC-CNR, National Research Council, Rome, ⁴Experimental Psychology, University of São Paulo

The landscapes that primates choose not to visit are as important as those they visit. Recent research on the travel paths of bearded capuchins (*Cebus libidinosus*) showed they repeatedly use an interconnected route network and frequently change direction at locations of high visibility, perhaps as a vantage point for travel decisions. In this study, we investigate the characteristics of the landscape beyond points of direction change (i.e., a vector from previous travel, distance: 0 - 300 m). These landscapes beyond change points (CPs) may reveal preferences that influence travel decisions. We followed individual bearded capuchin monkeys during three dry season months and visually interpreted and recorded their movements using a GPS-enabled tablet computer with a high resolution satellite image. We used the Byrne Change Point Test to identify locations where they significantly changed travel directions. CPs were found farther from roads than points at which individuals moved in a relatively straight line (move points or MPs). CPs were also found farther from areas of human influence (e.g., agricultural fields and homes) than MPs. However, CPs were significantly closer to steep ridges than MPs. These movement patterns indicate landscape preferences for move points and directional change points, with roads and human influence areas being preferred for movement and steep ridges being preferred for changes. Landscape preferences may reflect an animal's perceptions of risk, visibility, resource availability, or facility of rapid movement conferred by a given landscape type. Importantly, our work highlights the complex relationship between landscape features and movement decisions.

Semi-quantitative BSE-SEM evaluation of osteocyte and vascular porosity across complete bone cross section

BIN HU

Biomaterials, New York University College of Dentistry

Osteocytes are numerous and their large number is typically expressed as osteocyte lacuna density: n° lacuna/mm³, or n° lacuna/mm² in 3D or 2D respectively. Bone vasculature is similarly measured in 3D mm³ volumes or 2D mm² thin planes. In general, 3D methods are laborious or require sophisticated micro computed tomography. 2D methods employing light or electron microscopy imaging are simpler, and though values are relative, they scale directly with all

body mass-dependent measures of metabolic rate and life history. However, literature reports of 2D measures are quite variable, likely because of sample types and imaging modes used. We propose a highly reliable semi-quantitative method employing backscattered electron imaging in the scanning electron microscope (BSE-SEM). This method measures numbers and areas of lacunae and vascular pores from embedded bone block surfaces prepared free of topographic relief. Images obtained correspond to virtual sections of only 1 μ m thick, with gradations of grey according to mineral content and with lacunae and vascular pores appearing black. In this study, BSE-SEM imaging was performed with a Zeiss EVO 50 SEM at 15 kV, 600 pA, 8.5 mm WD, and 100 Pa. Whole human femur cross-section montages at 0.9793 μ m/pixel resolution were obtained using Zeiss SmartStich software. Monochrome 256 gray level images were processed and measured by the program "BSESEM", employing Matlab's Image Processing Toolbox. Lacunae and vascular pores have a characteristic roundness, perimeter, and area in BSE-SEM images that allow them to be identified and automatically measured relative to bone area in processed images.

Research support was provided by NSF award BCS-1062680 and the 2010 Max Planck Research Award to TGB.

Teaching race and gender as bioculturally relevant, not genetic proxies of human difference

AMELIA R. HUBBARD

Department of Sociology and Anthropology, Wright State University

Assessments of the public's understanding of human genetics continue to demonstrate misperceptions of social categories like race and gender as biologically determined and fixed categories of "human difference." Concomitantly, within and outside of the classroom there is a tendency to teach such concepts as either abiological or as socially real. Yet, numerous studies demonstrate that such myths persist precisely when we do not address the fact that racism and sexism (social constructs) have real impacts on our biology, in tandem with a deconstruction of the "myth of biological races."

This poster presents an approach used in a large format (100 student), non-major introduction to biological anthropology course, when discussing the nature of modern human variation and adaptation. Starting with a discussion of myth construction, cognitive bias, and the history of social classification schema this approach builds to a discussion of race and gender as "abiological," but socially powerful, myths based on our misunderstanding of the physical variation we can "see" with our own eyes. This approach

ends with a review of the ways in which racism and sexism lead to genetic and physiologically damaging outcomes that can become literally encoded in our physical bodies.

The landscape of Denisovan ancestry in the Americas

EMILIA HUERTA-SANCHEZ¹, KELSEY WITT-DILLON², ALYSSA FUNK² and LESLY LOPEZ²

¹Ecology and Evolutionary Biology and Center for Computational Molecular Biology, Brown University, ²Molecular Cell Biology, University of California Merced

Since acquiring sequences of archaic humans, we have increased our understanding of how archaic introgression is distributed across genomes in Eurasia and Oceania. By contrast, we know very little about how archaic introgressed segments are distributed across genomes from the Americas, and in fact these genomes are often excluded from analysis because most samples available exhibit confounding European and African ancestry. Recent work has examined Neanderthal and Denisovan admixture in a small sample set from the Americas, but very little discussion has been presented beyond quantifying admixture and observing higher levels than in Europeans and similar levels in East Asians. Here, we investigate the number and frequency of Denisovan variants along the genomes from the Americas. We find that populations in the Americas exhibit varying levels of Denisovan genetic variants likely due the effect of demographic history such as recent admixture from Europe and Africa and the effects of serial bottlenecks. For example, Peruvians harbor a larger number of high frequency Denisovan variants than other admixed populations in the Americas. We also investigate what regions of the genome have a large concentration of high frequency Denisovan variants, suggestive of adaptive introgression.

We thank both NIH (1R35GM128946-01) and NSF (DEB-1557151) for funding this research

Cradle Ambassadors: Public Palaeoanthropology in the Tourism Space

K. LINDSAY HUNTER

Archaeology, University of the Witwatersrand, National Geographic "Umsuka" Public Palaeoanthropology Project, African Digital Education Trust

"The Cradle of Humankind" (CoH) is the informal name of "the Fossil Hominin Sites of South Africa World Heritage Site" (WHS) in Gauteng Province just 47 km northwest of Johannesburg. Established as a cultural heritage site by UNESCO in 1999, "the Cradle," as it is known, today comprises approximately 47,000 hectares and more than a dozen dolomitic caves that preserve the remains of such assorted hominins

ABSTRACTS

as *Australopithecus*, *Paranthropus*, and *Homo*. It is a palimpsest where ancient seas, prehistoric villages, and recent battles are evident. It is in this landscape that a unique public education and development project was launched in 2016, catering to demographics as diverse as the setting. The "Cradle Ambassadors" is the flagship programme of the National Geographic "Umsuka" Public Palaeoanthropology Project. The programme seeks to provide tangible public benefits for a variety of different groups without recourse to passive trickle-down effects. This is accomplished through the active support of tourism stakeholders such as the CoHWS Management Authority, Maropeng the official visitors' centre of the CoH, the Cradle Tourism Company (TCTC), and the tourism/hospitality industries. Cradle Ambassadors is currently offered as a three-day overnight retreat that includes classroom learning, team-building, touring, and a public forum. This paper describes the development, implementation, and results of the Cradle Ambassadors and how the format and content of the programme have transformed over time, informed by both our international curriculum advisory committee (composed of palaeoanthropology and education professionals), as well as co-created through participant responses and shaped according to local needs.

Major support for this project has been provided by National Geographic Society grant numbers SP 36-16 and NGS-411E-18.

Feasibility of volumetric bone mineral density (vBMD) to predict rib structural properties

RANDEE L. HUNTER¹, YUN-SEOK KANG², KAREN C. BRILEY³ and AMANDA M. AGNEW¹

¹Skeletal Biology Research Laboratory, The Ohio State University, ²Injury Biomechanics Research Laboratory, The Ohio State University, ³Wright Center of Innovation in Biomedical Imaging, The Ohio State University

Bone mineral density (BMD) is often used as a surrogate for bone quality. However, little work has been done to investigate range of human variation in volumetric BMD, obtained from quantitative computed tomography (QCT), or its ability to predict structural properties especially in the axial skeleton. Meanwhile, rib fractures from traumatic events are a common source of increased morbidity and mortality. *Ex vivo* mid-level (5-7) human ribs from 41 males (50.9 ± 25 yrs.) and 30 females (54.7 ± 22.0 yrs.) were scanned at 0.167mm resolution prior to dynamic (2.0 m/s) anterior-posterior whole bone testing to failure. vBMD was calculated from CT using phantoms (0-800 mg/cm³) in Skyscan CTAn (Bruker), while histological sections were used to obtain section modulus (Z). Cortical vBMD demonstrated no significant differences between sides or levels (p=0.93, 0.20 respectively), indicating a lack of

intra-individual variation. When controlling for age, vBMD did not predict any structural properties in males or females (p>0.19). However, when vBMD was combined with Z to create a Stress Strain Index (SSI), SSI significantly predicted peak force (p<0.01), total energy (p<0.01), and stiffness (p<0.01) with stronger relationships in females. General linear models that included age and sex also support the advantage of SSI over vBMD in predicting rib structural properties. The amount of variation in peak force explained by the model increased from 39.2% (vBMD) to 79.0% (SSI). Thus, moving beyond simple measures of vBMD to include precise cross-sectional parameters may increase our understanding of sources of variation in rib fracture risk between individuals.

A developmental model of hominin brain evolution

SHAWN D. HURST¹, RALPH L. HOLLOWAY², LINDSEY M. KITCHELL³ and HEATHER M. GARVIN^{4,5}

¹Biology, University of Indianapolis, ²Anthropology, Columbia University, ³Psychological and Brain Sciences, Indiana University, ⁴Anatomy, Des Moines University, ⁵Evolutionary Studies Institute, University of the Witwatersrand

Sulcal homologies in the brains of *Homo sapiens* and *Pan troglodytes* are disputed, which impacts interpretations of hominin endocasts and brain evolution. The shared major sulci appear earlier during gestation and are deeper and less variable than the minor sulci. Here we use studies of human and non-human primate brain development as well as data from the Human Connectome Project and 190 chimpanzee brain MRIs to compare developmental similarities in the major deep sulci of these species, making their homologies clear. This comparison suggests that the frontal lobes of chimpanzees are less variable than has been claimed, that their inferior frontal sulci extend from the precentral sulci to near the frontal poles, and that the parieto-occipital arcus and more of the inferior parietal lobule than has been previously realized are present in chimpanzees but these are usually buried beneath the occipital operculum. This comparison also suggests that the frontal opercula in humans evolved through an inferior-posterior expansion and folding of the orbital and lateral frontal lobes. The loss of the occipital operculum in humans appears not to be due to obliteration of the lunate sulcus by new sulci and gyri, but by a posterior-inferior expansion and unfolding of already present but mostly buried sulci at the parietal occipital boundary, along with relative contraction of the occipital lobes. Using new multicolor curvature maps, we will discuss our interpretations of the hominin endocasts AL162-28, Taung1, STS5, MH1, DH3, LES1, ER1470, ER3733, and ER3883 in this light.

Ontogeny of intrinsic digit proportions in non-grasping mammals: a test of the grasping theory of primate hand and foot growth

ALEXANDER HYDE, REBECCA Z. GERMAN and JESSE W. YOUNG

Anatomy and Neurobiology, Northeast Ohio Medical University

Immature primates are characterized by relatively large hands and feet. Previous studies have suggested a functional explanation for this trend, arguing that proportionally larger extremities could improve grasping performance during passive transport or initial locomotor efforts. Ontogenetic changes in intrinsic digit proportions in capuchin monkeys and baboons are consistent with this hypothesis – fingers and toes are relatively long early on and become proportionally shorter with age. However, it may be that ontogenetic decreases in relative digit length is a common mammalian pattern, rather than being primate-specific. We tested this possibility by quantifying digit growth in growing laboratory rats (*Rattus norvegicus*), terrestrial mammals that lack primate-like power grasping abilities. We measured the length of metapodials and free digits (i.e., summed phalanges) in a mixed-longitudinal sample of 750 radiographs representing 28 individual rats. Raw bone lengths were converted to phalangeal indices (PIs: free digit length as a percentage of total ray length). Results showed that rats, like primates, show ontogenetic declines in relative finger length early in life. However, the magnitude of decline is much lower in rats (rats: 8.7% decline; capuchin monkeys: 20.3% decline). Relative toe lengths remained constant during rat growth, in contrast to the significant declines observed in both capuchin monkeys and baboons. Our results suggest that ontogenetic declines in relative digit length may be a common mammalian trend that has been co-opted and expanded in primates, particularly with respect to the foot. Overall, our study supports a functional grasping theory of primate hand and foot growth.

Never Done: A bioarchaeological study of women's work, task, and occupation in medieval Edinburgh, Scotland

LAUREN K. IDE¹, LINDA FIBIGER¹, CHARLOTTE Y. HENDERSON² and CATRIONA PICKARD¹

¹School of History, Classics, and Archaeology, University of Edinburgh, ²CIAS - Research Centre for Anthropology and Health, Dept. of Life Sciences, University of Coimbra, Portugal

Enteseal change (EC) morphology has been used within bioarchaeology to reconstruct behaviors of past peoples but ECs are known to have a complex and multifactorial etiology. Research on identified collections requires documented occupation, but females are often excluded due to the use of non-specific terms. This study of

ABSTRACTS

102 male and female skeletons dating from the medieval period (1130-1560) in Edinburgh, Scotland explores skeletal changes associated with a number of occupational activities. The research incorporates the socioeconomic history of medieval women and takes a broad approach to the analysis of occupation and activity by including paleopathological diagnosis, age, the new Coimbra Method EC scoring, and biomechanics. Preliminary results confirm higher Coimbra EC scores with increased age over 50 and with degenerative joint changes. While scores are higher in males, females have similar prevalence rates. Results also show that conditions such as leprosy, tuberculosis, or severe *genu valgus* are associated with lower EC scores in both males and females which implies a potentially lower level of activity for those with some chronic or debilitating conditions when compared to individuals of similar age and within the same population. Future research directions involve increasing sample size to 250, cross-sectional analysis of 3D scanned humeri, and a biomechanical case study with living volunteers performing one historic occupational activity. This research can help us to better understand the complex etiology of ECs and is developing approaches to study females, unknown skeletal collections, and the biomechanics of archaeological activity.

The effect of jaw muscle architecture dynamics on the biomechanics and evolution of the primate feeding system: a theoretical perspective

JOSE IRIARTE-DIAZ

Oral Biology, University of Illinois at Chicago

The ability of primates to produce precise movement during natural behaviors such as feeding depends on their capacity to generate and modulate force output of skeletal muscles. The most fundamental property of individual skeletal muscle fibers is the relationship between the amount of force they can generate and the length of their fibers, being maximal at intermediate lengths and decreasing at shorter and longer lengths. This tradeoff between muscle force and fiber length is usually reflected in muscles' internal architecture: muscles designed for producing large displacements tend to have long, parallel fibers, while muscles designed for force generation tend to have short, pennated fibers. In addition to the static implications of muscle architecture to mechanical output, morphological changes that occur dynamically during contraction can also affect muscle's mechanical performance. How these dynamic changes could affect the mechanical performance and evolution of the primate feeding system is still poorly understood. Using 3D models from 75 primate species of the cranium, mandible and jaw adductor muscles, the effect of different muscle architecture dynamics on mechanical output

was evaluated to test to test hypotheses about relationships between evolution of the primate feeding system, diet and feeding behavior. The data show that muscle dynamics can have substantial effect on the mechanical performance of masticatory muscles especially during large gapes. Clade-specific differences on the effect of muscle architecture dynamics were observed for the temporalis and the superficial masseter, suggesting a diversity of solutions to the muscle length-force tradeoff.

Variation in diet and foraging effort across seasons in the frugivorous Brown Lemur (*Eulemur fulvus*): Contrasts with a sympatric folivore (*Propithecus diadema*)

MITCHELL T. IRWIN^{1,3}, VOLOLONIRINA RAHALINARIVO², JEAN-LUC RAHARISON³, BRUNO RAMORASATA³, JEAN-FREDDY RANAIVOARISOA², JEANNOT RANDRIANASY² and JESSICA M. ROTHMAN^{4,5}

¹Anthropology, Northern Illinois University, ²Mention Anthropologie et Développement Durable, University of Antananarivo, ³Division of Research, SADABE, ⁴Anthropology, Hunter College, ⁵Graduate Center, CUNY

Many primatological models divide primates following broad dietary categories: frugivores, folivores, insectivores, etc. Although logical, much of our understanding of the contrasts among these types rests on untested assumptions. We studied the frugivorous brown lemur (*Eulemur fulvus*) in relatively undisturbed rainforest at Tsingy, Madagascar (one group, 13 months, 316 24-hour follows). We present the first diet record for this species in rainforest, quantify seasonal and age-sex variation, and compare with the sympatric folivore, *Propithecus diadema*, whose diet and nutrition are well-documented.

Diet was primarily frugivorous (fruit: 81%, leaves: 13%, flowers: 6%) and more frugivorous than conspecifics in Ankarafantsika's dry forest (68%, 25%, 5%). Seasonal diet shifts were as expected: relative to the abundant season (89%, 8%, 2%) the fruit-scarce lean season sees significantly less fruit consumption (72%, 18%, 9%). This shift to non-fruit resources is accompanied by significantly higher feeding effort (from 172 to 301 minutes per 24-h). Finally, 35% of feeding time was at night; although this was lowest in adult females, this was not significant. Brown lemurs seem to cope with the lean season as energy maximizers, working harder to find and ingest fruits as well as non-fruits, in contrast with sifakas, which are time minimizers (reducing ranging and feeding effort).

Further research is necessary: first, to quantify nutritional intakes, testing the hypothesis that lean seasons see reduced nutrient intakes, and to

test which nutrients are limiting and/or prioritized, and second, to search for behavioral correlates and consequences of the opposite lean-season strategies in the two sympatric species.

Funding provided by: National Geographic Society, Eppley Foundation, Northern Illinois University.

Exploring patterns of appositional growth amongst the urban child

RACHEL IVES and LOUISE HUMPHREY

Earth Sciences, Natural History Museum, London

Appositional bone attainment is a sensitive indicator of the cumulative impact of childhood growth disturbances. This research addresses the adequacy of childhood bone structural development by evaluating radiographic measurements of juvenile femoral medio-lateral cortical bone thickness from two documented 18th to 19th century urban groups: (1) Bethnal Green, London, known for extremely detrimental living conditions and a high burden of childhood illness, and (2) Christ Church Spitalfields, London, associated with economically more advantaged background. Results were compared to published data from medieval rural Wharram Percy, modern rural Finland and post-medieval St Martin's Church, Birmingham.

All archaeological populations show reduced cortical thickness compared to the modern population but the mechanisms underlying this trend differ between the groups. Most post-medieval sites show diminished periosteal apposition compared to the modern population and over-lapped each other, but children from post-medieval urban Bethnal Green showed markedly smaller total bone widths than rural medieval children, which were most like the modern population. These differences reflect variation in the amount of periosteal apposition.

Children from post-medieval urban London sites showed smaller medullary canal widths than modern children and children from post-medieval Birmingham. Medieval rural children had the largest medullary widths. Variation in cortical bone thickness between the archaeological populations was therefore additionally mediated by differences in endocortical remodelling. These findings indicate that whilst periosteal expansion appeared reduced in urban post medieval children, endocortical development appeared less compromised than in the rural medieval children.

The Guercy 1 Neanderthal cranium from Baume Moula-Guercy (Soyons, Ardèche)

REBECCA S. JABBOUR¹, GARY D. RICHARDS², GASPARD GUIPERT³ and ALBAN DEFLEUR⁴

¹Department of Biology, Saint Mary's College of California, ²Department of Biomedical Sciences, A. A. Dugoni School of Dentistry, University of the Pacific, ³Antenne de Préhistoire de l'Institut

ABSTRACTS

de Paléontologie Humaine, Centre Européen de Recherche et d'Enseignement des Géosciences de l'Environnement, ⁴Laboratoire de Géologie de Lyon, CNRS UMR 5276

The Moula-Guercy Cave overlooks the Rhone River, Ardèche. Work at this site provides one of the most important samples for reconstructing the paleoenvironment and culture of Mousterian peoples occupying this region during the Eemian Interglacial (MIS 5e, 127-117 kya). Whereas 20 stratigraphic levels have been recognized, hominin remains derive solely from level XV, biostratigraphically dated at 100-120 kya. Here we provide a metric and morphological assessment of the Guercy 1 cranium and an isolated occipital fragment.

Guercy 1 comprises portions of the frontal and right/left parietals. Morphologically the cranium is of a young adult female while the occipital is aged at ≈ 7.0 years. Both the cranium and the M-S-41/M-S-61 occipital were virtually reconstructed, with mirror-imaging of missing regions. Endocasts were segmented from volumes with 0.3mm isotropic voxels. Metric and morphological comparisons were made with European and Middle Eastern Middle-to-Late Pleistocene (\approx MIS 14 – MIS 2 to \approx 1) hominins ($n=183$).

Guercy 1 has a flat, broad, and short frontal (cf. Artenac 1). Supraorbital torus and sulcus development is weak but similar to Neanderthals. Parietal curvatures show affinities to Late Neanderthals, but the maximum breadth is midparietal. Cranial vault height is low relative to Late Neanderthals. The endocranium differs from Late Neanderthals in the absence of parietal lobe expansion in the vertex and euryonic regions. The middle meningeal vasculature is similar to Early/Late Neanderthals. The occipital fragment is typical of Early/Late Neanderthals. Moula-Guercy Neanderthals possess distinctive regional features and sample females of a poorly represented age range in Eemian age Neanderthals.

Human races owe their reality to inaccurate historical concepts of variation not genes

NINA G. JABLONSKI

Anthropology, The Pennsylvania State University

Race concepts and beliefs in the reality of human races have endured in the face of cogent statements and abundant scientific evidence about the nonexistence of race. This paradox can be understood better by examining the history of race definitions and the network of communication that existed between influential Enlightenment thinkers such as Hume, Kant, Blumenbach, Diderot, and Jefferson. Drawing from limited and inaccurate information on human physical variation, especially regarding skin color, Hume, Kant, and Blumenbach formulated definitions of human types or races and, in some cases, ranked them

in hierarchies. The influence of these scholars on one another can be reconstructed and, in the case of Blumenbach, the hardening and hierarchical organization of his human categories can be traced to his reading of Kant. When races were discussed in early encyclopedias, their reality was further validated and the information quickly propagated to scholars and politicians on both sides of the Atlantic. Reinforcement of notions of African inferiority contributed to the maintenance of chattel slavery in America after the transatlantic slave trade was abolished by France and Britain in the late 18th and early 19th centuries. The lived and enduring reality of race in North America exists not because of traits or gene frequencies, but because of the rapid permeation and persistent influence of Enlightenment pseudoscience on policy makers. We must constantly scrutinize the "new evidence" marshaled in support of the reinvention of race concepts and race groups, and understand the deep historical and psychosocial roots of its appeal.

Reconciling past injustices; building a future in African American genomics

FATIMAH L.C. JACKSON

Biology, Howard University

Acquiring and interpreting representative African genomic diversity is an essential prerequisite for reconstructing the evolutionary history of African descended peoples and that of our species. Recently, we have initiated the collection of integrative genomic data on a cross section of non-hospitalized African American and continental African individuals. This collection represents the initial acquisitions for our database initiatives: the 1000 African Diaspora Database, the 10,000 Continental African Database, and the 1000 Red Sea Diaspora Database.

In this preliminary collection effort, several weeks were devoted to community education and recruitment. Within 8 hours, 463 individuals provided informed consent for access to their DNA, salivary microbiome, ancestral background, and general health information. African Americans from North America and the Caribbean and continental Africans were the pre-identified target populations. While a total of 25 nationalities and 35 ethnicities were represented in this first sample, 260 of our participants (56.2%) self-reported as Black/African American

Participant data were subdivided based upon ancestral origins. 348 participants (75.2%) contribute to the 1000 African Diaspora Genomes Database, 31 participants (6.7%) from continental Africa will be included in the 10,000 Continental African Database, and 75 participants (16.2%) will go into the 1000 Red Sea Diaspora Database. Nine participants (2.0%) identified their ancestral origins in Eurasia or Oceania and were assigned to a Control cohort.

In collaboration with Helix and National Geographic, our strategy is to divide the completed databases equally into Discovery and Replication cohorts for the integrative testing of hypotheses regarding admixture, ancestry, migration, selection, disease susceptibility/resistance.

Support for these initial collections came from Helix and National Geographic's Genographic Project.

Multiple deeply divergent Denisovan ancestries in Papuans

GUY S. JACOBS¹, GEORGI HUDJASHOV^{2,3}, SAAG LAURI³, KUSUMA PRADIPTAJATI^{1,4}, CHELZIE C. DARUSALLAM⁴, DANIEL J. LAWSON⁵, MONDAL MAYUKH³, LUCA PAGANI^{3,6}, FRANÇOIS-XAVIER RICAUT⁷, MARK STONEKING⁸, MAIT METSPALU³, HERAWATI SUDOYO^{10,4,9}, J. STEPHEN LANSING^{1,11,12} and MURRAY P. COX²

¹Complexity Institute, Nanyang Technological University, Singapore, ²Statistics and Bioinformatics Group, Institute of Fundamental Sciences, Massey University, New Zealand, ³Institute of Genomics, University of Tartu, Estonia, ⁴Genome Diversity and Diseases Laboratory, Eijkman Institute for Molecular Biology, Indonesia, ⁵Integrative Epidemiology Unit, Population Health Sciences, University of Bristol, UK, ⁶APE Lab, Department of Biology, University of Padova, Italy, ⁷CNRS, Université de Toulouse, France, ⁸Department of Evolutionary Genetics, Max Planck Institute for Evolutionary Anthropology, Leipzig Germany, ⁹Department of Medical Biology, Faculty of Medicine, University of Indonesia, Indonesia, ¹⁰Sydney Medical School, University of Sydney, Australia, ¹¹Santa Fe Institute, Santa Fe, NM, ¹²Stockholm Resilience Center, Kräftriket, Sweden

Genome sequences are known for two archaic hominins – Neanderthals and Denisovans – which interbred with anatomically modern humans as they dispersed out of Africa. By excavating archaic haplotypes from 161 new genomes spanning 14 island groups in Island Southeast Asia and Papua, we find large stretches of DNA that are inconsistent with a single introgressing Denisovan origin. Instead, modern Papuans carry hundreds of gene variants from two deeply divergent Denisovan lineages, separated by over 350 thousand years. Geographical structure in these lineages implies introgression from Denisovans living east of the Wallace line and suggests considerable complexity in archaic contact among Papuan groups. A third Denisovan lineage occurs in modern Siberians, Native Americans and East Asians. This regional mosaic suggests that modern humans interbred with multiple Denisovan populations, which were geographically isolated from each other over deep evolutionary time.

ABSTRACTS

Gut microbiome community composition is significantly influenced by shared living-space in rural agriculturalists from Burkina Faso

DAVID K. JACOBSON^{1,2}, THÉRÈSE S. KAGONE³, NICOLAS MEDA⁴, HÉLÈNE CARABIN⁵, TANVI HONAP^{1,2}, KRITHIVASAN SANKARANARAYANAN^{2,6} and CECIL M. LEWIS, JR.^{1,2}

¹Department of Anthropology, University of Oklahoma, ²Laboratories of Molecular Anthropology and Microbiome Research, University of Oklahoma, ³Department of Biological Sciences, Centre MURAZ, Burkina Faso, ⁴Director, Ministry of Health, Burkina Faso, ⁵Département de pathologie et microbiologie, Université de Montréal, Canada, ⁶Department of Microbiology and Plant Biology, University of Oklahoma

Anthropological studies comparing gut microbiomes of individuals leading traditional lifestyles, such as hunter-gatherers, to urban, industrialized individuals, show that lifestyle impacts gut microbiome composition. These studies suggest that traditional communities have higher gut microbial diversity as well as increased abundance of certain bacterial taxa, especially those involved in fiber digestion. Still unresolved, however, are the ways in which lifestyle variation, including the built environment, impacts microbiome variation within traditional communities. For this study, we collected fecal samples from 120 individuals, stratified by age, sex, family, and multifamily “quarters” (compounds) from a village in central Burkina Faso. DNA was extracted at Centre MURAZ in Burkina Faso and the 16S rRNA V4 amplicon was sequenced at the University of Oklahoma. Amplicon sequences were bioinformatically processed with the USEARCH v10 pipeline for *de novo* Operational Taxonomic Unit (OTU) clustering at 97% sequence similarity. Overall, the Burkinabe samples were similar to other traditional populations, such as Matses hunter-gatherers from Peru, with high alpha diversity (OTU richness) compared to published data from industrialized American populations (p -value $< 4 \times 10^{-9}$), as well as the presence of taxa found in traditional, but not industrial, populations: *Treponema*, *Succinivibrio*, and *Prevotella*. Abundance of various taxa, including *Prevotella*, *Oscillibacter*, *Collinsella*, *Sporobacter*, and *Subdoligranulum* was significantly associated with *quartier* (fdr adjusted p -value < 0.003) but not other lifestyle variables. Thus, we demonstrate that intra-village gut microbiome variation is driven primarily by sharing (or lack thereof) of *quartiers*, providing a link between microbial ecological dynamics and living-space.

Investigating the Phenotypic Consequences of Archaic Hominin Introgression on Modern Human Biology

EVELYN JAGODA

Human Evolutionary Biology, Harvard University

A fundamental question of human evolution is, what are the adaptive genetic variants that underlie the remarkable ability of humans to inhabit diverse environments? While this is a daunting question in part due to the sheer size and diversity present in modern genomes, studies comparing ancient and modern genomes have added a new dimension to this question. They have revealed long stretches of DNA sequences (haplotypes), distributed across modern genomes that were introduced by interbreeding with archaic hominins. A subset of these haplotypes are under positive selection and have played beneficial roles during human dispersal and adaptation to different environments across the globe. Yet, as in all genomic studies, narrowing down these introgressed haplotypes to the actual causative base-pair(s) remains an enormous task. We are using a variety of computational and wet laboratory approaches track down these to identify actual causative base-pair(s) and their specific phenotypic consequences, particular in relation to impacts on the human immune system. By helping to understand phenotypes that were adaptive in the past and the genomic architecture of these phenotypes today, this research will provide a lens through which to view human adaptation to the modern environment of today.

Digestive and sensory adaptations for the grass-eating niche: Insights from the gelada (*Theropithecus gelada*) genome

MAREIKE C. JANIAK¹, KENNETH L. CHIOU², AMY LU³, THORE J. BERGMAN^{4,5}, JACINTA C. BEEHNER^{4,6}, NOAH SNYDER-MACKLER² and AMANDA D. MELIN¹

¹Anthropology & Archeology, University of Calgary, ²Psychology, University of Washington, ³Anthropology, Stony Brook University, ⁴Psychology, University of Michigan, ⁵Ecology & Evolutionary Biology, University of Michigan, ⁶Anthropology, University of Michigan

Geladas (*Theropithecus gelada*) are the only primates that feed almost exclusively on grass. This unique dietary niche poses distinct foraging and digestive challenges, which have likely exerted strong selective pressures on this species. Here, we investigated genetic adaptations for graminivory in digestive enzymes, taste receptors, and olfactory receptors in geladas, compared to their close phylogenetic relatives: baboons, macaques, and humans. We tested for gene families that have undergone expansion or contraction and/or have been subject to selection in the *Theropithecus* lineage. Preliminary results suggest that geladas have genetic adaptations for their unique graminivorous diet. We find significant expansions in gene families related to ubiquitin-conjugating enzymes ($p < 0.001$) and a significant contraction in the trypsin gene family ($p < 0.001$), which is related to protein digestion and may reflect the relatively low amount of

protein, especially animal protein, in the gelada diet. Further, *ALDH16A1* (aldehyde metabolism) has been under significant positive selection in geladas ($\chi^2 = 310.89$, $p < 0.001$), which may be linked to food detoxification. Unlike other cercopithecines, geladas do not retain any functional chitinase genes (*CHIA*), an enzyme that digests insect exoskeletons. Pseudogenization of these genes may be due to relaxed selection following the shift from an omnivorous to a specialized diet. Preliminary analyses of taste receptor genes suggest that geladas have 30 intact *TAS2R* genes and 6 pseudogenes, a lower pseudogenization rate (16.67%) than other primates (28-29%). Together, these results highlight several potential mechanisms that have allowed geladas to exploit a grass-eating ecological niche.

Cranial injuries in the Bronze Age sample from Bezdanjača cave, Croatia

IVOR JANKOVIC and MARIO NOVAK

-, Institute for Anthropological Research

Bezdanjača cave is located in the Lika region of Croatia. In 1965 excavations of the site yielded numerous human skeletons dated to Bronze Age, based on a series of radiocarbon dates (between 1350 and 1100 BC), pottery and metal objects found at the site. Due to a complex morphology of the cave (the entrance consists of a 30 meter deep vertical shaft, and the cave consists of two bigger and numerous smaller channels and chambers) it was not used as a living, but a burial site. There is evidence of elaborate burial rituals, such as presence of wooden and stone structures, traces of hearths, burnt animal bones, pottery, metal and bone artefacts. Skeletons were mostly placed in natural crevices or depressions, and not buried. In addition, alongside many human remains, animal skeletons (deer, wild pigs and other animals) were placed. Excavators note that remains of around 200 people were uncovered in the cave in a total of 57 graves, ten of which contained multiple (5-20) skeletons. Skulls of 35 individuals were given to the Institute for Anthropological Research for analysis. Based on morphological characteristics and details, sex, age, and data on pathologies have been obtained. Analyzed sample consists of 10 females and 10 males, one probable female and four probable males, one adult for which sex could not be established, and nine subadults. Five male skulls show blunt force trauma (3 antemortem and two perimortem). Further, one female adult skull shows signs of healed trepanation on the frontal bone.

The work was funded by the Croatian Science Foundation (grant no. HRZZ IP-2016-06-1450)

The wrist and hand of the StW 573 (“Little Foot”)

TEA JASHASHVILI^{1,2}, BIREN A. PATEL³, KRISTIAN J. CARLSON^{3,4}, JASON L. HEATON^{4,5}

ABSTRACTS

TRAVIS R. PICKERING^{4,6}, ROBIN CROMPTON⁷,
KATHLEEN KUMAN⁸, AMÉLIE BEAUDET⁹, JULIET
MCCLYMONT⁹, LAURENT BRUXELLES^{10,11,8},
DOMINIC STRATFORD⁹ and RONALD J. CLARKE⁴

¹Molecular Imaging Center, Department of Radiology, USC Keck School of Medicine, University of Southern California, ²Department of Geology and Paleontology, Georgian National Museum, ³Department of Integrative Anatomical Sciences, Keck School of Medicine, University of Southern California, ⁴Evolutionary Studies Institute, University of the Witwatersrand, ⁵Department of Biology, Birmingham-Southern College, ⁶Department of Anthropology, University of Wisconsin, ⁷Department of Rheumatology, Aintree University Hospital NHS Trust, ⁸School of Geography, Archaeology and Environmental Studies (GAES), University of the Witwatersrand, ⁹School of Health Sciences, Aldro Building, University of Brighton, ¹⁰French Institute for Preventive Archaeological Researches, (INRAP), ¹¹French Institute of South African Studies, (IFAS)

The human wrist and hand, as a manipulation organ, has undergone morphological modification over human evolutionary history. As the hand was emancipated from use during locomotion, its structure and proportions changed, and phalangeal curvature reduced. Here, we summarize the initial description and comparison of hand and wrist bones of the StW573 skeleton discovered in the Sterkfontein Member 2 deposit (3.67 Ma) within the Silberberg Grotto, South Africa.

Comparative study of StW573 and other Plio-Pleistocene hominins (e.g., *Australopithecus afarensis*, *A. africanus*, and *A. sediba*) demonstrates that geographical separation and adaptation to different habitats and terrain may have affected mosaic morphological adaptations in hand bones. For example, trapezium facet orientation, longitudinal angle, and the length/midshaft proportion of metacarpal 2 are morphologically modern human-like. In contrast, mediolateral base dimensions, head shape, and dorsal tapering of metacarpal heads are more like the features of *A. afarensis*. Overall, the wrist and hand bones of StW573 share morphometric features with *A. afarensis*, but they also express their own unique combination of characters. Even though climbing adaptations in the post-cranial skeleton may persist in combination with those of bipedal locomotion in both species, the presence long-distance terrestrial bipedalism did not eliminate an arboreal locomotor component. Instead, within the degeneracy, perhaps triggered complexity in partitioning the function of the hand as a locomotor or manipulative organ. In this context, the almost complete set of hand and wrist bones from the same individual provides a unique opportunity to further unravel this complexity.

South Africa National Research Foundation and Department of Science and Technology (KK82591, KK 82611, DS98808), the Center of Excellence in Palaeosciences (CoE-Pal), the Palaeontological Scientific Trust (PAST), NIH100D18500, NSF BCS-1719140

Selection for lifetime reproductive success among ethnic Tibetans residing at high altitude in Nepal

CHOONGWONG JEONG¹, DAVID B. WITONSKY²,
BUDDHA BASNYAT³, MANIRAJ NEUPANE⁴,
CYNTHIA M. BEALL⁵, GEOFF CHILDS⁶, SIENNA R.
CRAIG⁷, JOHN NOVEMBRE² and ANNA DI RIENZO²

¹Archaeogenetics, Max Planck Institute for the Science of Human History, ²Human Genetics, University of Chicago, ³Oxford University Clinical Research Unit, Patan Hospital, ⁴Mountain Medicine, Mountain Medicine Society of Nepal, ⁵Anthropology, Case Western Reserve University, ⁶Anthropology, Washington University, ⁷Anthropology, Dartmouth College

The genetic bases of reproductive traits in populations exposed to lifelong high-altitude hypoxia may provide insights into human evolution and adaptation. This presentation describes adaptive evolution among high altitude native, post-reproductive, Tibetan women residing above 3000m in Nepal. In 2012, 1,008 Tibetan women provided reproductive histories and saliva for DNA extraction. Data provided by 991 women with complete reproductive histories and genotypic data on 3.5 million single nucleotide polymorphisms (SNPs) permitted testing hypotheses about past and ongoing natural selection. The methods include genome-wide association analysis and analyses of signatures of selective sweep and polygenic adaptation using published techniques. 55 SNPs in six genome-wide association peaks associated with the number of pregnancies, births and the proportion of children surviving to 15 years of age. The analyses adjusted for covariates including age. The allele frequency of the SNP with the lowest p-value in each peak ranges from 0.552 to 0.752. These SNPs did not show evidence of selective sweeps associated with reproductive fitness. The frequency of many SNPs changed in similar direction and degrees compared lowlanders, consistent with polygenic adaptation. These findings reflect both past and ongoing selection favoring more pregnancies, livebirths, and surviving children in this sample. *EPAS1* and *EGLN1*, two loci showing strong signals of selection in this sample and others, did not associate with reproductive success phenotypes.

NSF award 1153911 to CMB and NIH award 1R01HL119577 to AD supported this research.

Predicting distribution of enamel on a tooth

JUKKA JERNVALL¹, TEEMU J. HÄKKINEN^{1,2}, S.
SUSANNA SOVA^{1,3} and IAN J. CORFE¹

¹Institute of Biotechnology, University of Helsinki, ²Department of Mathematics and Systems Analysis, Aalto University, ³Department of Geoscience and Geography, University of Helsinki

In primates, the thickness of the enamel layer relative to the tooth size ranges from thin to very thick, and the enamel distribution is not typically uniform across the crown. The overall differences in enamel thickness among species, and also increasingly within the tooth crown, have been used to examine taxonomic affiliations, life history, and functional properties of teeth. Nevertheless, it remains to be explained how the distribution of enamel on the tooth crown is developmentally regulated. Here we test a diffusion-limited model (DLM) of enamel matrix secretion that maps the dentin topography to the enamel surface topography. Micro-computed tomography was used to obtain enamel-dentin junction (EDJ) and enamel surface topographies of molars of *Gorilla*, *Pongo*, and *Homo*. Starting from these empirically measured EDJs for each taxon, simulations were used to secrete a virtual enamel matrix on top of the EDJs. The DLM was found to predict the empirically measured enamel surfaces better than models omitting the diffusion-limited matrix secretion. Together with high resolution 3D synchrotron tomography data on enamel structure from developing and erupted domestic pig molars, the DLM shows how convex and concave EDJ surface features have highly distinct effects on the final shape of the enamel surface. Complex patterns of enamel thickness on a tooth crown can result from a single developmental process, and models on matrix secretion help in part to explain how functional tooth forms are attained.

Genetic variation in body weight ontogeny and its contribution to body size sexual dimorphism in captive baboons (genus, *Papio*)

JESSICA L. JOGANIC^{1,2}, FRÉDÉRIC SANTOS²,
LAURA A. COX³, MICHAEL C. MAHANEY⁴, JEFFREY
ROGERS⁵, JAMES M. CHEVERUD⁶ and ANTHONY
G. COMUZZI⁷

¹Anthropology, Washington University in St. Louis, ²CNRS, MCC, PACEA UMR 5199, Univ. Bordeaux, ³Internal Medicine, Center for Precision Medicine, Wake Forest School of Medicine, ⁴South Texas Diabetes and Obesity Institute, University of Texas Rio Grande Valley School of Medicine, ⁵Molecular and Human Genetics, Human Genome Sequencing Center, Baylor College of Medicine, ⁶Biology, Loyola University Chicago, ⁷Executive Director, The Obesity Society

Organismal adult body size can be modified by altering the duration and/or rate of ontogenetic growth. In baboons, sexual dimorphism has been attributed to both an elongated male growth period and divergent sex-specific ontogenetic trajectories, yet the genetic underpinnings for these observations have never been studied. Applying a growth curve analysis, we address this deficiency by quantifying intraspecific variation in body size growth parameters in a pedigreed baboon sample (N=967). Body weight records

ABSTRACTS

(n=42,583) were collected opportunistically from birth to 15 years old (yo). We estimated genetic variance parameters and tested for sex-specific patterns of genetic architecture. Results indicate no sexual dimorphism in population average birth weight (F: 0.80 kg, M: 0.86 kg, $t=1.58$, $P=0.13$) and that both sexes follow a similar growth trajectory (7.3 g/day) until ~3.5 yo, at which point the male rate increases to 10.6 g/day until cessation at 7.7 yo (adult: 30.6 kg). In contrast, females gradually achieve adult weight (19.5 kg) by 10.8 yo. All growth parameters are significantly heritable (birth weight: 0.24 ± 0.1 , early growth rate: 0.45 ± 0.1 , adult weight: 0.50 ± 0.1) and adult weight is genetically correlated with both birth weight ($\rho=0.21$) and early growth rate ($\rho=0.78$). Genetic variance is greatest ($V_a=0.30$) at 3 yo, coinciding with the sex-specific growth trajectory divergence, and lowest ($V_a=0.11$) at 6 yo when males achieve peak growth rates. By building genetic models for polygenic trait ontogeny, we can help elucidate the gene regulation pattern changes necessary for understanding growth phenomena and heterochronic changes in mammalian evolution.

Funding for research from the French State in the framework of the "Investments for the Future" Program (ANR-10-IDEX-03-02) and for baboon care from the US National Institutes of Health (P51 OD11133).

Exploring Sex- and Age-Based Variations in Diet in Ancient Greek Sicily Using Dental Microwear Analysis

ASHLEY JOHNSON¹, LAURIE J. REITSEMA², APRIL K. SMITH², STEFANO VASSALLO³ and BRITNEY KYLE⁴

¹Department of Anthropology, Wayne State University, Detroit, MI 48202, ²Department of Anthropology, University of Georgia, Athens, GA 30602, ³Regional Archaeological Superintendence of Palermo, Italy, ⁴Department of Anthropology, University of Northern Colorado, Greeley, CO 80639

This study aims to identify intra-population diet variation at the Greek colony of Himera, Sicily using dental microwear analysis (DMA) of 20 males, 11 females, and 10 subadults from the 6-5th century BCE. DMA has been minimally utilized in bioarchaeological studies of complex human societies but as an indicator of diet texture, can play an important role in complementing other evidence of diet. We expand use of DMA to examine whether sex and age influenced diet at a diverse urban port city. Wear facet 9 on high-resolution casts of permanent first and second mandibular molars were viewed with a Teneo field emissions scanning electron microscope at 500X. Photomicrographs were analyzed using *Microware* (4.02) and statistical analyses were performed using *RStudio* (v. 1.1453). According to Levene's test of equality of variances, females exhibit significantly more variance in total features ($p=0.04552$) and number of pits ($p=0.04871$) than subadults, but significantly

less variance ($p=0.01758$) in pit length than males. Mann-Whitney U tests indicate females exhibit significantly smaller pits than males ($p=0.02345$) and subadults ($p=0.02004$). These results suggest females routinely consumed similar types of hard foods based on similarity in pit size. However, females varied in how often or how much of this type of food was eaten. We interpret the sex-based microwear difference to be an indicator that sex influenced diet at Himera, but that sex-based differences in diet did not appear until after adolescence. Future archaeological, paleodietary, and historical research can complement microwear data to explain why these differences occur.

This research was funded by National Science Foundation Research Experience for Undergraduates award numbers 1560227 and 1560158, the University of Georgia, and the University of Northern Colorado.

Frail young, Enduring Adults: Paleopathology of a Bronze Age Chinese Skeletal Sample

ELIZABETH JOHNSON¹, RUILIN MAO², HUI WANG², ELIZABETH BERGER^{3,4}, JENNA DITTMAR^{5,6} and IVY YEH-HUI YUAN⁷

¹Department of Anthropology, University of North Carolina at Charlotte, ²Department of Archaeology, Gansu Provincial Institute of Cultural Relics and Archaeology, ³Department of Anthropology, University of Michigan, ⁴Center for Chinese Studies, Lieberthal-Rogel Center for Chinese Studies, ⁵Department of Archaeology and Anthropology, University of Cambridge, ⁶Department of Archaeology and Anthropology, McDonald Institute for Archaeological Research, ⁷School of Humanities, Nanyang Technological University

Bronze Age China has consistently been an area of research foci for both domestic and international researchers; however, paleopathological analysis of certain cultures within the "Northern Zone" is relatively new and demands scholarly exploration. Located along the northern borders of modern-day China, this area was a critical arena for interregional contact which aided technological and cultural diffusion. The following research utilizes a "survivorship" framework and analyzes skeletal stress markers to make inferences about the health and lifestyles of Qijia (2200-1400 BCE) individuals. To do this, a small sub-sample (n=44) from the Qijia culture cemetery Mogou was analyzed for nonspecific indicators of stress, including osteomyelitis, periosteal reaction, porotic hyperostosis, cribra orbitalia, dental pathologies, and trauma. Preliminary results indicate paleopathological differences based on age and sex. While individuals under ten years composed 32% of the sample, only two of these individuals displayed stress markers. This may suggest an overall frail juvenile population, as individuals died before physiological insults displayed skeletally. Unexpectedly, the most common form of trauma was spinal fractures that often resulted

in significant new bone growth fusing multiple vertebrae. Developmental defects, such as spina bifida, were also present. The severity of spinal trauma and the presence of skeletal defects in mature individuals may speak to societal ideals and values regarding the care of injured or differently abled peoples. This research shows that the Qijia peoples located at Mogou were overall able to survive health assaults, developmental defects, and trauma.

Investigating social organization and community composition at the Tiwanaku-style temple complex of Omo M10 in the Moquegua Valley, Peru through analysis of phenotypic variation

KENT M. JOHNSON

Sociology/Anthropology, SUNY Cortland

The only Tiwanaku-style temple complex found outside the Tiwanaku homeland is located at the site of Omo M10 in the Moquegua Valley, Peru. Previous research on cranial modification style identified multiple corporate group cemeteries in the M10 mortuary complex. Mortuary analysis revealed greater diversity at M10 compared to other Moquegua Tiwanaku-affiliated sites. The present research explores patterns of phenotypic variation at Omo M10 to evaluate archaeological models of social organization and community composition. This study evaluates whether patterns of phenotypic variation at Omo M10 are consistent with a complex mortuary program wherein multiple social groups maintained cemeteries at Omo M10.

Odontometric data from 55 skeletons were analyzed using a variety of multivariate statistical approaches. Mahalanobis distances indicate the M10 sample is not phenotypically distinct from other Moquegua Valley Tiwanaku samples. Positive Relethford-Blangero residuals indicate higher than expected levels of extralocal gene flow and may corroborate archaeological evidence of cemetery use at M10 by members of a coastal community. Multidimensional scaling of Euclidean distances derived from principal components analysis provides limited evidence of cemetery structuring based on phenotypic similarity. Results of social network analysis indicate patterns of phenotypic variation and biological relatedness crosscut different cemeteries at M10. Together, the results are consistent with hypotheses based on archaeological data; multiple Tiwanaku communities and at least one non-Tiwanaku community maintained cemeteries at the site. Multiple corporate or

ABSTRACTS

kin-based social groups reflecting diverse ethnic and regional affiliations buried their dead in close proximity to the ritually and politically potent Tiwanaku-style temple at Omo M10.

Financial support provided by the Dean's Office in the School of Arts and Sciences at SUNY Cortland and NSF Doctoral Dissertation Research Improvement Grant No. 1441894.

Testing a computational approach for estimating age-at-death on a modern Portuguese population

LIAM J. JOHNSON and JONATHAN D. BETHARD
Department of Anthropology, University of South Florida

Age-at-death is a key parameter of the biological profile in forensic anthropological contexts and has a nearly 100 year history of innovation as numerous methods have been developed and refined. While there have been improvements in age-at-death estimations utilizing the pubic symphysis there are still issues of method and practitioner error. Reliance on visual comparison methodologies subjects skeletal remains to the risk of inaccurate analysis and necessitates the use of alternative methodologies that can quantify age-related changes to symphyseal surface topography.

By testing an approach that offers a more objective, quantitative method on a modern European population, questions concerning the validity and applicability of this approach can be better understood. The sample population consists of both male and female individuals (n=36) drawn from the University of Coimbra's 21st Century Identified Skeletal Collection (CEI/XXI). The mean age-at-death of the sample was 68.5 years. Three-dimensional surface scans of the pubic symphysis were analyzed with ForAge software and produced age estimates using five different regression models. Statistical analyses tested the bias, inaccuracy, and RMSE of each regression model. The age estimates produced by these regression models are comparable to recent publications testing computational quantitative methodologies on the pubic symphysis. While the results do support the need for more quantitative methods of age estimation these methods also produce methodological and practitioner issues of their own. As the medico-legal community pushes for more objective methods for evidentiary standards our field needs respond by pursuing methods that attempt to increase accuracy while lowering practitioner bias.

Do structural equation models work to explain the factors shaping cortical bone morphology?

ROBYN A. JOHNSTON and LIBBY W. COWGILL
Anthropology, University of Missouri

Increased muscle strength and total bodyweight load have both been suggested to influence the bending strength of the femur. However, many other factors, such as sex, age, and other life history factors can also contribute to the current morphology. Structural equation models are an ideal method to examine how a variety of factors influence the relationship between body mass and the final cortical measurements. This project uses the Third National Health and Nutrition Examination Survey (NHANES III) dataset to create a structural equation model that examines how these factors modify the relationship between body mass and proximal femoral geometry. The sample includes 850 individuals, all who reported exercising in one of three types of exercise (running, weightlifting, and swimming) a minimum of 10 times in the past 30 days. Body composition was calculated using skinfold and bioimpedance measurements. Cross-sectional area was estimated using dual energy x-ray absorptiometry (DEXA) scans of the femoral shaft, directly below the lesser trochanter, and the Hip Structure Analysis program. Based on this study, total mass was related to proximal femur cortical properties, with lean muscle mass, weight at age 18 significantly affecting the relationship. Increased activity positively affected lean muscle mass amount. We propose that structural equation models are a useful tool for understanding the complex relationships affecting cortical morphology.

New Estimates of Hunter-Gatherer Mortality Patterns From Improved Fits of the Siler Model

JAMES HOLLAND JONES¹, MICHAEL D. GURVEN² and MICHAEL H. PRICE³

¹Department of Earth System Science, Stanford University, ²Department of Anthropology, University of California Santa Barbara, ³ Santa Fe Institute

Low-dimensional parametric models of human mortality are important tools in biodemography and comparative evolutionary studies. These models allow researchers to smooth mortality data drawn from small samples, which tend to yield volatile estimates of age-specific mortality hazards as a result of limited observations in adjacent age-classes, without imposing particular age-specific patterns. The Siler competing-hazards model is a theoretically appealing and commonly-used parametric model for human mortality. The Siler model contains five parameters and captures the overall bathtub-shape of human mortality without otherwise making large assumptions about the level of different mortality components. Unfortunately, the model can be quite challenging to fit because of correlations between the different parameters. Gurven and Kaplan (2007) compiled data on the age-specific mortality of hunter-gatherers and other small-scale subsistence populations.

Because of the small samples, which are characteristic of studies in anthropological demography, Gurven and Kaplan fit Siler models to the estimated hazards to smooth and extend curves to the full age range. We present a greatly improved optimization algorithm for fitting the Siler model to empirical data and reanalyze the age-specific mortality of the hunter-gatherer groups in the original sample. Focusing in particular on four groups (Ache, Hadza, Hiwi, Tsimane), we find that previous fits under-estimate increases in senescent mortality and over-estimate the decay of infant/early-childhood mortality. We synthesize these results and present new mortality standards for research into the mortality of people in small-scale subsistence populations.

Identity and Dental Modification in Prehispanic Ecuador

SARA L. JUENGST

Anthropology, University of North Carolina at Charlotte

Body modification in the Andes has long been associated with identity display of various indigenous groups, with practices ranging from labret piercings to artificial cranial and dental modification. While body modification has been well-documented in the Peruvian, Bolivian, and Chilean Andes, we know significantly less about body modification in prehispanic coastal Ecuador. In this poster, I present evidence for dental modification from collection of 42 crania curated at the Museo de Antropológico y de Arte Contemporáneo (MAAC) in Guayaquil, Ecuador. While many of these crania were collected in the mid-1900s and lack secure archaeological context, all are of Prehispanic origin. Bioarchaeological assessment of the dentition from 42 individuals identified two distinct types of important antemortem modification. Four individuals had intentional dental modification such as incisive crosshatching, gold appliques, and metal inserts. Eleven individuals had lost their central and lateral maxillary incisors and maxillary canines prior to death (as marked by alveolar resorption), a pattern of tooth extraction noted by Spanish chroniclers when they arrived to Ecuador in the early 1500s. One individual presented with both modifications, with gold insets on mandibular incisors and canines and missing maxillary incisors with alveolar resorption. While the archaeological context is not secure for these crania, it is clear that people living in coastal Ecuador prior to Spanish colonization were communicating important messages about status and identity through dental modification.

Funding for this research was provided by the College of Liberal Arts and Sciences at the University of North Carolina Charlotte.

ABSTRACTS

Osteoarthritis and osteophytosis in the vertebral column in two prehistoric populations from the semi-arid north of Chile

DANIELLE K. JULIEN and KIMBERLY M. RAYMOND
Anthropology, Binghamton University, State University of New York

Past research on osteoarthritis and osteophytosis in hunter-gatherer and agricultural societies have generally focused on postcranial elements, with few studies done on the vertebral column. For this study, prehistoric individuals from the Archaic and Diaguita cultures, which occupied the semi-arid North of Chile, were examined. Using methods originally presented by Stewart (1958), Chapman (1973), and Ubelaker (1999), data were collected on the location and severity of osteoarthritis and osteophytosis from 58 Archaic and 41 Diaguita individuals. Five age categories, 15-24, 25-34, 35-44, 45+, and adult, age unknown, were used in this study. Univariate analysis of variance (ANOVA) was completed on data collected from individuals with 18 or more vertebrae present in order to study the relationship between each vertebra, age, sex, and differences between the Diaguita and Archaic. Statistical results demonstrated that the upper cervical vertebrae and lower lumbar spine were the most severely affected by osteoarthritis and osteophytosis. The data demonstrated that age and time period had a significant effect on these pathologies in the cervical and lumbar spine. Moreover, the results obtained from studying osteoarthritis revealed that the individuals between the ages of 35-44 did not show a significance between age and the effect of the disease. While considering osteophytosis, individuals between 25-44, and the adults, age unknown, also did not demonstrate significance between age and severity of disease. This information is critical because these results are not consistent with other research done on the paleopathological information previously obtained from the semi-arid north of Chile.

Morphological integration in thoracolumbar vertebrae of *Macaca fascicularis*

HYUNWOO JUNG and NOREEN VON CRAMON-TAUBADEL

Buffalo Human Evolutionary Morphology Lab,
University at Buffalo, SUNY, NY

The purpose of this study is to examine the pattern of magnitude of integration in thoracolumbar vertebrae. It is hypothesized that 'anticlinal' pairs will show higher magnitudes of integration than the two adjacent vertebrae for stable dorso-ventral flexion.

For this, 45 *Macaca fascicularis* (23 males and 22 females) were used and 18 landmarks were digitized on 3D scanned T1, T2, T9, T10, T11, T12, L1, and L2 vertebrae. 'Anticlinal' pairs were defined as the two adjacent vertebrae around T10 as T10 is the first caudal thoracic vertebra

with spinous process perpendicular to the body. Magnitudes of integration was calculated by integration coefficient of variation (ICV) from inter-landmark distances, which were pooled within-sex mean standardized. A resampling method was applied for generating distributions of ICV for a single vertebra and adjacent pairs of vertebrae. Comparison between ICV scores were conducted with Mann-Whitney U test and Bonferroni adjustment (significant when $p < 0.0033$). All analyses and ICV calculations were conducted with R 3.4.4. and *evolqg* package.

The results did not support the hypothesis as ICV scores of T9 and T10, or T10 and T11 pair were significantly lower than other adjacent vertebrae pairs ($p < 0.0001$). T1 and T2 pair showed the highest ICV scores followed by T11 and T12 pair. Moreover, within single vertebrae, T1 showed the highest ICV scores followed by T11. Thus, it can be inferred that changes in vertebral identity may be an important factor for maintaining high morphological integration within and between vertebrae but not 'anticlinality'.

Physical Activity as Evidenced by Degenerative Joint Disease in Adults from a Rural and Urban Medieval Polish Comparison

HEDY M. JUSTUS¹, TRACY K. BETSINGER² and AMANDA M. AGNEW³

¹Forensic Anthropology, SNA International,
²Anthropology, SUNY Oneonta, ³Skeletal Biology Research Laboratory, The Ohio State University

Polish populations experienced subsistence and lifestyle changes associated with increasing urbanization during the early medieval period (10th-12th centuries). It is hypothesized that urban populations engaged in less arduous physical activity and thus experienced a decrease in the frequency of degenerative joint disease (DJD) compared to rural populations, particularly those that continued to participate in farming activities. Adult skeletal remains from medieval urban Poznan (n=86) and rural Giecz (n=170) were used to test this hypothesis. They were analyzed for DJD according to the Global History of Health Project (Steckel *et al.*, 2006) for 15 joint groups (cervical, thoracic, and lumbar vertebrae and left and right shoulders, elbows, wrists, hips, knees, and ankles). A series of statistical tests, including two-tailed t-tests and Mann-Whitney U-tests, were conducted on various data subsets. When considering the greatest extent of degeneration in each individual, 29% (n=25) of the urban sample exhibited mild DJD (slight marginal lippling and/or osteophyte formation and porosity) and 20% (n=17) exhibited more severe DJD (extensive marginal lippling, osteophyte formation, degeneration, and, in some cases, eburnation). In the rural sample, 44% (n=75) of individuals exhibited mild DJD and 44% (n=75) exhibited severe DJD, in addition to 1% (n=2) of individuals suffering

from near fusion and 1% (n=2) complete joint fusion. Tests confirmed that urban populations were significantly ($p < 0.01$) less affected by DJD than rural populations, for the populations as a whole, as well as when considering age cohorts and sexes separately. Furthermore, urban populations suffered from less severe DJD compared to rural populations.

Commingle skeletons in Cussac cave (Gravettian, Dordogne, France): Paleobiology and mortuary behaviors

SACHA KACKI^{1,2}, IRENE DORI^{1,3}, PIERRE GUYOMARC'H¹, ELINE M.J. SCHOTSMANS^{1,4}, VITALE S. SPARACELLO¹ and SÉBASTIEN VILLOTTE¹

¹PACEA, CNRS-Université de Bordeaux, France,
²Department of Archaeology, Durham University, UK, ³Department of Biology, Laboratory of Anthropology, University of Florence, Italy,
⁴Centre for Archaeological Science, University of Wollongong, Australia

Cussac cave (France) hosts a unique combination of parietal art (600+ engravings) and human remains dating to the Gravettian (31,000–22,000 BP). The skeletal remains are located deep in the cave in three different loci. One of them contains the largely complete, well-preserved skeleton of an adult male, who was placed in a prone position in a former bear hibernation nest. His bones were then disturbed by flooding events. The other two loci were not affected by these natural phenomena. They consist of accumulations of disarticulated bones and share common features, including the presence of red pigment, the association of the bones of several individuals, and the absence of cranial remains. The distribution of the remains suggests that these bone accumulations are the result of secondary deposit of body parts or skeletal elements. Some evidence also points to selection of bones and post-deposition manipulations (e.g. consistent separation of upper and lower limb elements in one of the locus, accumulation of maxillary teeth suggestive of the deposition and subsequent removal of a cranium in the second one).

Based on these observations, it seems clear that previously unknown Gravettian mortuary practices took place at Cussac. These observations make a significant contribution to the knowledge of the variability in mortuary practices in the Upper Paleolithic. They add to the rare evidence of Gravettian post-mortem manipulations known to date, which were previously limited to a few cases in the sites of Abri Pataud (France), Pavlov (Czech Republic) and Sungir (Russia).

This work was supported by the Agence National de la Recherche (ANR) (Gravett'Os Project; Principal investigator: Sébastien Villotte; grant number: ANR-15-CE33-0004).

ABSTRACTS

The Impact of the Roman Conquest of Egypt on the Non-Elite - Evidence from the Wall of the Crow Cemetery at Giza

JESSICA E. KAISER

Near Eastern Studies, University of California Berkeley

Written sources suggest that the change in Egypt's status from an independent power to a province of the Roman Empire had far-reaching consequences for the Egyptian population. The Romans raised taxes and instituted a more or less segregationist policy towards native Egyptians. Women, in particular, became increasingly marginalized when the Egyptian laws were abandoned in favor of the more patriarchal Roman legal system. However, a historical narrative based on textual sources will mainly reflect the situation among the literate elite. This study, in contrast, employed a multidimensional bioarchaeological approach that considered evidence of skeletal stress in combination with archaeological and historical data to examine the extent to which a non-elite population from the Wall of the Crow Cemetery in Lower Egypt were affected by the Roman conquest. The cemetery material comprised 228 individuals divided into two distinct phases: an earlier phase dating to the relatively stable Saite period (664-525 BCE), and a later phase dating to the early to mid-Roman period (1st-2nd Century CE). To investigate whether the historical narrative is supported by skeletal evidence, frequencies of non-specific skeletal stress markers were compared between the phases, as well as between the sexes, within and between the two periods. The results suggest that there was indeed a decline in living conditions from the Saite to the Roman period, though not as steep as expected. In particular, the study found no statistically significant evidence for a decline in living conditions among women following the Roman conquest.

Morpho-functional traits of the mandible suggest no hard food adaptation in the hominin lineage

THOMAS M. KAISER¹, JORDI MARCÉ-NOGUÉ^{1,2}, THOMAS A. PÜSCHEL³ and ALEXANDER DAASCH¹

¹Mammalogy, Paleoanthropology, Center of Natural History, University Hamburg, ²Institut Català de Paleontologia M. Crusafont, Universitat Autònoma de Barcelona, Cerdanyola del Vallès, Barcelona, ³School of Earth and Environmental Sciences, University of Manchester

An on-going debate concerning the dietary adaptations of Australopithecines and early *Homo* has been fueled by contradictory inferences obtained using different methodologies. This work presents an extensive comparative sample of 30 extant primate species that was assembled to perform a morpho-functional comparison of these taxa with 12 models corresponding to eight fossil hominin species. Finite Element Analysis

and Geometric Morphometrics were employed to analyze chewing biomechanics and mandible morphology to, firstly, establish the variation of the group, secondly, relate stress and shape variables, and finally, to classify fossil individuals into broad ingesta related hardness categories using a support vector machine algorithm. Our results suggest that some hominins previously assigned as hard food consumers (e.g. the members of the *Paranthropus* clade) in fact seem to rely more strongly on soft foods, which is consistent with most recent studies using either microwear or stable isotope analyses. By analyzing morphometric and stress results in the context of the comparative framework, we conclude that in the hominin clade there were probably no hard-food specialists. Nonetheless, the biomechanical ability to comminute harder items, if required as fallback option, adds to their strategy of increased flexibility.

German Research Foundation, KA1525-9/1, FOR 771

Linking female sociability and infant survival in capuchins: the roles of direct and indirect social connections, food competition, and energetic status

URS KALBITZER¹, MACKENZIE L. BERGSTROM², FERNANDO A. CAMPOS³, SARAH D. CARNEGIE², MELISSA EMERY THOMPSON⁴, KATHARINE M. JACK⁵, AMANDA D. MELIN² and LINDA M. FEDIGAN²

¹Anthropology, McGill University, ²Anthropology and Archaeology, University of Calgary, ³Anthropology, University of Texas at San Antonio, ⁴Anthropology, University of New Mexico, ⁵Anthropology, Tulane University

Many female primates form differentiated relationships with other female group members, and there is increasing evidence that socially integrated females exhibit higher fitness. In accordance with observations from baboons and macaques, there is also a link between social integration and infant survival in white-faced capuchin monkeys. Two important questions that require further attention are 1) which dimensions of social relationships confer such benefits, and 2) how these benefits are conferred. To address the first question, we analyzed long-term data on capuchin monkeys in Santa Rosa, Costa Rica, to evaluate the importance of different social network parameters to infant survival. To address the second question, we assessed whether social integration was related to female urinary C-peptide levels (which reflect energetic status), considering the degree of feeding competition. The most important social network parameter to infant survival was maternal 'eigenvector centrality' (GLMM with the lowest AIC-value), which reflects the social integration of a female plus the integration of her social partners, and, therefore, direct and indirect social connections. However, we did not detect a relationship between a female's

eigenvector centrality and her energetic status (LMM: P-value = 0.64). Our results indicate that, for female capuchins, being socially, and possibly spatially, central within the group is the most important factor determining the survival of her infant. However, centrality does not seem to lead to better energetic status, and the mechanism by which maternal sociability is linked to infant survival in capuchins and other primate species remains to be determined.

Sodium content in plant & insect food resources consumed by chimpanzees in Gombe National Park, Tanzania

AXELLE KAMANZI SHIMWA¹, CARSON M. MURRAY², MICHAEL L. POWER³ and ROBERT C. O'MALLEY⁴

¹Center for the Advanced Study of Human Paleobiology, George Washington University, ²Center for the Advanced Study of Human Paleobiology, George Washington University, ³Nutrition Laboratory, Smithsonian Conservation Biology Institute, ⁴Dialogue on Science, Ethics, and Religion Program, American Association for the Advancement of Science

Many primate diets are dominated by plant foods, yet plant tissues are often poor sources of sodium (Na) - a necessary mineral for mammalian metabolism and health. Previous studies suggest that some wild primates seek out and consume certain aquatic plants, soils, clays, and decaying wood due to their high sodium content. Among such primates are chimpanzees (*Pan troglodytes*), who are characterized as ripe fruit specialists but consume a diverse spectrum of animal and plant resources. Animal prey, including insects, have been proposed as a source of dietary sodium for chimpanzees, yet published data on the Na values for specific foods are limited.

We used AA spectroscopy to determine the Na content of key plant foods and insects consumed by the chimpanzees of Gombe National Park, Tanzania. On a dry matter basis, the mean Na value of plant foods (n=49; Mean = 91.4ppm, S.D. = 93.8ppm) was significantly lower than insect foods (n= 7; Mean = 1,532.2ppm, S.D. 767.4ppm) (Kruskal-Wallis = 15.812, df=1, p<0.001). Furthermore, all plant values were below the suggested sodium requirement (2000ppm) for primates. While the values of assayed insects were quite variable, the Na content of the two most commonly consumed insect prey for Gombe chimpanzees (*Macrotermes* soldiers and *Dorylus* ants) were 4-5x greater than the highest plant values and likely would meet requirements. We conclude that major plant foods available to

ABSTRACTS

Gombe chimpanzees are poor sources of dietary sodium. In contrast, insect prey are important, and perhaps critical, sources of this mineral for this population.

This research was supported by a GWU-SI Opportunity Fund Research Grant and a Mazuri Research Grant

Are there clade level differences in the sexual dimorphism of primate hair morphology?

JASON M. KAMILAR^{1,2}, AMANDA N. SPRIGGS³, ALYSE MAKSIMOSKI¹ and BRENDA J. BRADLEY⁴

¹Department of Anthropology, University of Massachusetts Amherst, ²Graduate Program in Organismic and Evolutionary Biology, University of Massachusetts Amherst, ³Department of Anthropology, University at Albany – SUNY, ⁴The Center for the Advanced Study of Human Paleobiology (CASHP), Department of Anthropology, The George Washington University

In primates, body mass sexual dimorphism is relatively high in catarrhines, moderate in platyrrhines, and low in strepsirrhines. These differences likely reflect variation in the strength of sexual selection across clades. In addition to body mass, some primates exhibit sex differences in hair morphology (i.e. length, width). Some of the best-known examples are from species where males have hair-related ornaments, such as capes. Though, we still have little knowledge if sex differences in hair morphology show consistent differences across clades or if hair morphology dimorphism is associated with other traits, such as body mass dimorphism. Here we examined if the degree of hair length and width dimorphism differs across the three major primate clades (catarrhines, platyrrhines, and strepsirrhines) and test whether these traits are associated with body mass dimorphism across primates. We measured hair length and width at six body regions (dorsal torso, ventral torso, proximal and distal tail, crown, and cheek) for males and females representing more than 60 primate species and analyzed these data using phylogenetic generalized linear models. We found differences in hair length dimorphism across clades for the ventral torso and cheek regions, with catarrhines exhibiting the most dimorphism. In contrast, clades exhibited similar levels of dimorphism in hair width for each body region. Also, we found little association between hair morphology and body mass dimorphism across species. We suggest that evolutionary forces on hair length differ across body region and across clades, which has interesting implications for human and nonhuman primate evolution.

Funded by National Science Foundation (BCS #1546730, BCS #1606360), the Wenner-Gren Foundation, The George Washington University, the University of Massachusetts Amherst

Moving through ecology: orangutan positional behavior in a mosaic habitat

ERIN E. KANE¹, ANDREA BLACKBURN¹, TRI WAHYU SUSANTU² and CHERYL D. KNOTT^{1,2}

¹Anthropology, Boston University, ²Gunung Palung Orangutan Conservation Project

Documenting the ways in which organisms physically move through space and the influences of habitat structure on their movement and posture are fundamental to understanding their spatial ecology. Movement ecology is thus a significant influence on animal cognition, morphology, diet, group structure, etc. Evidence to date demonstrates that orangutans of different species (*Pongo abelii*, *P. wurmbii*) living in similar habitats exhibit positional behavior more similar to each other than to conspecifics in disparate habitats. Therefore, it is a reasonable hypothesis that orangutan positional behavior is a function of habitat rather than morphological constraints. Here, we test this hypothesis by examining the positional behavior of orangutans living in Gunung Palung National Park in West Kalimantan, Indonesia, a primary forest mosaic composed of seven distinct habitats. We use 33,358 instantaneous scan samples collected every 5 minutes during full day follows of habituated adult orangutans (N=27) to examine postural behavior, locomotor modes, and structure use with a null hypothesis of no differences in positional behavior or support use profiles between habitats. We found significant differences in the profiles of orangutan postural behavior (G=216.2, p<0.001), locomotor behavior (G=45.34, p<0.001), and support use (G=137.8, p<0.001) in 5 distinct habitats within Gunung Palung National Park. Orangutans within the same population move through and use distinct habitats in different ways. This underscores the role of local ecology in structuring organisms' space use as well as the importance of behavioral plasticity to primates' movement ecology.

National Science Foundation (BCS-1638823, BCS-0936199); National Geographic Society; US Fish and Wildlife (F15AP00812, F12AP00369, 98210-8-G661); Leakey Foundation; Disney Wildlife Conservation Fund; Wenner-Gren Foundation; Nacey-Maggioncalda Foundation

Late Copper Age multiple inhumation burials with subadults in the Carpathian Basin

AMY N. KARABOWICZ

Anthropology, University of Pittsburgh

Settlements, burials, and isolated finds associated with the Baden culture appear in and around Europe's Carpathian Basin during the Late Copper Age (3500-2800/2700 BC). The present study focuses on subadults interred with one or more individuals at extramural Baden mortuary sites in Hungary and Austria (e.g., Budakalász, Alsónémedi, and Ahrenberg). Baden burials within

settlements mimic their extramural counterparts or exhibit diverse methods through which the deceased were manipulated and deposited in (unusual) features. In contrast, extramural burials are generally found in isolation or in small clusters, with many consisting of single inhumations or cremations. The extramural Baden cemetery of Budakalász near Budapest is atypical due to its size: more than 450 individuals excavated from 436 graves. Of the 38 double or triple inhumation graves, 23 graves (61%) at Budakalász contain at least one subadult (individuals aged 15 years or younger). Multiple inhumations consisting of one or more subadults were identified at an additional eight extramural Baden sites. Of the 31 multiple inhumation graves, 15 graves (48.3%) contain only subadults. The remaining graves consist of a minimum of one adult (>15 years of age) and one subadult. Although this dataset is small, the demographics are explored within social contexts proposed for the Baden including the role of ideological influences, genetic relatedness, and seasonal shifts in habitation. Potential sources of complication are noted. This project aligns with ongoing efforts to reconstruct Copper Age lifeways for the Carpathian Basin.

Interdisciplinary evidence of the effects of physical activity in the patterns of human hand entheses

FOTIOS ALEXANDROS KARAKOSTIS¹ and KATERINA HARVATI^{1,2}

¹Paleoanthropology, Senckenberg Centre for Human Evolution and Palaeoecology, ²DFG Center for Advanced Studies "Words, Bones, Genes, Tools", Eberhard Karls University of Tübingen

Even though entheses are routinely used to reconstruct activity in the past, their interpretation has been hampered by low precision in their scoring and the absence of rigorous multivariate statistical analysis. Furthermore, even though several works report an association between activity and aspects of enthesal variation, recent studies have argued against this connection. However, these works have important methodological shortcomings. Specifically, they did not analyze the multivariate relationship among different entheses and did not address the widely supported notion that enthesal form is mainly affected by a complex interaction between biological age and long-term systematic physical activity. Some important factors of enthesal variation (such as old age) were often completely ignored.

By contrast, our research group has recently provided original and interdisciplinary evidence of a significant functional signal in human hand entheses. Using a novel and precise 3-D measurement method, we found that the multivariate patterns among hand entheses reflect fundamental muscle synergy groups, directly related either with power or precision grasping behavior.

ABSTRACTS

An anthropological sample with uniquely detailed and lifelong documentation of the individuals' occupational activities, showed clear differences between heavy manual workers (exclusively presenting a power grip enthesal pattern) and precision workers (with a precision grasping pattern). The recent application of our method on Neanderthals reported that their enthesal patterns are directly linked to manual behaviors which reflect on the most recent and reliable archaeological evidence. Furthermore, our presentation discusses new and supportive evidence for our methodology, relying on our latest histological, geometric morphometric, and experimental research.

German Research Foundation (DFG FOR 2237), European Research Council (ERC CoG 724703), German Academic Exchange Service (91584619), and the A. G. Leventis Foundation (12386).

An analysis of the trabecular morphology of the *Homo naledi* talus, and its inferred functional implications

COLIN P. KASL¹, ANNA J. RAGNI^{2,6} and WILLIAM E.H. HARCOURT-SMITH^{3,4,5,6}

¹Department of Anthropology, New York University, ²Vertebrate Paleontology, Richard Gilder Graduate School, American Museum of Natural History, New York, ³Department of Anthropology, Lehman College, 250 Bedford Park Blvd. W., Bronx, New York, ⁴Department of Anthropology, CUNY, Graduate Center, New York, ⁵Division of Paleontology, American Museum of Natural History, New York, ⁶New York Consortium of Evolutionary Anthropology

The *Homo naledi* foot has previously been described as relatively modern in external morphology, with an adducted hallux, rigid midfoot, elongated tarsus, and a talus falling just within the range of modern human shape variation. However, the proximal pedal phalanges are markedly curved, and there is a reduced or possibly absent medial longitudinal arch. Given the mosaic nature of the foot, a better understanding of its precise functional affinities is important. Here we focus on internal trabecular structure, which has long been considered to reflect loading regimes during locomotion. Previous studies have found important differences in talar trabecular morphology between extant apes, modern humans and fossil hominins. This study assesses the trabecular morphology of four *H. naledi* tali: UW-101-148/149, UW101-520, UW101-1215, and UW101-1417. Specimens were microCT scanned (<40 microns), separated into nine spherical regions of interest directly plantar to the trochlear surface, and processed to analyze standard trabecular parameters, including thickness (Tb.Th) and number (Tb.N), bone volume/trabecular volume (BV/TV), and degree of anisotropy (DA). Results show that Tb.Th and BV/TV of *H. naledi* are similar to values for extant apes and other fossil hominins, and

higher than in modern humans. The degree of anisotropy follows a similar pattern of anatomical distribution to modern humans, with highly anisotropic trabeculae on the lateral side of the trochlea. We conclude that the *Homo naledi* upper ankle joint was subjected to predominantly modern human-like loading regimes, though the more ape-like Tb.Th and BV/TV values indicate that these were not exclusively modern human-like.

Predicting skull shape from admixture history in a multigenerational macaque cross sample

DAVID C. KATZ^{1,2}, LAURA T. BUCK², JAY DEVINE¹, REBECCA R. ACKERMANN^{3,4}, BENEDIKT HALLGRIMSSON¹, LESLEA J. HLUSKO⁵, SREETHARAN KANTHASWAMY⁶ and TIMOTHY D. WEAVER²

¹Cell Biology & Anatomy, University of Calgary, ²Department of Anthropology, University of California, Davis, ³Department of Archaeology, University of Cape Town, ⁴Human Evolution Research Institute, University of Cape Town, ⁵Integrative Biology, University of California, Berkeley, ⁶School of Mathematical and Natural Sciences, Arizona State University

The extent to which skeletal morphology reflects admixture history is an important issue for studies that seek to infer ancient admixture when genetic data is not available. Most admixture studies focus on the earliest generations of crosses. Yet, often enough in nature, some introgressed genetic material persists in a parental population over many generations of reproduction. In the case of interbreeding among Late Pleistocene archaic humans, the evidence supports such a scenario.

Here, we quantify the admixture signal preserved in the skulls of admixed rhesus macaques (*Macaca mulatta*), a close relative of humans. We use a multigenerational sample of Chinese and Indian *M. mulatta* subspecies and approximately 100 of their admixed progeny. The sample is drawn from a colony maintained at the California National Primate Research Center, and includes many animals with only a small genetic contribution (~ 10%) from one subspecies line. We tested the extent to which admixture proportion predicts shape in the cranium as a whole and for masticatory morphology. Percentage Chinese ancestry is a good predictor of shape ($R^2=0.4$, $p=0.002$) along the primary axis of variation (first principal component, 56% of variation). The ability to predict shape from ancestry is much weaker for masticatory morphology ($R^2=0.115$, $p=0.006$; PC1 accounts for 28.4% of variation). We discuss the implications of our findings for efforts to infer

admixture from skeletal data, and provide further details about the macaque sample, which will become available to the scientific community over the next several years.

This research was generously supported by grants from the National Science Foundation (#1623366, #1720128) and Leakey Foundation.

Managing an undergraduate research lab at a teaching-focused university

LAURIE KAUFFMAN

Biology, Oklahoma City University

It is essential that undergraduate students be afforded the opportunity to participate in research. Research experiences for undergraduates have many benefits including improving student soft-skills, increasing student retention and satisfaction, and preparing students for graduate school. At teaching-focused institutions, faculty are often encouraged to provide undergraduate research opportunities, but may lack time and resources to do so. Often, primarily undergraduate institutions have fewer resources for research, and faculty likely carry a large teaching load, making it difficult to allot time to mentoring undergraduates in research. Here I discuss my experiences running a primate behavior undergraduate research lab. In the last seven years I have worked with more than twenty students to carry out research projects on wild squirrel monkeys, zoo-housed orangutans, and long-tailed macaques at a local monkey sanctuary. I describe my use of regular structured meetings, intentional mentoring, and small scale research projects. These approaches have allowed me to complete a significant amount of undergraduate research within a limited time budget. I share my tips for maintaining an undergraduate research lab in light of limited resources, and also invite discussion and tips from others working in similar circumstances.

Relations between cultural perceptions of childhood and childhood stress in an ancient Greek colony

MADISON R. KAYE¹, BRITNEY KYLE², STEFANO VASSALLO³ and LAURIE J. REITSEMA⁴

¹Department of Anthropology, Washington College, MD, ²Department of Anthropology, University of Northern Colorado, CO, ³Soprintendenza di Palermo, Italia, ⁴Department of Anthropology, University of Georgia, GA

Every culture develops its own conceptualization of childhood. Therefore, the culture in which a child is indoctrinated may influence stress experienced during childhood. This study uses social age categories, defined by the ancient Greek's cultural ideology of childhood based on cognitive development stages, to assess the prevalence of childhood stress indicators within individuals who died during childhood or adulthood in

ABSTRACTS

the Greek colony of Himera (648-409 B.C.). We assume this Sicilian colony followed the ancient Greek idea of childhood. We observed 739 individuals from the 6th-5th century BCE for three skeletal markers of childhood stress: cribra orbitalia (CO), porotic hyperostosis (PH), and linear enamel hypoplasia (LEH). Individuals observable for at least one pathological lesion were assigned to the age-at-death categories of subadult (below age 18) and adult (age 18+) to examine whether individuals who died in childhood (subadults) exhibited a different prevalence for each stress marker than individuals who survived childhood (adults). The subadults were divided into five social age categories specific to ancient Greece: babyhood (birth-2), early preschool (3-5), real preschool (6-7), school (8-14 [puberty]), and adolescence (15-18). No significant differences between subadults and adults in the prevalence of any stress marker were observed ($X^2 p_{co}=0.09$; $p_{ph}=0.72$; and $p_{leh}=1.00$). Adolescents exhibited significantly more PH and LEH than 3 of the 4 other stages of childhood. Perhaps experiencing early childhood stress led these individuals at Himera to develop a survival strategy that proved maladaptive to future environmental conditions, making these adolescents more susceptible to another stress event later in childhood.

This research was funded by National Science Foundation Research Experience for Undergraduates award numbers 1560227 and 1560158, the University of Georgia, and the University of Northern Colorado.

The Krapina Neandertal Site: Using Dental Metrics To Determine Population Variability In Neandertals

BRIAN A. KEELING

Anthropology, Binghamton University

Krapina is a Neandertal rockshelter site dating back to $130,000 \pm 10,000$ BP located in Northern Croatia. This site was discovered over a century ago by Karl Gorjanović-Kramberger and remains the largest amount of Neandertal skeletal remains ever found in a single site. This large assemblage is excellent for investigating issues of sample variation. This study analyzed dental metrics, specifically the buccolingual diameter of each tooth to determine if the hypothesis that Krapina represents a distinct Neandertal "population" among Neandertals is supported. A total of sixteen comparative sites were compiled to best determine the relationship of Krapina to human populations and other groups of genus *Homo*. Variation was analyzed through comparisons of the coefficient of variation and from several statistical significance tests. The results of this study determined that Krapina was too variable to be a Neandertal population. The critical dental element, the first and second molars, demonstrate a level of variation not significantly different from that of the full Neandertal sample used. However, Krapina does show some features and

variation in other elements that suggest some genetic continuity at the site. Krapina's high within-sample variation is likely attributable to the probably 10,000-year span of occupation at the site and to the possibility of extensive interbreeding with other Neandertal groups during the long period of the rockshelter's use.

"Active learning" in the anthropology classroom improves student engagement, retention, and inclusion

T. JOSHUA KEETON and AMELIA R. HUBBARD

Department of Sociology and Anthropology, Wright State University

Phrases like active learning, team-based learning, and flipped classrooms have become increasingly common in college level discussions of teaching, yet many remain wary that such approaches to teaching are "passing trends." Ongoing scholarship of teaching and learning suggests that such approaches are not only effective in conveying information that is more readily retained but also creates a classroom that is more inclusive to diverse perspectives and promotes the retention of underrepresented groups in science.

This poster presents three years of faculty and student perspectives on the effectiveness of such techniques in a large-format (100 student), non-major intro to biological anthropology course. Results of such approaches in this course broadly include students having: 1) both an improved understanding of the scientific process and a deeper appreciation of anthropology as a science, 2) an enhanced sense of belonging in the classroom, and 3) greater investment in the material. Specific examples of successful activities, principles of group formation, and scaffolded teaching will be provided.

Socio-ecological predictors of maternal uncle investment in the bilateral, semi-nomadic Shodagor

MONICA H. KEITH¹ and KATHRINE E. STARKWEATHER²

¹Department of Anthropology, University of Missouri, ²Department of Anthropology, University of New Mexico

The Shodagor are a bilateral, semi-nomadic boat-dwelling population in Bangladesh that exhibit a range of social and economic strategies dependent upon specific ecological circumstances. Their flexibility includes some behaviors characteristic of matrilineal societies, such as investment from maternal uncles into their sisters' children in 39% of Shodagor families. Maternal uncle investment has often been considered puzzling from an evolutionary perspective given that these men are presumably investing resources into their sisters' children rather than their own. We investigate household-level socio-ecological predictors of three types of

maternal uncle investment: direct investment of childcare, indirect investment of resources such as food or clothing, and a general category of any maternal uncle investment. Bayesian linear models indicate that residence patterns significantly influence direct care from maternal uncles, and families residing on boats as well as those living matrilocally are more likely to receive direct investment. Informative predictors of indirect investment indicate that a mother's birth history corresponds with more tangible contributions such as food and clothing. Mothers who are firstborn in their natal families as well as those who have more older brothers are more likely to receive any brotherly investment at all. The bilateral, behaviorally flexible nature of this population allows us to make evolutionary inferences from these associations, revealing circumstances that may lead to the development of female-biased kinship.

The data collection for this research was funded by the Wenner-Gren Foundation, Dissertation Fieldwork Grant 8578.

Bioarchaeological analysis of Nasca 'trophy' head individuals from the site of Zorropata in Peru (AD 450-1000)

CORINA M. KELLNER¹ and SARAH DOST KERCHUSKY²

¹Anthropology, Northern Arizona University, ²Anthropology, University of California, Santa Barbara

Various factors shaped cultural practices such as 'trophy head' taking in Andean prehistory. Zorropata, located in the Las Trancas Valley, Nasca, Peru, was a large domestic site with likely ceremonial function occupied relatively continuously from the Late Nasca period (c. AD 450-600) until the early Middle Horizon/Loro period (c. AD 600-1000). Archaeological survey conducted by Katharina Schreiber in the 1990s at Zorropata identified at least one and possibly two adobe compounds that were similar to structures described by Julio C. Tello at Huaca del Loro, the largest Las Trancas site and local hub dating to the Middle Horizon. At both Huaca del Loro and Zorropata these structures appear to be *barbacoa* style tombs. Excavations conducted at Zorropata in 2014 recovered eight 'trophy head' individuals from the largest cell (Structure 21) of the adobe compound. 'Trophy head' individuals were analyzed using bioarchaeological methods to investigate this practice just prior to and concurrent with Wari imperial influence in the Nasca Region. Most exhibited typical Nasca cranial vault modification and were in the style of Nasca 'trophy' heads. Isotopic values show that maize was an important part of their diet. However, the inclusion of subadults and one possible female in this group is unusual for the time period. Additionally, strontium isotope values show that the majority were non-local, deviating

ABSTRACTS

from previous studies. These results illustrate that the Nasca experience with environmental and sociopolitical challenges differed between valleys within the Southern Nasca Region.

NSF Archaeology Doctoral Dissertation Improvement Grant #1441840 and University of California, Santa Barbara Social and Behavioral Sciences Grant

The interaction of climatic and energetic factors on human nasal morphology

ALEXA P. KELLY and SCOTT D. MADDUX

Center for Anatomical Sciences, University of North Texas HSC

While a narrower nose enhances inspiratory air-conditioning in cold-dry climates, such environments are also metabolically expensive, requiring greater oxygen intake than tropical environments. Accordingly, it has previously been hypothesized that volumetric restriction of oxygen intake due to nasal narrowing may necessitate an increase in nasal height to meet energetic demands. To test this, we employed 17 linear measurements from the nasal skeleton of modern humans from 10 climatically diverse geographic areas (Arctic Circle, Europe, Iran, Australia, North Africa, Khoisan, South African Bantu, East Africa, West Africa, Papua New Guinea). Femoral head diameter (FHD) was further employed as a proxy for body size and metabolic requirements. In conjunction with climatic data, these morphological data were employed in multivariate analyses to examine the relationship between nasal dimensions, climate, and metabolic demand. Our results indicate that most breadth measurements of the nasal aperture and internal cavity are significantly correlated with climate (all r -values=0.64–0.81, p -values<0.045), but not FHD. Conversely, height and length measurements of the aperture and cavity were found to be more strongly correlated with FHD (r -values=0.53–0.68, p -values<0.047) compared to climate. Further, overall nasal passage area was found to be positively associated with FHD (r =0.54, p =0.039), while nasal passage shape retained a significant relationship with climate (r =0.76, p =0.001) with relatively tall/narrow airways associated with colder-drier environments. Collectively, these results support the assertion that airway height represents a compensatory mechanism for ensuring a metabolically sufficient intake of oxygen. Additional studies employing more direct measures of metabolic demands are accordingly warranted.

Impact of urbanization on tuberculosis and leprosy prevalence in medieval Denmark

KIRSTEN S. KELMELIS¹ and DORTHE D. PEDERSEN²

¹Anthropology, Pennsylvania State University,

²ADBOU, Institute of Forensic Medicine, University of Southern Denmark, Odense

Urbanization and consequences of urbanization, such as increased exposure to pathogens, is one source of heterogeneity that has long been considered detrimental to human health. The following study analyzes the relationship between urbanization and disease prevalence – specifically leprosy and tuberculosis – in four skeletal samples from medieval Denmark ($n = 210$) using a paleoepidemiological approach. Skeletal samples were selected from the early-middle medieval (AD 1200-1400) period from four sites (Ribe and Ole Wormsgade urban cemeteries, Sejet rural cemetery, and Øm Kloster lay cemetery) located in the Jutland region of Denmark. Six dichotomous lesions indicative of leprosy and six dichotomous lesions indicative of tuberculosis were analyzed using a probabilistic approach based on lesion sensitivity and specificity, and it was possible to score at least one of these conditions on each adult skeleton. Prevalence of leprosy at death varied between 4-20% among the different cemeteries, with Ole Wormsgade having the highest prevalence (CI 11-30%) (CI 11-30%). The Sejet sample had an estimated prevalence of 13% (CI 4-24%), Øm an estimated 8% (CI 2-14%), and Ribe with an estimated 4% (CI 0-8%). Prevalence of tuberculosis at death varied between 34-55%, with Sejet having the highest prevalence (CI 34-80%). Øm Kloster had an estimated 46% (31-63%), Ole Wormsgade an estimated 38% (CI 26-53%), and Ribe with an estimated 34% (CI 24-47%). These results suggest disease prevalence in skeletal samples cannot be explained by urbanization alone; rather, there are likely other sources of heterogeneity that are contributing factors to past disease experience.

This research was funded by the National Science Foundation (1825362), the Wenner-Gren Foundation (Gr.9604), the American-Scandinavian Foundation, and the College of Liberal Arts, Pennsylvania State University.

Effects of Binocular Field Width on Grasping Performance in *Cheirogaleus* and *Microcebus*: Implications for Primate Origins

ADDISON D. KEMP

Anthropology, UT Austin

The Angiosperm Coevolution and Nocturnal Visual Predation hypotheses propose that diagnostic crown primate traits, including a large field of binocular vision, evolved to facilitate feeding on fruits and catching prey at night, respectively. We tested the ability of these hypotheses to account for the evolution of primates' wide binocular field by experimentally determining whether a wider binocular field provides an advantage in grasping fruit and insect prey. The effect of binocular field width grasping performance was tested in two small-bodied nocturnal strepsirrhine species— *Cheirogaleus medius* and *Microcebus murinus*. Five individuals per species were filmed

grasping equally-sized fruit and insect prey under normal ($n=400$) and reduced binocular field ($n=360$) conditions. Binocular field restriction was achieved using a head-mounted blinder that blocks the medial visual field of one eye. Generalized linear mixed effects models were used to evaluate the effect of visual condition, species and individual on grasp success rate and six variables characterizing grasp mechanics. In a subset of 100 *M. murinus* grasps, the reduced binocular condition significantly decreased grasp success rate for both food types ($p < 0.05$) and caused significant changes in three of the grasp variables ($p < 0.05$). However, the performance deficit under the reduced binocular condition was also significantly greater when individuals were grasping insects than when they were grasping fruit ($p < 0.01$). These results suggest that while a wider binocular field is beneficial for both fruit and insect grasping, the latter may have provided a stronger selective pressure favoring the evolution of forward facing eyes in primates.

This work was supported by NSF Bio-Anth DDRIG 1650734 and a Harrington Fellowship

A validation of dental methods to estimate ancestry

DORI E. KENESSEY, ANDREA SBEI, MASON MCKINNEY and MARIN A. PILLLOUD

Department of Anthropology, University of Nevada, Reno

The use of dental data in the estimation of ancestry is growing in the field of biological anthropology. While several methods have been proposed, there has been little work done to test the accuracy of these methods. This study serves to validate two methods based on dental data: the rASUDAS proposed by Scott et al. (2018) and a set of dental metric data outlined by Pilloud et al. (2014). To test these methods, data on dental metrics ($n=265$) and morphology ($n=226$) were collected on a documented skeletal sample at the American Museum of Natural History. The sample represented Asian (Melanesia, Micronesia, South East Asia, East Asia, Middle East, Native American), African (East, West, and Sub-Saharan Africa), European, and South American populations. Morphological data were input into the web-based application rASUDAS, and metric data were analyzed using the custom database function in Fordisc. Ancestry was assigned based on the group with the highest posterior probability. In rASUDAS, 38.3% of individuals from six groups classified correctly. Positive predictive values ranged from 26.3% (American Indian) to 52.9% (Sub-Saharan Africa). Using the metric data, 52.7% of individuals were correctly classified into one of four groups. Positive predictive values ranged from 23.1% (East Asia) to 81.1% (Western Eurasia). While the methods are working, there are clear patterns in terms of misclassifications

ABSTRACTS

that will require a growth of the reference sample. Future research will also incorporate both data sets in model development as an additional way to improve allocation accuracy.

Mitochondrial haplogroup variation from the archaeological site of Cundisa, Bolivia

JENNIFER KENNEDY¹, TANVI HONAP², STANISLAVA CHÁVEZ³, SERGIO CHÁVEZ¹ and KRITHIVASAN SANKARANARAYANAN⁴

¹Sociology, Anthropology and Social Work, Central Michigan University, ²Anthropology, University of Oklahoma, ³Anthropology, Wayne State University, ⁴Microbiology, University of Oklahoma

The Cundisa archaeological site has a complex and continuous history of human occupation covering over 2,500 years. The site is located in the modern town of Copacabana, Bolivia located on the shore of Lake Titicaca. Excavations by the International and Interdisciplinary Yaya-Mama Archaeological Project under the direction of Sergio and Stanislava Chávez, revealed Tiahuanaco burials that date from the Early Intermediate to the Middle Horizon Periods (50 BCE – 1000 CE). This makes it one of the largest cemeteries uncovered within the Tiahuanaco cultural sphere of influence and one of the first studied using ancient DNA methods. Ancient DNA from 18 selected Cundisa individuals from different time periods identified at the site were extracted, target-enriched for the complete mitochondrial genome, and sequenced on an Illumina MiSeq. Post enrichment ~3-79% of reads were mitochondrial with 12 of 15 samples having an average depth of coverage of >10X (min: 14X, max 100X). Eight individuals were identified as haplotype B2 and the other four appear as A2. This data was used to propose questions about genetic continuity at Cundisa mirroring the proposed cultural continuity as seen in the archaeological record by Chávez. Also examined are the individual genetic relationships at the site as well as comparing the population of Cundisa to other studied ancient populations within the broader region.

Post-cranial diversity in Catarrhines

BRITTANY A. KENYON and NOREEN VON CRAMON-TAUBADEL

Department of Anthropology, University at Buffalo

Most research in primate, including human, evolution use similarities and differences in cranial morphology to address questions relating to systematics and phylogeny. While primate cranial diversity tends to reflect primate taxonomy, the phylogenetic efficacy of the primate post-cranium tends to be less clear, even though assessment of these bones is necessary given that many fossil remains include post-cranial elements.

Here, we test the hypothesis that post-cranial bones of the limb girdles reflect taxonomy using data collected from a representative male and female from 11 catarrhine species (n=22). The scapula and innominate were 3D scanned using an HDI structured light scanner. Scapula (n=17) and pelvic (n=20) landmarks were applied to the scans using Landmark Editor.

Following Procrustes superimposition, Procrustes distance matrices were subjected to a 2D multidimensional scaling (MDS) to visualize the affinities among individuals. For the scapula, cercopithecoids and hominoids tend to group separately, thereby reflecting gross taxonomic differences, although both *Nasalis* and *Hylobates* were exceptions to this, as both fell outside their expected groups. For the pelvis, individuals also separated based on gross taxonomy, but with clear differences between more arboreal and terrestrial cercopithecoids. Principal Components Analysis were performed to evaluate the morphological shape differences associated with each major taxonomic group. A Mantel test found that among individual scapula and os coxa, Procrustes distances were significantly correlated ($r = 0.31$, $p = 0.006$), but it remains to be tested to what extent these post-cranial patterns match the expectations based on genetic or cranial diversity patterns.

Funding provided by the Mark Diamond Research Fund.

“Anthropologically, socially and politically sound”: American eugenics, anthropology, and the Galton Society

KEVIN F. KERN

History, The University of Akron

Scholars tend to regard the Galton Society primarily as the scholarly “Brain Trust” of the early 20th-century American Eugenics Movement. However, this assessment obscures its fundamentally anthropological outlook and effects. An analysis of thousands of documents from a number of archives reveals not only that the organization was founded and operated as a physical anthropological organization, but also that it had an immense—if largely unintended—influence on the larger field of anthropology.

While its members included famous (some might say infamous) eugenicists, others were among the foremost physical anthropologists and anatomists of the day, including Earnest Hooton, Adolf Schultz, and T. Wingate Todd. Furthermore, according to its charter the Society's purpose was “the promotion of study of racial anthropology, and more especially, the origin, migration, physical and mental characters, crossing and evolution of human races. . .”; and most of its scholarly programming focused on physical

anthropological topics. In its origins, membership, and practice, the group was consistent with an early 20th-century conception of a physical anthropology society.

The Galton Society also secured a large Rockefeller Foundation grant to study the physical anthropology of Australian Aborigines. Due to an unusual turn of circumstances the project instead helped launch some of the most important cultural anthropological classics of the early 20th century, including work by A.R. Radcliffe-Brown, Reo Fortune, and Raymond Firth. In a way that might have mortified some of its founders, the Galton Society had a significant and lasting impact on the cultural anthropological literature.

Saving face: the role of artificial intelligence in evaluating craniofacial variation for the treatment of orofacial dysfunction

MATTHEW J. KESTERKE¹, GANESH SANKARANARAYANAN², MACKENZIE SAUTTER¹, RAKTIM BHATTACHARYA³, RITESH BHATTACHARJEE¹, ANDREW READ-FULLER^{2,4} and LIKITH V. REDDY^{2,4}

¹Biomedical Sciences, Texas A&M College of Dentistry, ²Department of Surgery, Baylor University Medical Center, ³Department of Aerospace Engineering, Texas A&M University, ⁴Department of Oral and Maxillofacial Surgery, Texas A&M College of Dentistry

Every year over 11.4 million Americans experience orofacial dysfunction in various forms, ranging from myofascial pain to disorders associated with head and neck cancers, traumatic injury, and other associated conditions. The accurate and replicable evaluation of craniofacial variation is integral to the clinical treatment of such conditions. Anthropology has a long history of studying craniofacial variation, but advances made by the field seldom find their way into contemporary clinical procedures that rely heavily on the accurate quantification of variability. This results in unnecessary medical and financial burdens for patients and hospitals alike, and demands a new generation of tools that can accurately assess normal variation and diagnose orofacial dysfunction. Using data from cephalometrics, 3D photogrammetry, motion capture, bite force metrics, and CT imaging, we developed a novel deep-learning artificial intelligence (AI) system for automated assessment of the varied causes of orofacial dysfunction to incorporate a patient's unique craniofacial anatomy into clinical diagnosis. The tenets of functional craniofacial morphology provide the foundation for this novel approach of evaluating normal and abnormal variation. Presented here are three preliminary case studies using this AI system to quantify and evaluate shape changes in patients undergoing procedures from routine

ABSTRACTS

tooth extraction to complex orbital fracture repair. These studies provide the framework for ongoing clinical studies in the field of anthropoengineering and its application to clinical and surgical fields.

Funded by Texas A&M University Health Science Center X-Grant Development Award and the Texas A&M University College of Dentistry Department of Biomedical Sciences Development Award

Secular change in macromorphoscopic trait frequencies in modern European Americans

GRACE S. KILROY, B.S.¹ and SEAN D. TALLMAN, PH.D.^{1,2}

¹Department of Anatomy and Neurobiology, Boston University School of Medicine, ²Department of Anthropology, Boston University

Secular change has been documented in several studies focused on cranial and postcranial morphometrics and nonmetric traits. However, to date, few studies have addressed the potential of temporal changes occurring in the expression of cranial nonmetric traits utilized in ancestry estimation. This study examines whether secular change affects the expression of 23 cranial and mandibular nonmetric traits frequently used in ancestry estimation; with the age, sex, and birth year of each individual documented for data analysis. Data was collected for European American individuals from the Hamann-Todd Skeletal Collection (n=518) and from the William M. Bass Donated Skeletal Collection (n=602). Individuals were divided into birth-year cohorts as follows: Hamann-Todd Skeletal Collection: 1824-1849 (cohort 1), 1850-1874 (cohort 2), 1875-1899 (cohort 3), and 1900-1924 (cohort 4); William M. Bass Donated Skeletal Collection: 1900-1924 (cohort 4), 1925-1949 (cohort 5), and 1950-1987 (cohort 6). Pearson's chi-square analysis produced significant p-values (< 0.01) in 20 of the 23 traits between the six cohorts. Correspondence analysis was used to visually assess the relationship of trait expression between the cohorts. Factor maps produced by correspondence analysis show that cohorts 1 and 2 tend to cluster together while cohorts 5 and 6 also cluster together. The relationship of cohorts 3 and 4 to the other cohorts varies depending on the trait. This study demonstrates that significant secular change in nonmetric cranial and mandibular traits has occurred over the last two centuries with the greatest change appearing at the turn of the twentieth century.

A comparison of cercopithecoid molar outlines using elliptical Fourier analysis

ALEXANDER C. KIM and FRANK L. WILLIAMS
Department of Anthropology, Georgia State University

Cercopithecoid monkeys are adapted to various dietary niches, including folivory, durophagy and omnivory, represented by molar differences in *Colobus*, *Cercocebus* and *Papio*, respectively. Phylogenetic relationships suggest that *Cercocebus* should be similar to *Papio* in shape and both should be distinct from *Colobus*. A total of 24 first permanent maxillary molar epoxy resin dental casts, evenly divided between the three genera, were digitized and measured using a camera microscope system and measurement software to estimate buccolingual and mesiodistal lengths and occlusal area. Outlines of the occlusal surface were binarized through media editing software and input into SHAPE v.2.0 to calculate elliptical Fourier coefficients. The resulting amplitudes of the harmonics were subsequently reduced to principal components scores. *Papio* is substantially larger in all measurements, whereas area measurements fail to separate *Cercocebus* and *Colobus* due to their similar size. However, *Cercocebus* differs from *Colobus* by having mesiodistally longer molars, while *Colobus* molars are relatively wider given the pronounced bilophodonty resulting in a reduced constriction of the buccal and lingual extremes. The first ten principal components scores explain 94.2% of the variance. The first principal components axis (PC1) explains 31.4% of the variance and polarizes *Colobus* from the other two taxa, whereas PC2, accounting for 19.4% of the variation, imperfectly separates *Papio* from *Cercocebus*. PC3, which represents 15.8% of the variance, separates *Cercocebus* and *Colobus* but with some overlap. Results indicate body size, rather than dietary adaptations alone, separate the cercopithecoid genera, whereas shape differences reflect the closer phylogenetic relationship between *Papio* and *Cercocebus*.

Funding was provided by Fulbright-Belgium and the Commission for Educational Exchange between the USA, Belgium and Luxembourg.

Evaluating the effects of maternal prenatal stress on fetal growth patterns and birth outcomes in Soweto, South Africa

ANDREW W. KIM^{1,2}, RIHLAT S. MOHAMED², LUKHANYO NYATI², CHRISTOPHER W. KUZAWA^{1,3} and SHANE A. NORRIS²

¹Department of Anthropology, Northwestern University, ²MRC/Wits Developmental Pathways for Health Research Unit, School of Clinical Medicine, Faculty of Health Sciences, University of the Witwatersrand, ³Institute for Policy Research, Northwestern University

Recent evidence has implicated the role of maternal prenatal stress as a distinct risk factor for adverse birth outcomes such as low birth weight and preterm birth. Insights from life history theory conceptualize the gestational processes that lead to smaller birth size and shorter gestational periods based on two major considerations. Greater maternal prenatal stress is

understood to shift maternal energetic resources away from fetal development towards maternal investment in her survival and future reproductive success. Additionally, stronger signals of poor environmental quality are assumed to shift fetal developmental trajectories towards faster life history strategies, leading to faster growth *in utero* and smaller birth size. While this theoretical reasoning provides testable hypotheses for predicting infant birth outcomes, these proposed pathways have been largely understudied and only tested in Western, high-income contexts, where maternal-fetal demands and environmental exposures are likely to be quite distinct compared to conditions in low- and middle-income settings. This study evaluates the impacts of maternal psychosocial stress during gestation on fetal growth patterns and birth outcomes in the Soweto First Thousand Days study (n=603), based in Soweto, South Africa, a historically marginalized urban township of Johannesburg. Preliminary findings report that prenatal stress is significantly correlated with infant birth weight (p=0.016). Additionally, maternal social support during gestation is significantly correlated with maternal diastolic blood pressure (p=0.0373) and pulse (p=0.0432) during the third trimester. Findings from this study will elucidate the developmental influences of prenatal stress on fetal development and birth outcomes in an understudied, non-Western study population.

Testing the applicability of shape-based computational age-at-death estimation methods using pubic symphyseal surface scans of Asian Origin

JIEUN KIM¹, BRIDGET FB. ALGEE-HEWITT^{1,2,4}, DETELINA K. STOYANOVA^{1,3}, CRISTINA FIGUEROA-SOTO⁴ and DENNIS E. SLICE^{1,5}

¹Scientific Computing, Florida State University, ²Center for Comparative Studies in Race and Ethnicity, Stanford University, ³Mathematics and Statistics, University of North Carolina at Charlotte, ⁴Anthropology, University of Tennessee, ⁵Anthropology, University of Vienna

Recent computational age-at-death estimation methods developed using 3D laser scans of the pubic symphysis have been shown to provide robust estimates of age for documented White individuals. While validation testing has demonstrated reduced within-/between-observer error, improved objectivity, invariance to asymmetry, and equal applicability to female and males pubic symphyses, no study has explored the issue of population diversity. Concerns over broad applicability arise from the facts these methods were developed using a reference sample composed of modern American White males and that the same sample is used to produce the final age estimate in the associated software, *forAge*, which implements the shape algorithms and multiple regression analyses. There is, therefore, a need to determine their utility for peoples

ABSTRACTS

from different geographic regions. The present study seeks to assess the applicability of these computational methods for age estimation of Asians, focusing on a mixed-sex sample from Asia. Three shape-based measures, capturing the gradual flattening of the face and changes in the ventral margin of the symphysis, are used to build a series of regression models and the final age estimates are assessed for error and bias. Preliminary results from 69 scans suggest statistically significant relationships exist between ages-at-death and the three shape measures ($p < 0.05$). R-squared values indicate that 30-50% of the shape variation can be explained by age. RMSE values of 10-11 years are lower than those originally reported. These preliminary results suggest the utility of these methods for Asia and support further investigation for the rest of the region.

This project is supported by a National Institute of Justice grant (2015-DN-BX-K010) awarded to the senior authors, Slice and Algee-Hewitt.

Canine-root size variation and its influence on the pattern of sexual dimorphism in the facial skeleton of *Australopithecus afarensis*

WILLIAM H. KIMBEL¹, YOEL RAK^{1,2} and JULIE LAWRENCE¹

¹Institute of Human Origins, Arizona State University, ²Sackler Faculty of Medicine, Tel Aviv University

Reduced canines and low canine-size dimorphism are derived features shared by modern humans and the earliest hominins (*Ardipithecus*, *Australopithecus*). Accordingly, attributing sex to fossil canines not at the size extremes is risky. This uncertainty extends to the *Au. afarensis* sample of maxillary canines ($n=12$) from Hadar (3.4-3.0 Ma). Inspired by recent findings that temporal patterns of canine crown and root reduction are uncorrelated in early *Australopithecus*, we asked whether a measure incorporating both crown and root size revealed an underlying distribution of Hadar canine morphs. We used the ratio of maxillary mesiodistal canine-root length/maximum mesiodistal crown length devised by Jay Kelley (*AJPA*, 96:365, 1995) to investigate canine dimorphism.

Because the Hadar sample root-size CV is more than double the crown-size CV, the ratio more effectively separates the Hadar teeth than crown size alone. As for great ape samples of known sex composition, the ratio demarcates one subset with smaller crowns and relatively small roots and another with larger crowns and relatively large roots. These subsets comprise female and male canines, respectively, in the apes, and presumptively in the fossils. The index classifies several Hadar specimens as female whose sex is indeterminate on crown size alone. Hadar "males" and "females" average ~10% smaller

than the corresponding values for chimpanzees, but the difference between the sex categories in the fossil and chimpanzee samples is the same. These results substantiate suggestions that variation in canine-root size underlies a unique pattern of sex-based shape differences in the *Au. afarensis* midface independent of facial size.

Quantitative genetics of sexually-selected traits in male rhesus macaques

CLARE M. KIMOCK^{1,2}, CONSTANCE DUBUC¹ and JAMES P. HIGHAM^{1,2}

¹Anthropology, New York University, ²New York Consortium in Evolutionary Primatology

Sexual selection favors the evolution of traits that increase an animal's reproductive success. Sexually-selected traits are often perceived as being under strong directional selection, which increases the frequency of extreme trait values in a population. However, many sexually-selected male primate traits display considerable variation, and we have a limited understanding of how this variation is generated and maintained. Here, we explored the production and maintenance of variation in male sexually-selected traits in the free-ranging rhesus macaques of Cayo Santiago. We collected morphometric data from 103 adult male rhesus macaques and 21 of their closely related females during the 2015 trapping season. We measured canine size, body mass, crown-rump length, abdominal skinfold thickness, and testis volume. We employed long-term pedigree data to conduct heritability and selection analyses on these traits. Animal models revealed that canine size, body mass, crown-rump length, and skinfold thickness were moderately or highly heritable ($h^2 > 0.3$). Heritability estimates for testis volume were lower ($h^2 < 0.3$), indicating considerable developmental and environmental variance. Selection gradients showed no evidence for directional or stabilizing selection on any of the above traits, though we discovered some evidence for disruptive selection on testis volume. These results suggest that non-directional selection processes (such as balancing selection) may maintain variation in male traits in this population. Studies of other species are required to determine whether directional selection is a common mechanism acting on primate male traits.

This research was supported by The Leakey Foundation.

Famine and Tooth Decay: Assessing the Relationship between Famine and Caries Frequencies

ABIGAIL K. KINDLER¹ and BRITTANY S. WALTER²

¹Anthropology, University of Central Florida, ²Defense POW/MIA Accounting Agency Laboratory, Department of Defense

In bioarchaeology, famine has been associated with poor health, specifically elevated risk of infectious disease, skeletal lesions from malnutrition,

and reduced stature. Famine may also affect dental health, as individuals undergoing famine faced reduced access to protein-rich foods (e.g. animal meat, dairy, and fish), resulting in a higher proportion of carbohydrates in the diet and thus an elevated risk of cariogenesis. Given that individuals experiencing famine consumed a more cariogenic diet and that cariogenic foods are associated with tooth decay, it is expected that individuals experiencing famine would exhibit a higher frequency of caries compared to individuals not experiencing famine. This study investigates the effect of famine on dental health by comparing caries frequencies of adults interred in famine graves and attritional graves ($n=656$) from a medieval London cemetery (c. 1120-1539 CE). Preliminary chi-square results indicate caries frequencies are significantly higher for individuals interred in famine graves. However, results of hierarchical log-linear analysis indicate a significant three-way interaction among caries, sex, and grave type and between all lower-order interactions. These results suggest that though there is a higher frequency of individuals with caries in famine burials, this difference is likely an artifact of more females with caries compared to males, and a higher proportion of females in famine burials. This study demonstrates how sex differentials in mortality and pathology (e.g. famine mortality and caries frequencies) can obscure more complex patterns of health in skeletal assemblages, underscoring the importance of investigating other factors that may affect frequencies of potential famine-related pathologies.

Assessing the impact of duration versus bout frequency data in studying infant handling

ALLYSON G. KING, TIANNA C. RISSLING and PASCALE SICOTTE

Anthropology & Archaeology, University of Calgary

Research into infant handling has focused solely on frequency of events by nonmaternal handlers, often disregarding the impact of handling variation on infant development. The lengths of handling bouts vary, with nonmaternal handlers typically performing shorter duration handling behaviors than mothers. Yet, studies have not used duration data or investigated the relationship between bout frequency and duration data (except in the context of biological markets). This approach may obscure variation in the quality or amount of total handling time that infants receive from both maternal and nonmaternal handlers. Importantly, differences in the amount of handling received may influence the timing of developmental milestone acquisition. Here we examine (1) whether the duration and frequency of maternal and nonmaternal handling received by infants are associated and (2) how use of the two data types influences estimates

ABSTRACTS

of individual variation in infant handling. We collected and analyzed 112.98 hours of handling observations from 20 *Colobus vellerosus* infants (newborn–86 weeks) over 10 months at Boabeng-Fiema Monkey Sanctuary, Ghana. Duration and frequency data were associated ($T_b=0.52$, $p=0.002$) for nonmaternal handling, but were not for maternal handling ($T_b=0.17$, $p=0.28$). Frequency data was significantly more variable than duration data when comparing the amounts of maternal and nonmaternal handling infants received ($F(1)=71.15$, $p<0.001$). These findings suggest that duration data may be a more effective measure for accurately describing handling variance, and that future handling research consider the appropriateness of incorporating both duration data and maternal handling to more fully understand the role handling plays in infant development.

Funding for this research was provided by the Natural Sciences and Engineering Research Council of Canada.

Determining dominance rank order in wild female white-faced capuchins: a comparison of three methods

GILLIAN L. KING-BAILEY and KATHARINE M. JACK
Anthropology, Tulane University

Dominance hierarchies are a common feature of mammalian social groups and are important for reducing conflict and maintaining order within groups. Deciphering dominance relationships is crucial for furthering our understanding of the costs and benefits of group living.

Numerous methods are used for determining dominance hierarchies in non-human primates, however researchers rarely use more than one method. Such comparisons could help discern a hierarchy, clarify the variability inherent in dominance structures in some species, and determine which method is most accurate or appropriate.

We recorded dyadic dominance interactions between 23 wild adult female white-faced capuchin monkeys (*Cebus capucinus imitator*) in three social groups in the Sector Santa Rosa (SSR) of the Área de Conservación Guanacaste in Costa Rica. Using Landau's test of linearity and the directional consistency index we found that two of three groups meet criteria for linearity (the third group comes close). We applied three different methods for linearly ranking females within groups, David's scores, the I&SI method, and Elo-rating.

All three methods were strongly positively correlated ($p<0.01$). We conclude that all three methods are accurate for determining dominance hierarchies in female white-faced capuchins. Elo-rating has the additional benefit of tracking changes over time and may best be used when exploring dominance over shorter timescales, such as when comparing hormone levels, rather than averaging dominance across

an entire study period. Our study demonstrates that these three methodologies are comparable, can be used for differing purposes, and applying multiple methods can help elucidate variation within populations and species.

Funding was provided by The Nacey Maggioncalda Foundation, The American Philosophical Society, The International Primatological Society, Sigma Xi, The Leakey Foundation, and Tulane University

The role of social status in spinal degenerative joint disease outcomes: Evidence from Medieval Villamagna, Italy (800-1450 AD)

KATHERINE M. KINKOPF¹, SABRINA C. AGARWAL¹, CAROLINE GOODSON², FRANCESCA CANDILIO^{3,4}, ALFREDO COPPA⁵ and MAURO RUBINI^{6,7}

¹Department of Anthropology, University of California, Berkeley, ²Faculty of History, University of Cambridge King's College, ³Anthropological Service, Soprintendenza Archeologia, Belle Arti e Paesaggio per la città metropolitana di Cagliari e le province di Oristano e Sud Sardegna, ⁴Physical Anthropology Section, University of Pennsylvania Museum of Archaeology and Anthropology, ⁵Department of Environmental Biology, Sapienza University of Rome, ⁶Department of Archaeology, Foggia University, ⁷Anthropological Service, S.A.B.A.P.-LAZ

We present the results of a multifactorial analysis of degenerative spine disease (vertebral osteophytosis [VO] of the amphiarthrodial intervertebral joints and vertebral osteoarthritis [VOA] of the diarthrodial articular facet joints) at the Medieval site of Villamagna in Italy (c. 800-1450). Villamagna served as a monastic center, and later as a rural village center for a lay (non-religious) population who were agriculturalists. This skeletal assemblage includes individuals from three time periods: the Early (800-950), Central (1000-1300), and Late Medieval (1300-1450) with multiple high and low status groups, based on mortuary archaeology evidence.

Spinal degenerative joint disease is demonstrated to have a clear relationship with aging in clinical and bioarchaeological studies, and where the pathogenesis of vertebral osteophytosis has genetic and environmental components. Bioarchaeological research has demonstrated the efficacy of employing analyses of degenerative joint disease in the spine in order to understand gendered divisions of labor and how inequality intersects with activity.

Severity and occurrence of VO and VOA across four functional regions of the spinal column (cervical, upper thoracic, lower thoracic, lumbar) for $n=120$ individuals from the rural Medieval site of Villamagna show differential patterning dictated by age and sex for VO and by social status for VOA. Analyses of sex differences in VOA severity and occurrence show no difference

between sexes across or within time periods and statuses. The results of this study point to the importance of status in determining degenerative joint disease outcomes in Medieval populations.

Stahl Faculty Grant, Archaeological Research Facility, University of California Berkeley

Covariation among dental wear, craniofacial morphology, and pathologies in *Macaca fascicularis*

CLAIRE A. KIRCHHOFF¹, SIOBHÁN B. COOKE^{2,3}, CLAIRE E. TERHUNE⁴ and ASHLY N. ROMERO⁴

¹Biomedical Sciences, Marquette University, ²Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine, ³New York Consortium in Evolutionary Primatology Morphometrics Group, ⁴Department of Anthropology, University of Arkansas

Dental and craniofacial morphologies are a frequent focus of analysis in comparative studies, but have been infrequently linked to one another and/or to pathologies. Thus, how these different components of the masticatory apparatus may influence one another, both in non-pathological and pathological conditions, is unclear. The goal of this study is to evaluate how these disparate lines of evidence covary; we use *Macaca fascicularis* as a test case for integrating these datasets.

For a sample of adult *M. fascicularis* (49 females, 60 males), we collected surface scans of the cranium and mandible and high-resolution scans of the maxillary and mandibular dentition. We evaluated specimens for temporomandibular joint (TMJ) osteoarthritis (OA), antemortem tooth loss (AMTL), and other trauma and pathologies using standard criteria. Dental relief and a measure of wear asymmetry was calculated for upper and lower first and second molars. The degree of fluctuating asymmetry in the cranium was also quantified.

Results indicate that TMJ shape varies significantly in relation to TMJOA, pulp cavity exposure, and periapical abscesses. No significant relationships were found between craniofacial shape and pathology. Further, we observed no significant correlations between any pathology and dental relief or between craniofacial/TMJ morphology and dental relief. There was a significant positive correlation between wear asymmetry and the presence of teeth with exposed pulp cavities. Lower levels of fluctuating asymmetry were observed in individuals with carious lesions or periodontal disease. Further analyses will focus on how these pathologies vary across species and in relation to dietary patterns.

NSF BCS-1551722 (CAK), NSF BCS-1551669 (SBC), NSF BCS-15511766 (CET)

ABSTRACTS

Patterns of mobility in the early stage of urbanization of Viking Age Sigtuna, Sweden

ANNA S.E. KJELLSTROM

Osteoarchaeological Research Laboratory,
Department of Archaeology and Classical studies,
Stockholm University

In the 10th century, the late Viking age - early Middle Age town, Sigtuna, was founded. The town contrasted with preceding hubs in the region, demonstrating a structured town plan with royal and religious administrations. The urbanization process, as read through the inhabitants, has been investigated in several studies during recent years. In this overview, a holistic approach is taken, combining results from these previous surveys based on genomic-, isotopic- and health data, from individuals buried in Sigtuna. The homogenous character of most graves is contrasted to the complexity demonstrated by aDNA and isotope analyses. While the dietary patterns overall suggest cultural similarities involving only a small level of social stratification, there are also indications of long-distance mobility, disparate ancestry, and, probably, second generation immigrants. Additionally, gender-related activities have been shown in the bioarchaeological data. The cosmopolitan character of the town may well have had an impact on the citizens since there is a dietary difference ($\delta^{13}C$ - and $\delta^{15}N$ -values) between people buried in Sigtuna and those buried at the preceding Viking center Birka, and at contemporary farmstead cemeteries. Collectively, the data demonstrate the social networks and influx of ideas in the forming of the urban Sigtuna society.

This study is based on the work done within two projects funded by The Swedish Research Council (VR 2013-04959 & RJ M13 0904:1 and VR 2016-02532).

Assessing the influence of Hox11 genes on calcaneal trabecular bone formation

KELSEY M. KJOSNESS¹, TIMOTHY M. RYAN² and PHILIP L. RENO¹

¹Department of Bio-Medical Sciences, Philadelphia College of Osteopathic Medicine, ²Department of Anthropology, Pennsylvania State University

The calcaneus and pisiform have substantial functional significance to human and non-human primate locomotion. While the pisiform and calcaneus are developmentally paralogous structures, these bones have undergone drastically different morphological changes during human evolution: the pisiform has lost its growth plate and experienced truncation since divergence from *Australopithecus*, while the calcaneus has ballooned and increased the proportion of trabecular to cortical bone compared to apes. Hox11 genes are known to influence wrist and ankle development and *Hoxa11* and *Hoxd11* are known to be expressed around both the pisiform and calcaneus. Mutations to *Hoxa11* or *Hoxd11*

produce dosage dependent changes in pisiform morphology, including truncation and disorganization of the pisiform growth plate, while mice with both genes knocked out lack a calcaneus. We test the hypothesis that alterations to *Hoxa11* and *Hoxd11* genes impact the internal trabecular structure within the calcaneus in a dosage-dependent manner. MicroCT scans indicate that calcanei of mice with mutations to three of the four *Hoxa11* and *Hoxd11* alleles are shorter than wild type, however no discernable differences were found in trabecular bone volume, thickness, connectivity, or orientation across genotypes. We found trabecular bone volume in male mice to be higher than in female mice, possibly making genotype differences difficult to determine. These results suggest that Hox11 patterning may impact calcaneal ossification and overall size, but appears to have little impact on trabecular formation. Further work is needed to parse the roles that pattern formation and mechanical responses during growth have on trabecular bone morphology.

This work was funded by the National Science Foundation NSF BCS-1540418, NSF IOS-1656315 & NSF BCS-1638812

A Re-Evaluation of the Sinodont and Sundadont Dental Complexes for the Peopling of the Japanese Archipelago

SHANNON A. KLAINER and GEORGE R. SCOTT
Anthropology, University of Nevada, Reno

The peopling of Japan revolves primarily around two principal models: (1) the longstanding continuity model wherein the Jomon are ancestral to the modern Japanese population; and (2) the dual structure model wherein the modern Japanese population is descended from Neolithic East Asian farmers and the Ainu are descended from the Jomon. The Sinodont and Sundadont dental complexes defined by C.G. Turner II can be used to assess the relationships between East and Southeast Asians, the Jomon, the Ainu, and modern Japanese populations. To address models of Japanese origins, 35 groups from Asia and the Pacific (Jomon, Ainu, East Asia, Southeast Asia, Polynesia, Micronesia, Australia, and New Guinea) were analyzed for 23 crown and root traits. Trait frequencies were analyzed using Bray-Curtis dissimilarity statistics, in association with cluster analysis. Findings show the Jomon and Ainu cluster tightly together and are next closest to a cluster that contains samples from East Asia (Japan, An-yang, Urga) and Southeast Asia (Taiwan.) The isolation of Australo-Melanesia and New Guinea from Asian clusters does not support the hypothesis that Sundadonty was a product of gene flow between Sinodonts and Australo-Melanesians. The pattern suggests that the Jomon and Ainu are related ultimately to the Sundadont populations of Southeast Asia

whereas the modern Japanese population was derived from North and East Asian Sinodont populations, albeit with some evidence for Jomon admixture.

Secular Change in Popular Morphological Traits of the Skull and Pelvis

ALEXANDRA R. KLALES and HOLLY LONG

Forensic Anthropology Program, Department of Sociology and Anthropology, Washburn University

In order to examine secular change in morphological skull and pelvic traits frequently used for sex estimation, score data of the five Walker (2008) traits (nuchal crest-NC, mastoid process-MP, glabella-G, supra-orbital margin-SO, mental eminence-ME) and the three Kales et al. (2012) traits (ventral arc-VA, subpubic contour-SPC, medial aspect of the ischio-pubic ramus-MA) were collected from 1,734 individuals of known sex and ancestry from multiple skeletal collections. Temporal variation was assessed by comparing trait score frequencies between contemporary and historic samples using the Mann-Whitney U test. Significant differences between the modern and historic samples were found for the G ($p=0.012$) and left SPC ($p=0.039$) in black females and for G ($p=0.008$), left MP ($p=0.012$), and the SPC ($p=0.037$ left; $p=0.002$ right) in black males. In all cases, the contemporary black sample had significantly lower (i.e., more gracile) scores. In whites, significant differences between temporal periods were found for the MP ($p=0.000$ left and right), G ($p=0.000$), and NC ($p=0.03$) in females and the NC ($p=0.000$) in males. All three traits of the pelvis were significantly different at the $p>0.05$ level for both white males and females. All traits exhibited significantly lower scores (i.e., more gracile) in the modern sample except for the NC which has more robust/higher scores in the modern white samples. Overall there are patterned changes occurring in these skull and pelvic traits over time which can impact the utility of these traits for accurate sex estimation in bioarchaeological and forensic contexts.

This research was funded by National Institute of Justice Grant 2015- DN-BX-K014. Opinions expressed herein do not necessarily represent the official position or policies of the U.S. DOJ or NIJ.

In search of the missing, the overlooked, and the invisible: paleodemographic conundrums, sexuality and gender, and epigenetics in Lambayeque bioarchaeology

HAAGEN D. KLAUS

Sociology & Anthropology, George Mason University

Over the last few decades, conceptual, theoretical, epistemic, and philosophical advances have woven their way throughout bioarchaeology

ABSTRACTS

– including the growing awareness that much that remains unseen via bioarchaeological approaches to the human past. Such issues speak to the vagaries of preservation, problematic sampling design, and investigator bias. To these ends, three contextualized case studies are considered from the Lambayeque region of northern Peru.

First, the vexing paleodemographic issue of “missing children” is examined in the pre-Hispanic record. Despite representative sampling and modern excavation techniques, subadults under the age of 15 are starkly underrepresented. This is not a methodological shortcoming, but an encounter with ancient cultural filters involving starkly different concepts of personhood involving children in the pre-Hispanic Andes – and the perception that children were not “human.” Second, gender and sexuality has been long and egregiously neglected in Andean bioarchaeology. In particular, where are the people of diverse genders or non-heteronormative sexualities in the Andean bioarchaeological record? Here, burial patterns and skeletal data suggest that such phenomenon may have been constrained by dualistic, binary Andean cosmologies and gender roles – as well as highlighting decades of implicit and evidence-blinding investigator biases. Third, the rise of epigenetics has shown there is a whole new world of previously missing or otherwise invisible biocultural phenomena awaiting study, especially regarding sociopolitical marginalization. An overview of our initial forays into life history and phenotypic plasticity approaches is revealing, but also illustrates why authentic epigenetic perspectives still remain out of reach.

This work has been supported since 2005 by the Wenner-Gren Foundation, the National Science Foundation, the National Geographic Society, and George Mason University.

Functional correlates of jaw shape diversity in platyrrhine sclerocarpic harvesters

ZACHARY S. KLUKKERT

Doctoral Program in Anthropology, City University of New York Graduate Center, New York Consortium in Evolutionary Primatology (NYCEP)

Jaw shape is routinely used in discussions of relationships among living and extinct platyrrhines, though few efforts have aimed to parse the phylogenetic and functional signals that affect the variability in this morphology. Among the living taxa, the cebid *Aotus* and the pitheciids exhibit similar mandible shapes related to a common specialization, principally-focused on the ingestion of hard-skinned fruits. This study tests for functional correlates of the mandibular morphology that distinguishes the pitheciids from the predominately-frugivorous, and similarly-sized cebids, to assess the contribution of mechanical signals to the morphology that is also used in phylogenetic reconstructions

of the platyrrhine radiation more generally. 3D geometric morphometrics and principal components analysis is used to identify the leading sources of the variability in the shapes of 145 landmarked mandibles of pitheciids (*Cacajao*, *Chiropotes*, *Pithecia*, *Callicebus*) and cebids (*Sapajus*, *Cebus*, *Aotus*, *Saimiri*). Biomechanically-significant measurements of the mandible were derived from the landmark coordinates and regressed against the shape components to test for correspondence between the phylogenetic and functional signals in the shapes of the jaws. Results link the variability in this sample with jaw function and distinguish the studied taxa in terms of feeding strategies, not phylogeny. These results are consistent with a mechanical explanation for the diversity in jaw shape whereby *Aotus* and the pitheciids are unified as sclerocarpic harvesters, i.e., a group that emphasizes anterior-tooth loading, while the jaws of pitheciids and *Sapajus* overlap in values associated with support for eccentric loading during mastication, e.g., cracking and masticating seeds.

This work was supported by the National Science Foundation, NSF 0966166 (NYCEP IGERT)

Repeatability of female odor preferences in mate choice

LESLIE A. KNAPP

Anthropology, University of Utah

Human Leukocyte Antigens (HLA) play a key role in immune response and regulation. Genes encoding HLA are the most polymorphic loci in the human genome. While parasite and pathogen resistance may be a driving force behind HLA polymorphism, HLA diversity may be important for kin recognition and mate choice since only related individuals share HLA genotypes. Negative assortative mating for HLA type has been observed in some human populations. It is hypothesized that HLA-based odor preferences mediate this mating choice. Although research has shown female preference for odors from HLA-dissimilar males, our understanding of odor preference in mate choice remains limited. This study investigates HLA-based odor preference and evaluates repeatability of odor preferences. Thirty-one women were asked to smell pairs of T-shirts, worn by five different men, and identify the most “pleasant” odor. One hundred T-shirt pairs were presented to each woman over two sessions under identical conditions. For 17 women (Group 1), a male researcher presented T-shirt pairs. A female presented T-shirts to the other 14 (Group 2). All participants were genotyped for HLA Class I and Class II loci. Overall, repeatability of odor preference was highly significant ($p < 0.001$) but not related to HLA. Twenty-one out of 31 women showed significant repeatability of odor preference ($p < 0.05$). In Group 2, 13 of 14 women exhibited repeated odor preferences. However, only half the women

showed consistent preferences with a male researcher, suggesting that odor preference can vary in the presence of one (or more) additional competing males.

Disease ecology and the relationship of human- and nonhuman primate-infecting *Treponema pallidum*

SASCHA KNAUF¹ and CHRISTIAN ROOS^{2,3}

¹Infection Biology Unit, German Primate Center, ²Gene Bank of Primates, German Primate Center, ³Primate Genetics Laboratory, German Primate Center

In contrast to Asian macaques, *Treponema pallidum* (TP) infection is widespread in African nonhuman primates (NHPs). In humans, TP causes syphilis (subsp. *pallidum*), bejel (subsp. *endemicum*), and yaws (subsp. *pertenue*; TPE). One of the first confirmed reports of a TP infected baboon (*Papio papio*) came from Guinea in West Africa in the 1960s. Today, the associated Fribourg-Blanc strain represents the first fully sequenced TP genome of NHP origin. Its genetic and functional similarity to human yaws-causing strains has led to its proposed classification into the subsp. *pertenue*. This finding supported our *pertenue*-like classification of earlier and current studies on TP in Tanzanian NHPs and remains supported by a growing number of published whole genome sequences of strains of NHP origin from West and East Africa. TPE strains of NHP origin fall paraphyletic with human yaws-causing strains and the existence of TPE in a number of different NHP species indicates that interspecies transmission must have occurred at least at some evolutionary stage. While the close genetic relationship of TPE of NHP and human origin does not provide evidence for ongoing transmission across the different primate taxa, our most recent data on the diversity of strains in a larger number of Tanzanian monkeys shows that interspecies transmission is likely ongoing but represents a sporadic event. TP remains an elusive pathogen and we are at the beginning of understanding how this pathogen has co-evolved with its primate host and whether or not human and NHP infecting strains are (still) ecologically connected.

Recent work on NHP and human infecting TPE strains was funded by the German Research Foundation (DFG): KN1097/3-1 and KN1097/4-1 (to SK) and RO3055/2-1 (to CR).

Fecal isotopes as indicators of weaning and diet in wild Bornean orangutans

CHERYL D. KNOTT¹, BROOKE CROWLEY², MICHELLE BROWN³ and TRI WAHYU SUSANTO⁴

¹Anthropology, Boston University, ²Geology and Anthropology, University of Cincinnati, ³Anthropology, University of California, Santa Barbara, ⁴Biology, National University of Indonesia

ABSTRACTS

Orangutans have a 7.6 year average inter-birth interval, the longest of any mammal. Suckling occurs throughout that interval, until the birth of the next offspring, but it is unclear how important milk consumption is during that period, as we cannot assess the actual intake amount. Measurement of stable carbon isotope ratios ($d^{13}C$), stable nitrogen isotope ratios ($d^{15}N$) and nitrogen content of feces (%N) provide evidence of the transition between breast milk to solid food. Here we present pilot data on these isotopic ratios from matched fecal samples of mothers and offspring ($n=43$), collected from wild orangutans in Gunung Palung National Park, Borneo, Indonesia. We found that the youngest infant (2.3 yrs) had the highest $d^{15}N$ values overall, indicative of a higher percentage of animal products (milk) in the diet. Older juveniles (5.8 yrs) did not consistently show higher $d^{15}N$ than their mothers. This may indicate variation in suckling frequency or the amount of breast milk consumed per suckling session. Adolescents (10-13 yrs) showed significantly (GLMM, $p < 0.007$) lower $d^{15}N$ than samples taken from the same day on their mothers. This is surprising given that they were eating similar diets. We thus compare the isotopic signature of the plants consumed to examine the sources of this variation. We conclude that analysis of fecal samples collected from wild orangutans can be used to assess the relative importance of breast milk in the diet, but caution that isotopic excretion may also be effected by differences in the isotopic content of the diet.

NSF (BCS-1638823, BCS-0936199); National Geographic; USFish/Wildlife (F15AP00812, F13AP00920, 96200-0-G249, 96200-9-G110); Leakey; Disney Wildlife Conservation; Wenner-Gren; Nacey-Maggioncalda; Orangutan Conservancy; Conservation-Food-Health; Woodland Park Zoo; Holloman Price; AZA; Ocean Park Conservation; USAID; Arcus

A Method for Identifying Source Populations in Genetic Ancestry Studies

ANTHONY J. KOEHL and JEFFREY C. LONG
Anthropology, University of New Mexico

We outline a novel approach to identify the sources of ancestry of a contemporary mixed population when the sources of ancestry are uncertain. In this approach, we propose multiple models that differ in the number of source populations, and use proxy samples to represent these sources. In addition to supervising members of proxy samples to their respective sources, we place constraints on which sources can contribute to individuals with unknown mixed ancestry. Thus, for $K > 2$ potential sources of ancestry, unknown individuals can be constrained to have ancestry from $2 \leq K^* \leq K$ of the potential sources. We use the Akaike Information Criterion (AIC) to rank the performance of competing models. A novel feature of our method is that our constrained

models all estimate the same number of allele frequencies and thus differ only in the number of ancestry coefficients estimated. This increases the potential to differentiate the performance of different models.

We apply our approach to the Cape Mixed Ancestry (CMA) population from South Africa. There are three previously published studies of this population. The earlier studies differ substantially in terms of postulated sources of ancestry and their final results. In total, these studies proposed 18 samples as proxies for four ancestral sources. Using microsatellite data, we show that 10 of these proxy samples are unlikely to have contributed ancestry to the CMA population. However, from the eight remaining ancestry proxies, we are able to demonstrate that they represent six independent ethno-geographic sources of ancestry.

Risk of injury in two Asian colobines

ANDREAS KOENIG^{1,2}, JACOB A. FEDER², AMY LU^{1,2} and CAROLA BORRIES^{1,2}

¹Department of Anthropology, Stony Brook University SUNY, ²Interdepartmental Doctoral Program in Anthropological Sciences, Stony Brook University SUNY

Escalated aggression, while rare, is presumed to result from competition over highly-prized resources and expected to occur only if benefits outweigh costs. However, the context of escalation is often unknown, and the causes of variation across species are unclear. Here, we investigated the occurrence of injuries in two Asian colobines (*Semnopithecus schistaceus*, Nepal gray langurs, NGL and *Trachypithecus phayrei crepusculus*, Phayre's leaf monkeys, PLM) to highlight the impact of age, dispersal, and reproduction on injury risk. We used generalized linear mixed models to analyze the monthly occurrence of injury based on 6 years (NGL, 84 individuals) and 7 years of data (PLM, 87 individuals). In both species, subadults were at the highest risk of injury, suggesting that they face challenges as they compete for group membership or establish rank or both. This was especially true for the dispersing sex (males in NGLs, females in PLMs). In NGLs males received more injuries than females, but we did not find a sex difference in PLMs. This may again relate to the different dispersal patterns, as PLM females compete not only over food but also over group membership. In NGLs, who have a shorter reproductive season than PLMs, males received more injuries during the mating season, indicating strong competition for mates. Females experienced more injury prior to conception, suggesting feeding competition to improve energy balance to resume cycling. Our

results indicate that escalated aggression was most likely linked to high-stakes gains related to establishing group membership, achieving high rank, and facilitating reproduction.

Fieldwork supported by Alexander von Humboldt-Foundation, American Society of Primatologists, Ernst-Stewner-Foundation, German Academic Exchange Service, German Research Foundation, Leakey Foundation, National Science Foundation, Society for Technical Cooperation, Wenner-Gren Foundation.

Stature estimation as allometry

LYLE W. KONIGSBERG and SUSAN R. FRANKENBERG

Anthropology, University of Illinois at Urbana-Champaign

The statistical problem of extrapolating stature estimates for the very tall and very short has a long history. Pearson (1899) suggested using quintic equations and provided (seldom-used) charts for his equations. We present a simpler approach that treats stature estimation as a problem in allometry, following Konigsberg et al. (1989) but focusing specifically on bivariate allometry. This approach regresses organ size (bone lengths) onto body size (stature) and then solves the regression equation for stature. To find the full posterior distribution of stature we use a simple approximate method from Hunter and Lamboy (1981) for small sample size reference collections and an even simpler method from Konigsberg et al. (1989) for larger sample size collections. Both methods can be applied using summary statistics, so it is not necessary to have access to the raw data.

For reference sample information we use summary statistics on long bone lengths and stature from Konigsberg and Meadows Jantz (2018), metacarpal lengths and stature from Musgrave and Harjena (1978), and metatarsal lengths and stature from Bidmos (2008). We apply these summary statistics to find the full posterior distributions of stature from individual bones of a female Aka individual, of Patrick Cotter (one of the "Irish Giants"), *A. sediba*, and *H. naledi* and *floresiensis*. The modern humans' stature estimates from individual bones are consistent with and near the known statures for individuals. The fossil stature estimates confirm previous statements about allometric departures.

New methods for quantifying enthesal shape and adaptation to functional loading

NICOLAI KONOW¹, JULIE M. WINCHESTER², DOUG M. BOYER² and IAN J. WALLACE³

¹Biological Sciences, University of Massachusetts Lowell, ²Evolutionary Anthropology, Duke University, ³Human Evolutionary Biology, Harvard University

ABSTRACTS

To gain insight into the behavioral patterns of ancient humans, anthropologists analyze the surface morphology of entheses (muscle/tendon attachment sites) on fossil long bones to infer adaptation to functional loading during life. Such analyses have become increasingly common due to the greater availability of 3D scanning technology, and a variety of methods of quantifying enthesal shape from scan data have been proposed. Despite major advances in the analysis of enthesal morphology, however, the lack of consistency in shape quantification methods has made it difficult to interpret and compare the results of different studies. In an attempt to provide a potential solution to this problem, here we present methods of quantifying topographic shape from 3D meshes representing entheses. In particular, we discuss three topographic metrics: Dirichlet normal energy (describing surface curvature), relief index (describing surface relief), and orientation patch count rotated (describing surface complexity). Together, these metrics offer a comprehensive assessment of surface morphology that encompasses nearly all variables of interest in analyses of enthesal shape. These metrics can be computed using MorphoTester, a relatively automated, free, open-source application for quantifying and visualizing surface topography from 3D meshes. We illustrate the promise of topographic methods for accurately characterizing enthesal shape and adaptation to functional loading using the femora of turkeys that were experimentally exercised on a treadmill. Ultimately, we propose that more widespread adoption of topographic methods (and software like MorphoTester) in analyses of enthesal surface morphology would greatly enhance comparability and thus interpretability of different studies.

Supported by NSF BCS1341120 and NIH AR055295.

Humans have relatively larger lumbar vertebrae than African apes

NIINA KORPINEN, MARKKU NISKANEN, JUHO-ANTTI JUNNO and TIINA VÄRE
Archaeology, University of Oulu

Back problems are a major, worldwide health problem of modern day. Previous studies have indicated an association between the size and shape of the vertebrae and vulnerability to back diseases. In this study, we aimed to clarify how the dimensions of lumbar spine differ between humans and African apes. We hypothesized that bipedal humans should have larger vertebral bodies compared to quadrupedal apes. To conduct this study, we had sample of 119 individuals from the Robert J. Terry Anatomical skeletal collections and 66 specimens of *Pan* and *Gorilla* from Powell-Cotton Museum collections (which included 34 *Pan troglodytes* and 32 *Gorilla gorilla*). The measurements collected included anterior-posterior depth, mediolateral minimum

and maximum width and anterior and posterior heights of L4 in humans and L3/L2 in apes. In addition, vertebral cross-sectional area and volume were calculated. Since apes are more variable in number of the lumbar vertebrae, we also tested the connection between the dimensions of L3/L2 lumbar segments. Values were analyzed with IBM SPSS Statistics v.24 using ANOVA analysis. We found no statistically significant difference in L2/L3 dimensions between specimens with 3 or 4 lumbar vertebrae. Our results indicated that in relation to weight humans did have overall largest vertebrae. However, we did not find clear dimensional differences between humans and *Pan*, especially in width. The expected divide between apes and humans also did not merge, instead it seemed there was divide between humans/*Pan* and *Gorilla*.

This research was funded by Finnish Cultural Foundation

The Life History of Hunting Skill: Cross-cultural and Individual Variation

JEREMY KOSTER^{1,2} and RICHARD MCELREATH²
¹Anthropology, University of Cincinnati, ²Human Behavior, Ecology, and Culture, Max Planck Institute for Evolutionary Anthropology

Human adaptation depends upon the integration of slow life history, complex production skills, and extensive sociality. Anthropologists have hypothesized that unique life history traits of humans permit the gradual mastery of highly complex foraging strategies, such as hunting, as part of a multi-generational adaptation of food production and sharing. In turn, refining and testing models of the evolution of human life history and cultural learning benefits from increasingly accurate measurement of knowledge, skills, and rates of production with age. We pursue this goal by inferring individual rates of skill gain and loss from empirical data on subsistence hunting contributed by researchers from their respective field sites. The cross-cultural database includes 23,000 hunting records generated by 1,800 individuals at 40 locations. The statistical model provides an improved picture of ages of peak productivity as well as variation within and between ages. The data reveal an average age of peak productivity around 30 years of age, but with substantial heterogeneity among individuals and across study sites. Heterogeneity among individuals depends more upon variation in rates of decline with age than variation in rates of increase, implying that older hunters exhibit more heterogeneity in skill than younger hunters. This analysis sharpens questions about the co-evolution of human life history and cultural adaptation, clarifying needs for future empirical research. It

also demonstrates the potential for new statistical algorithms to allow for successfully marrying substantive models of human behavior with data collected in the field.

National Science Foundation (#1534548)

Application of the 3D quantitative shape analysis method for age assessment from os coxae in European samples

ANEZKA KOTEROVA¹, JANA VELEMINSKA¹, EUGÉNIA CUNHA² and JAROSLAV BRUZEK¹

¹Department of Anthropology and Human Genetics, Charles University, ²Department of Life Sciences, University of Coimbra

An accurate and reliable age-at-death estimation is of paramount importance in establishing a biological profile. Advanced technologies have shifted the direction of methodological development towards the more objective assessment of skeletal senescence markers. Stoyanova et al. (2017) proposed a computational method quantifying the pubic symphyseal surface of the os coxae of Euro-American adult males. In the present contribution, we tested the performance of this method in European populations. Together four different samples (n=96, aged from 20 – 83 years) from three populations (two Portuguese collections, Swiss and Crete collections) were used. The tested quantitative method is based on five regression models of which two were multivariate and three univariate. When we used the whole sample of individuals without an age limitation, the values of RMSE were unacceptably high (over 20 years), which is in compliance with the results of previous studies. However, the tested method in a subsample limited to individuals under 40 years outperformed the results of the original study. The best results were achieved with the thin plate spline algorithm (root mean square error – 5.93 years and inaccuracy – 4.47 years). Our results did not confirm that multivariate models contribute to better age estimation. The quantitative approach has contributed to more objective age evaluation but the skeletal age indicators have to be used with regard to the biological possibilities expressed in the aging process.

This research has been supported by the research grant GAUK No. 642218.

Mixed support for the patterning cascade model in bears: Implications for understanding the evolution and development of hominoid molar morphology

EMMA A. KOZITZKY^{1,2} and SHARA E. BAILEY^{1,3}

¹Center for the Study of Human Origins, Department of Anthropology, New York University, ²New York Consortium in Evolutionary Primatology, ³Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology

ABSTRACTS

The patterning cascade model (PCM) postulates that the spacing and timing of signaling centers in a growing tooth determine the number and size of cusps in the completed crown. Under the PCM, accessory molar cusps sometimes used to assess hominoid phylogeny may actually be homoplastic. The PCM was originally conceived to explain variation in the mesiodistally-oriented, conical molar cusps of piscivorous seals, and there is only partial support for the PCM's ability to explain variation in accessory cusps among hominoids. Deviations from PCM predictions may be related to differences in tooth shape, cusp height and/or phylogenetic distance from the model mammal. To better understand how tooth shape and phylogeny relate to the PCM, we tested model predictions in Carnivora taxa with buccolingually-expanded, low-cusped lower first molars: *Ursus arctos* and *U. americanus*. Binary logistic regression and Kendall's τ correlation coefficients for the pooled *Ursus* sample show that the presence of an accessory cusp between the metaconid and entoconid is significantly predicted by decreasing relative metaconid-entoconid distance, in agreement with the PCM. However, the presence of an accessory cusp between the hypoconid and entoconid is not correlated with relative hypoconid-entoconid distance. We suspect that deviations from the PCM like those found in hominoids and bears may be related to functional changes in molar shape, specifically the orientation of low cusps on a wide, basined molar. The PCM should be tested in a broader sample of mammals with diverse molar shapes to further elucidate the relationships among function, phylogeny, and development.

Arboreal Positional Behavior in Humans, Chimpanzees, and Gorillas

ELAINE E. KOZMA^{1,2,3}, HERMAN PONTZER³, CRICKETTE SANZ^{4,5} and DAVID MORGAN^{5,6}

¹Anthropology, City University of New York Graduate Center, ²New York Consortium in Evolutionary Primatology, NYCEP, ³Evolutionary Anthropology, Duke University, ⁴Anthropology, Washington University in St-Louis, ⁵Goualougo Triangle Ape Project, GTAP, ⁶Lester E Fisher Center for the Study and Conservation of Apes, Lincoln Park Zoo

Many human populations regularly climb trees, but their arboreal positional behavior is not well studied. Adaptations to terrestrial bipedalism are generally thought to limit arboreal behavior in humans and earlier hominins as compared to living apes. Here, we tested whether and how humans and apes differ in arboreal ecology, using a comparative data set of human positional behavior in trees compared with sympatric chimpanzees and gorillas in northern Republic of Congo (IACUC and IRB approved). Data were collected during full day follows. At two-minute intervals we recorded a subject's position,

height, support diameter, and location within the tree. The sample consisted of *P. troglodytes troglodytes* (22 individuals; Goualougo Triangle research site), *G. gorilla gorilla* (19 individuals; Goualougo Triangle and Mondika research sites), and indigenous Mbendjele men (17 individuals; Makao village). Among key results we find that: 1) In trees, humans spend significantly more time standing bipedally than apes; 2) humans spend significantly more time in the core region near the main trunk (as opposed to the peripheral branches) than apes; and 3) minimum support diameter is not significantly different in humans and other apes. These data suggest humans use trees differently than apes, but are nonetheless adept in an arboreal environment and capable of foraging in the canopy. We discuss the implications of these results for understanding the ecology and evolution of living hominoids and fossil hominins.

This work was partially funded by the Leakey Foundation (general grant) and the National Science Foundation (1732194 and 1646736)

Sex Differences in Orangutan Long Bone Skeletal Strength in Relation to Flanging Status

ALEXANDRA E. KRALICK
Anthropology, University of Pennsylvania

Bimaturism is rare among primates and most pronounced in adult male orangutans, who are either flanged with secondary sexual characteristics or unflanged with arrested secondary sexual characteristic development. Yet, the effect of developmental arrest on the orangutan skeleton remains relatively unexplored. Initial work with collections from the Smithsonian National Museum of Natural History (NMNH) in 2018 indicated that the timing between dental and skeletal development can be disjointed and differs between females, unflanged males, and flanged males. To further evaluate these findings, data from a small group of orangutans (64 individuals, including 36 adults of known sex) at the Smithsonian NMNH, the Harvard Museum of Comparative Zoology (MCZ) and Museum für Naturkunde (MfN) in Germany were collected. The humeri and femora of these orangutans were measured for length, midshaft diameter and periosteal circumference. Despite adult female orangutans climbing more often than adult males, females were similar to males in the ratio between humeral circumference-to-length compared to femoral circumference-to-length. Females and unflanged males also showed a positive correlation between long bone length and circumference, while the flanged male relationship between these variables was more complex. Flanged male bone lengths and circumferences were larger than females, while unflanged males had circumferences smaller than flanged males. These observations suggested that adult

unflanged male orangutan bone strength could be affected by a delayed puberty mechanism of bone growth. Overall, these new data will contribute to our understanding of the effect that differing sexual strategies have on the orangutan skeleton.

Urban-rural differences in respiratory tract infections in medieval and early modern Polish subadult samples

MARTA KRENZ-NIEDBAŁA and SYLWIA ŁUKASIK
Department of Human Evolutionary Biology, Faculty of Biology, Adam Mickiewicz University in Poznań

We tested a hypothesis that the development of urban centers in medieval Poland characterized by overcrowding and poor sanitary conditions resulted in higher rates of respiratory tract infections (RTI) in urban than rural children. RTI in skeletal remains can be detected through observing inflammatory new bone formation in the maxillary sinuses, on the ear bones, and on the visceral surfaces of the ribs. We examined the skeletal indicators of RTI in maxillary sinuses, auditory ossicles, and ribs in subadults (<20 years of age) from two sites: early urban Cedynia dated to 10th-14th AD, and rural Staboszewo dated to 14th-17th AD. Rib lesions were observed additionally in subadult remains from a cemetery in Łekno dated to 13th-16th AD, which served for rural dwellers. The total sample consisted of 309 skeletons. The skeletal remains with severe taphonomic changes were excluded from the analysis. We found more individuals affected by RTI in the urban, than the rural sites: 42.2.4% vs 25.9% for ear bone changes, 18.0% vs 7.1% for maxillary sinusitis, and 28.8% vs 16.5% for rib lesions, respectively, while the results were statistically significant for the lesions of auditory ossicles (FET, $p = 0.0339$) and ribs (FET, $p = 0.0239$). From our study it appears that the prevalence of risk factors for RTI, such as poor air quality and high population density, was higher in urban than rural environments, although the complex and multifactorial etiology of the observed bone changes should be taken into account.

The role of grit in dental microwear textures: evidence from Artificial Resynthesis Technology (ART)

KRISTIN L. KRUEGER¹, EVAN CHWA², ALEXANDRIA PETERSON³, RALPH DELONG⁴ and ALEX FOK⁴

¹Anthropology, Loyola University Chicago, ²College of Dentistry, University of Illinois at Chicago, ³Environmental Dynamics, University of Arkansas, ⁴Minnesota Dental Research Center for Biomaterials and Biomechanics, University of Minnesota

The formation of dental microwear on the posterior dentition is largely attributed to the dietary proclivities of an organism. More recently, some have suggested that dietary and environmental

ABSTRACTS

grit, such as sand, contributes more to the dental microwear signature than the material properties of food, questioning the applicability of dental microwear to reconstructing the diet of fossil organisms. This study seeks to better untangle the contributions of food and grit to dental microwear textures using Artificial Resynthesis Technology (ART).

ART is a mastication simulator with the ability to replicate dental wear as well as respond to changes in food texture. It also simulates the actions of the entire oral cavity, including the cheeks, tongue, and saliva. This simulator was used to assess the production and formation of dental microwear textures on surgically extracted third molars ($n=8$) using different textures of meat (cooked and dried) with and without sand. High-resolution molds were taken at regular intervals up to 5000 simulated chewing cycles. Results show that meat alone did not produce microwear textures, but did show enamel prism exposure at 5000 cycles. Meat with sand shows enamel prism exposure and texture formation, with microwear forming at approximately 2500 cycles.

Initial results show that food texture affects microwear formation, and that dietary grit can produce microwear textures. Expanding this research to include other food items hypothesized to be a component of fossil hominin diets, including leaves, stems, insects, and underground storage organs, will help to better untangle these variables.

This study was funded by the LURUP Mulcahy Fellowship to KLK and EC.

Life History Perspectives on Carious Lesion Formation

KAYLA KUBEHL and DANIEL H. TEMPLE
Anthropology and Sociology, George Mason University

This study evaluates survivorship in relation to carious lesion formation. Carious lesion presence was recorded by tooth surface in a sample of 754 individuals of known age and sex from the Terry Collection. Kaplan-Meier survival analysis was used to evaluate mortality differences between groups with and without carious lesions by sex and tooth surface (crown, CEJ/root). Females without carious teeth experienced higher survivorship than females ($p < 0.052$) and males ($p < 0.42$) with crown lesions. The same group had lower survivorship than females with CEJ/root lesions ($p \leq 0.050$). Females with crown lesions had lower survivorship than females and males with lesions present at the CEJ/root ($p \leq 0.001$). Females with carious lesions involving the CEJ/root have a higher survivorship than males without carious lesions ($p \leq 0.001$), males with crown lesions ($p \leq 0.001$), and males with CEJ/root lesions ($p \leq 0.011$). Males without carious

lesions have lower survivorship than males with CEJ/root lesions ($p \leq 0.001$). Males with carious lesions involving the crown had lower survivorship than males with CEJ/root lesions ($p \leq 0.001$). Differences in survivorship and carious lesion presence between females begins around 30 years during the reproductive lifespan, while differences in CEJ/root caries between males and females is found around 50 years indicating age and sex specific differences in carious lesion formation due to alveolar bone loss during the post-reproductive lifespan. These results suggest that mortality estimates associated with carious lesions reflect varied life history factors including reproductive ecology and age-progressive alveolar bone loss.

Enamel extension rate patterns in the great apes

CHRISANDRA KUFELDT

Research Centre in Evolutionary Anthropology and Palaeoecology, Liverpool John Moores University

The enamel extension rate reflects the number of enamel-secreting cells differentiating along the inner enamel epithelium and the subsequent lengthening of the enamel-dentine junction (EDJ). The timing of enamel growth is central to understanding patterns of development. Studies of modern humans and fossil hominins suggest an exponential decline in extension from the cusp to cervix and faster extension rates are related to shorter enamel formation times. This study describes enamel extension in great apes to determine the relationships between extension rate, crown formation time, and the EDJ, and what variation in rate means for differences in enamel growth. Differences in timing of enamel formation are important to consider when using modern humans and non-human great apes as analogues for fossil hominins. The results show apes have rapid rates of extension greater than $20 \mu\text{m/day}$ within the first two months of enamel development followed by a reduction in rate in the lateral enamel. *Gorilla* show the fastest rate of enamel extension and some individuals of *Pan* and *Pongo* showed an increase in rate in the cervical enamel and although this occurrence is not well understood, it may be related to rapid root extension rate. The suggestion that faster rates of extension are related to shorter enamel formation times in molars is rejected in this study given the fast rates and longer formation times measured in *Gorilla*. The difference in timing observed across modern humans and the great apes may be related to life history rather than other aspects of enamel growth.

Do primates really trapline?

TAMARA L. KUMPAN^{1,3}, EVE A. SMELTZER¹, WILLIAM D. AGUADO⁴, ALEXANDER Q. VINING⁵ and JULIE A. TEICHROEB²

¹Anthropology, University of Toronto, ²Anthropology, University of Toronto Scarborough, ³School of the Environment, University of Toronto, ⁴Anthropology, Rutgers University, ⁵Animal Behavior Graduate Group, University of California, Davis

Trapline foraging, a term originally proposed for pollinating insects, is defined as repeated sequential visits to several feeding locations. Primates are often suggested to form traplines but, to our knowledge, no one has systematically tested this assumption. We analyzed primate foraging data ($n=43$ individuals) from three small-scale foraging arrays ($n=1480$ trials) on four different species, vervet monkeys (*Chlorocebus pygerythrus*), fat-tailed dwarf lemurs (*Cheirogaleus medius*), grey mouse lemurs (*Microcebus murinus*), and aye-ayes (*Daubentonia madagascariensis*). We modified a similarity index (SI) previously used for bees (Saleh & Chittka 2007) to determine the likeness of visitation sequences as animals gained experience in the array, where an SI of 0 indicates no similarity between successive foraging routes and an SI of 1 indicates an identical path. We calculated SI for individuals of each species two ways: 1) over all of their trials and, 2) when they started at the same platform in the array. SI values were examined to see if they increased with experience in the array using Pearson correlations. Overall, the frugivorous species showed a greater tendency to trapline. Twelve percent of individual vervets ($n=3/25$, mean SI=0.32) and 66.7% of dwarf lemurs ($n=4/6$, mean SI=0.26) showed SI values that increased significantly ($p < 0.05$) with experience. For the more insectivorous species, one mouse lemur ($n=1/6$, mean SI=0.04) and none of the aye-ayes ($n=0/6$, mean SI=0.03) showed SI values that increased significantly with experience. Our data show that the tendency to trapline in primates varies by species and individual and may depend on dietary specialization.

This research was funded by a Natural Science and Engineering Research Council of Canada Discovery Grant issued to Dr. Julie Teichroeb, and the University of Toronto.

Three-dimensional tarsal morphology and movements in anthropoid primates

SHARON KUO¹, MICHAEL C. GRANATOSKY², MYRA F. LAIRD³, BIREN PATEL^{3,4}, CALEY ORR^{5,6}, CALLUM F. ROSS² and CAROL V. WARD¹

¹Pathology and Anatomical Sciences, University of Missouri, ²Organismal Biology and Anatomy, University of Chicago, ³Integrative Anatomical Sciences, University of Southern California, ⁴Biological Sciences, University of Southern California, ⁵Cell and Developmental Biology, University of Colorado School of Medicine, ⁶Anthropology, University of Colorado Denver

ABSTRACTS

Reconstructing locomotor adaptations in Miocene hominoids is complicated by the lack of modern analogs, and a paucity of postcranial fossils for many taxa. However, tarsals are among the most abundant remains. Given that the foot directly contacts the substrate, pedal remains have the potential to be particularly informative. Arboreal taxa, especially those relying on strong pedal grasping, should emphasize more inversion of the foot. Because these motions are thought to occur primarily at the talocrural, subtalar, and transverse tarsal joints, understanding the morphology of these joints in a functional context can provide important new inferences into locomotor adaptation in fossil apes.

This research combines comparative 3D geometric morphometric (GM) analysis of anthropoid tali, calcanei, naviculars, and cuboids with *in vivo* analysis of joint motion during locomotion collected by XROMM (x-ray reconstruction of moving morphology). XROMM involves mapping *in silico* polygonal models onto biplanar fluoroscopic films of moving animals, enabling 3D posture and motion of the bones to be quantified and visualized. For this study, two macaques were filmed. For the comparative analysis, 1007 tarsal bones from 250 individuals of 17 anthropoid genera were evaluated using standard landmark-based geometric morphometric approaches. The GM analyses not only separated taxa emphasizing different positional behaviors ($p < 0.01$), but the XROMM analysis revealed that intertarsal rotation about the long axis of the foot (i.e., inversion) corresponded with the articular surface morphologies that separated taxa in the GM analysis. This combination of approaches provides functionally informed inferences with which to assess fossil hominoids.

NSF MRI-DBI 1338066; Wenner-Gren Foundation, Leakey Foundation, AAPA Professional Development Program, George Washington University, University of Southern California, Midwestern University-Downers Grove, and National Science Foundation (BCS-1316947; BCS-1317047; BCS-1317029 and BCS-153974)

Using cranial morphology to investigate population history in the genomic age: insights from the study of a 9500-year-old human skeleton from San Miguel Island, California

SUSAN C. KUZMINSKY

Anthropology Department, University of California, Santa Cruz, Instituto de Alta Investigación, Universidad de Tarapacá, Chile, Department of Sociology & Anthropology, University of Idaho

Morphological assessments of human cranial shape have long been used to address questions of biological affinities and population dynamics among extinct hominins and prehistoric populations. Recently, this work has been overshadowed by human paleogenomics, now widely used to investigate human population history in the

Old and New World. However, both genetic and cranial data offer invaluable insights into questions about ancient human dispersals, biological relationships and evolutionary adaptations, as exemplified in this study of a 9500-year-old skeleton excavated on San Miguel Island, located off the coast of central California. After its discovery, researchers were tasked with establishing biological and cultural affiliation as defined under NAGPRA. Attempts to extract ancient DNA from this skeleton were unsuccessful, but 3D morphometric assessments from the cranium proved to be a critical component in establishing an ancestor-descendent relationship. Using 3D imaging methods, geometric morphometrics, ordination (PCA), pairwise distances and probability assignments, this ancient skeleton was compared to 250 individuals excavated from early-mid Holocene sites in North and South America. Results demonstrated that this individual has a close biological relationship not only to skeletons from the California Channel Islands, but to prehistoric populations from all along the Pacific Coast of North and South America. These results align closely with genetic and archaeological data that support an early Pacific coastal migration during the initial peopling of the Americas. This study highlights the continued importance of non-destructive cranial morphological assessments and 3D geometric morphometric methods to address questions of biological relationships and ancient human dispersals.

This work was funded by an IIE Fulbright Fellowship #03102656, University of California Pacific Rim Research Grant #20090940, and NPS/NAGPRA Grant #P14PX01204.

The Evolution and Morphological Diversification of the Subtribe Papionina

SOPHIE B. LABELLE¹, MICHELLE SINGLETON² and JAMES M. CHEVERUD³

¹Biology, Loyola University Chicago, ²Anatomy, Midwestern University, ³Biology, Loyola University Chicago

Analysis of variation is critical in understanding evolutionary processes. The subtribe Papionina, defined commonly as baboons and their closest relatives, is a highly morphologically diverse group of primates that is useful for the examination of the relationship between variation and evolution. The subtribe is also a valuable behavioral, ecological, and morphological analogy for hominins. This study uses landmark-based cranial geometric morphometric data and multivariate analysis to test whether the pattern of morphological diversification present in Papionina is consistent with genetic drift and/or selection. The sample consists of all six extant genera of Papionin, represented by ~500 individuals collected by Michelle Singleton and Stephen R. Frost from predominantly wild populations. Multivariate analysis was performed on 17 linear

measurements obtained by following principles of morphological integration. The proportionality of variance/covariance matrix structure within and between populations was compared in order to identify the mode of morphological diversification present in the subtribe. Our results indicate that the mechanism driving diversification is unlikely to be drift alone and requires selection. The facial prognathism distinguishing baboons and mandrills from the rest of the subtribe is primarily the result of selection having acted on an immediate common ancestor.

Age-related decline in executive function in primates

AGNES LACREUSE

Psychological and Brain Sciences, University of Massachusetts at Amherst

Executive function encompasses several cognitive abilities that can be conceptualized as planning, updating, inhibiting, and set or task switching. Decline in executive functioning is a hallmark of aging in humans, which correlates with a number of age-related changes in the prefrontal cortex. This talk will review emerging evidence that age-related decline in executive function is pervasive among primates. Cognitive and neurobiological (when available) data from prosimians, New World and Old World monkeys, apes and humans will be presented. While it is clear that executive function declines with age in all species studied, the relationship with age-related alterations in the prefrontal cortex is not entirely understood, due to the scarcity of neurobiological studies focusing on the aging brain in most species. In addition, the influence of sex and hormonal status on age-related patterns has rarely been considered. A comprehensive integration of cognitive and neurobiological data across species is needed to understand how aging shapes neurocognitive trajectories in primates with different life histories, lifespans and brain architectures. Such comparative investigations will have important implications for understanding healthy and pathological aging in our own species.

Supported in part by R01 AG046266 and P01 AG02642

Neandertal oral health: new techniques and future directions

SARAH A. LACY

Department of Anthropology, California State University, Dominguez Hills

As Erik Trinkaus' pivot towards a greater focus on issues of paleobiology in both Neandertals and early modern humans culminated, he chaired my doctoral research on differential oral pathology prevalence between these two Late Pleistocene hominin taxonomic groups. Paleoanthropology research has long been

ABSTRACTS

largely disconnected from research methodology coming out of bioarchaeology, and both Trinkaus' and my own work have attempted to connect the two subdisciplines. Moving into the next phase of this interdisciplinary research, there are many areas of inquiry that have yet to be explored within Neandertal and early modern human "health." Recent methodological directions within bioarchaeology and paleogenomics suggest questions can now be posed about Late Pleistocene human microbiomes, paleoparasitology, and even cancer risk. Trinkaus' multiple syntheses of the results of individual assessments of Neandertal and early modern human trauma, infection, and chronic disease provide a foundation to begin exploring the application of these new techniques to human skeletal remains from the Late Pleistocene. Specially within and intersecting with oral health research, this may include oral microbiome assessments, evidence of attempts at dental hygiene, and indicators of digestive and respiratory health. The study of the paleobiology of Late Pleistocene humans has many potential future directions, and Trinkaus will be recognized as one of those who shepherded the field into maturity.

Bone remodeling in the macaque (*Macaca fascicularis*) skeleton: effects of loading frequency and magnitude

SUSAN E. LAD¹, W. SCOTT MCGRAW² and DAVID J. DAELING¹

¹Anthropology, University of Florida, ²Anthropology, The Ohio State University

Haversian remodeling is a process by which damaged cortical bone is resorbed and replaced by new bone, resulting in the formation of secondary osteons. Remodeling is incited by the microdamage caused by high strain and/or fatigue loading, but the relative effects of load magnitude and frequency on microdamage accumulation, and thus remodeling, are uncertain. We test whether strain magnitude or strain frequency results in more remodeling activity by measuring secondary osteon population density (OPD), osteon cross-sectional area (On.Ar), and relative osteonal area (%HAV) in adult macaque (*Macaca fascicularis*) mid-level ribs and mid-diaphysis femora, tibiae, and fibulae (n=5 individuals). Ribs experience relatively low strain, but relatively high loading frequency (breathing at a rate of 33 times per minute) in terms of cycles per day. Limb bones have lower daily loading frequency than ribs, but femora and tibiae presumably undergo the greatest load magnitude due to impact loads involving gravitational forces. The fibula experiences a fraction of the total gravitational loads. ANOVAs returned significant differences in OPD ($P=0.010$) and On.Ar ($P<0.001$). Post hoc pairwise t-tests revealed significantly lower On.Ar in the rib than in all other bones, presumably because the rib's narrow cortex imposes a constraint on

osteon size. OPD was significantly higher in the rib than tibia or femur, and higher in the fibula than femur. The high fibular OPD was surprising given that the femur and tibia are more weight bearing. The high rib OPD implies that remodeling activity is more responsive to loading frequency than strain magnitude.

Supported by NSF BCS-1440278 and -1440532.

Corn, Culture, and Caries: A Temporal Study of Carious Lesions on the Mississippian Periphery

EMMA M. LAGAN, ROBERT A. COOK and MARK HUBBE

Anthropology, The Ohio State University

Contemporary with Mississippians, Fort Ancient cultural groups are considered the first maize farmers in the region. Isotopic evidence from the Miami River Valley demonstrates diachronic and geographic shifts in maize consumption. Late (AD1400–1675) Fort Ancient populations consumed less maize than Earlier (AD1020–1280) ones. Those closer to the mouths of the Ohio River consumed more maize than groups along the upper portions of the Great and Little Miami Rivers. To further explore the agricultural transition in the region, this study examines skeletal samples from four Fort Ancient sites: three with extensive paleobotanical and isotopic analysis from the Great and Little Miami River Valleys—Guard (12D29), Turpin (33Ha19), and Anderson (33Wa4)—and one site farther east along the Ohio River, Fox Farm (15MS1).

A total of 3111 permanent teeth were examined for prevalence of carious lesions (Guard n=365, Turpin n=1100, Anderson n=873, Fox Farm n=773). All sites show high caries prevalence, ranging from 13.97% (Fox Farm) to 17.18% (Anderson), in accordance with the expectations of maize agriculturalists. Chi-squared tests show no significant differences between the sites ($\chi^2=3.598$, $df=3$, $p=0.308$). Interestingly, there are also no significance differences by sex at any of the sites (largest prevalence difference observed: 19.74% male, 15.66% female at Turpin, $p=0.086$). This suggests that access to cariogenic foods (i.e. maize) was similar for individuals across sites, supporting a temporal continuity in diet. Moreover, our results show equal consumption of cariogenic food between males and females, despite studies that have shown that females are more susceptible to caries.

Best Practices for the Macerating Human Thyroid Cartilage

ALEXIS M. LAGOY, TESSA SOMOGYI, ELIZABETH A. EVANGÉLOU and ELIZABETH A. DIGANGI

Anthropology, SUNY Binghamton

The thyroid cartilage is the uppermost cartilage in the human larynx. Thyroid cartilage supports and protects the vocal cords as well as provides an attachment site for the hyoid bone via the thyrohyoid membrane. In forensic contexts, visible abnormalities on the thyroid cartilage may be indicative of perimortem trauma including ligation marks or stab wounds. During autopsy, the thyroid cartilage must be freed of surrounding soft tissue before these marks can be clearly observed; however, there is scant information on best practices for processing the thyroid cartilage.

We tested several processing methods on a sample of 40 donated human thyroid cartilages obtained through an anatomical supply company. Three main processing methods were utilized: (1) dermestid beetles; (2) heat maceration (160°F); and (3) chemical maceration with 300 mL solutions of (a) laundry detergent, (b) sodium borate, (c) bleach, (d) multi-purpose cleaner, and (e) papain. A 19-point scoring system adapted from Steadman and colleagues (2006) was used to test the efficacy of each maceration method. The scores are based on odor (0-3), soft tissue texture (0-3), ease of soft tissue removal (0-5), cartilage quality (0-5), and duration (0-3). Methods receiving a higher point score are deemed better as they performed well in multiple categories. With a final score of 18/19 (94.7%), chemical maceration using bleach was found to be the best method for removing the surrounding tissue from the thyroid cartilage. The recommended bleach method is inexpensive, quick, and requires almost no additional mechanical removal of soft tissue.

This project was supported by an award from the National Institute of Justice: 2016-DN-BX-0155.

Another massive distal humerus of *Paranthropus boisei* from Koobi Fora, Kenya

MICHAEL R. LAGUE

School of Natural Sciences & Mathematics, Stockton University

A 1.9 Ma hominin distal humerus (KNM-ER 45510) was recovered in 2004 from Area 123 (Upper Burgi Member) of the Koobi Fora Formation. KNM-ER 45510 preserves the entire distal articular surface and a short portion of the distal diaphysis, though it suffers from minor bone loss on the lateral capitulum and posterior trochlear crests. This study examines the morphology of KNM-ER 45510 to assess whether it can be confidently attributed to (or excluded from) any particular hominin species (*P. boisei*, *H. habilis*, *H. erectus*). Multivariate ordination techniques are applied to landmark and linear data to compare KNM-ER 45510 to other early Pleistocene hominin humeri, including those associated with taxonomically secure skeletons.

ABSTRACTS

Distance metrics reflecting shape dissimilarity between KNM-ER 45510 and other fossils are assessed in the context of intraspecific variation within modern hominid species. Comparisons indicate that KNM-ER 45510 exhibits the distinctive morphology of the elbow joint and distal diaphysis observed among specimens attributed to *P. boisei*. Shape-based distance metrics indicate a much higher probability that KNM-ER 45510 belongs to *Paranthropus* than to *Homo*. KNM-ER 45510 is larger in diaphyseal size than the humeri of most chimpanzees and modern humans and similar in size to an average female gorilla humerus. It therefore represents one of four massive humeri now allocated to *P. boisei*, all of which likely belonged to a males. This study also demonstrates that specimens of *P. boisei* (and *Australopithecus*) have unusually small elbow joints relative to diaphyseal size compared to other Plio-Pleistocene hominins and extant hominids.

Supported by the National Science Foundation, the Leakey Foundation, and the Wenner-Gren Foundation.

The influence of dietary grit on capuchin feeding behavior

MYRA F. LAIRD, MICHAEL C. GRANATOSKY and CALLUM F. ROSS

Organismal Biology and Anatomy, University of Chicago

Dietary grit is proposed to be a major factor in dental microwear formation. While several studies have examined the influence of dietary grit on microwear formation, the behavioral response to grit has received relatively little attention. Modern humans change their feeding behavior if grit is detected, presumably to protect their teeth from wear. It is unknown whether non-human primate feeding behavior changes with the introduction of exogenous dietary grit. We examined the effect of dietary grit on feeding behavior in three female tufted capuchins (*Sapajus apella*): we hypothesized that foods containing grit of larger particle sizes would elicit lower muscle activation, increased tongue and jaw kinematic variation, and be chewed with a greater number of gape cycles.

We tested these hypotheses using a combination of X-ray Reconstruction of Moving Morphology (XROMM) and fine wire electromyography. Subjects were fed cubes of jello containing no grit or 10 ml of silt-like (75 microns), sand-like (180 microns), or granular (1400 microns) grit. Our results show tufted capuchins feed with greater variance in tongue and jaw kinematics, and a greater number of gape cycles when chewing food containing dietary grit. These results indicate non-human primates modify their behavior when exogenous dietary grit is detected, and

suggest interactions between bite forces, movement of grit particles within the mouth, and the number of chewing cycles may have an effect on dental microwear formation.

Funding was provided by the American Association of Physical Anthropologists Cobb Professional Development Program

Isotopic Analyses in Contemporary Forensic Cases from Coconino County, Arizona

TAYLOR LAMBRIGGER¹, CORINA M. KELLNER¹, LAWRENCE CZARNECKI² and FRANK RAMOS³

¹Anthropology, Northern Arizona University,

²Medical Examiner, Coconino County Public

Health Services District Medical Examiner's Office,

³Geological Sciences, New Mexico State University

Stable isotope analysis as a technique in forensic anthropology is quickly growing in popularity. Isotopic analyses have helped in bringing closure to loved ones in unidentified forensic cases in different regions. Coconino County encompasses the Grand Canyon, which attracts over 4 million visitors per year, and neighbors the Navajo Nation and Hopi tribe. In an attempt to gain information on unidentified individuals housed at the Coconino County Public Health Services District Medical Examiner's Office, the Northern Arizona University Paleodiet Lab was provided bone and tooth samples from 12 unidentified individuals for isotopic analysis of diet (carbon and nitrogen), geolocation (strontium and oxygen), and water consumption (oxygen) to narrow the possibilities for identification. We analyzed the samples at the Colorado Plateau Stable Isotope Laboratory at NAU and the Johnson Mass Spectrometry Laboratory at New Mexico State University. The forensic isoscape for the United States is still being developed, and this is the first study to our knowledge in Coconino County. The range of carbon, oxygen, and strontium values in these individuals is wide in tooth enamel, suggesting significantly different geolocations and diets during childhood. In bone, however, the range in values is narrow and shows a C3/C4 mixed diet during adulthood. Paired bone/teeth results show likely migration and different diets from childhood to adulthood. When placed on oxygen and strontium isomaps of the United States, these results suggest that most of these individuals likely lived in hot arid regions near the Colorado Plateau, western New Mexico, Nevada, or west Texas.

The Northern Arizona University Hooper Undergraduate Research Award funded this research.

From Cheap Chicken to Genome Instability: Arsenic, Diabetes, and the Social Nature of One-Carbon Metabolism

HANNAH LANDECKER

Sociology/Institute for Society and Genetics, UCLA

Metabolism constitutes a unique meeting point of biology and culture, being the multi-species system of enzymes, catalysts and substrates through which synthesis, breakdown, incorporation and detoxification occurs in any human body. What goes into human bodies (which is more than food) is inevitably socially formatted and historically specific. This paper uses the example of anthropogenically-generated dietary arsenic exposures to discuss the resulting social character of one-carbon metabolism, a key metabolic cycle that generates the substrates for DNA and histone methylation as well as cellular detoxification processes. Microbial metabolism of soil and gut microbiomes is equally important to understanding how arsenic moves through human bodies and societies. Epidemiological and physiological links between arsenic exposure and diabetes provide a macro-level picture of these micro-level interactions. This example demonstrates how the anthropogenic industrial impact on biological life is increasingly central to science and society, and how we might think about reframing methods and research questions in the social sciences to keep up.

USC Dornsife Berggruen Institute Fellowship

Maxillary sinus growth and development in Neanderthals and *H. sapiens*

FEDERICA LANDI¹, ANTONIO PROFICO² and PAUL O'HIGGINS¹

¹Department of Archaeology and Centre for Anatomical and Human Sciences, Hull

York Medical School, University of York (UK),

²Department of Environmental Biology, Sapienza, University of Rome (IT)

We investigate and compare facial and maxillary sinus ontogeny among Neanderthals and *H. sapiens* to understand the extent of any differences and to investigate if these might arise through differences in developmental interactions.

3D facial and sinus landmarks were acquired from virtual reconstructions of *H. sapiens* and Neanderthals (*H. sapiens* N=60, Neanderthals=5). Geometric morphometric analyses compared ontogenetic trajectories of size and shape as well as patterns of covariation among the maxillary sinuses, facial skeleton and its sub-regions.

Our results show that facial ontogeny diverges and that maxillary sinuses develop divergently among Neanderthals and modern humans. In both, maxillary sinus, facial and maxillary form are strongly associated. Further, PLS analyses indicate that the ontogeny of maxillary sinus form is strongly associated with that of several facial regions in infancy but becomes most closely associated with the form of the maxilla and nasal cavity in older individuals. In part, this is because the great changes in size that occur in the first few years of life dominate the analyses. However

ABSTRACTS

when shape alone is considered a similar shift in patterns of association is observed, albeit with lower correlations indicating that ontogenetic size changes alone do not explain the observed interactions.

These findings suggest that despite differences in facial form and ontogenetic trajectories between modern humans and Neanderthals, their maxillary sinuses develop similarly, showing similar patterns of interaction with other facial components, but attaining larger sizes, consistent with the greater space available for expansion provided by the larger maxilla of Neanderthals.

Fracture Patterning and Distribution in the Appendicular Skeleton as a Result of a Blast Event

KATHERINE M. LANE¹ and ALICE F. GOODING²

¹Anthropology, Georgia State University,

²Geography and Anthropology, Kennesaw State University

Improvised explosive devices are increasingly utilized as a weapon in cases of human rights abuses and domestic terrorism. Forensic anthropologists who investigate remains from these contexts must differentiate and interpret blast trauma from other types of assaults such as blunt or ballistic traumas. Experimental studies on the fracture types and dispersion of trauma in blast scenarios are necessary in order to identify and document blast trauma. This study utilized 32 wild pigs (*Sus scrofa*) that were exposed to controlled explosions at close range (1.5 meters). The pigs were either exposed to mixed metal shrapnel materials or positioned in front of a plywood wall to test how these variables affect the presentation of trauma. The appendicular skeleton was macroscopically analyzed for fracture types as well as their locus. Walls were insufficient in producing a significantly different pattern of trauma ($p > 0.05$), while shrapnel was found to significantly increase the severity of injuries ($p < 0.039-0.001$). Body size was a notable factor in the total number of fractures sustained. Traumatic amputations of the innominates and lower limbs were also observed. Overall, trauma was extensive with dispersion of injuries concentrated in body regions in the horizontal trajectory of the blast wave. Blast trauma in this scenario was characterized by multiple presentations of trauma across the skeleton and localized amputations as a result of victim positioning. This pattern differs from the more discrete presentation of traditional trauma, and these results aid in the identification and analysis of blast trauma in a forensic medicolegal setting.

A Closer Look at Global Prevalence of Obstetric Fistula

LEXI R. LANG and CHERYL KNOTT

Anthropology, Boston University

Obstetric Fistula (OF) is a fistula in which a passage forms between the vagina and either the rectum, ureter, or bladder. OF is usually the result of untreated difficulties during childbirth. The estimated 2 million women suffering from OF globally are often in pain, immobilized, and ostracized from their families and communities. Reducing global rates of maternal mortality and morbidity is of international concern and a target of the UN Millennium Development Goals. OF research has been conducted almost exclusively in African and South East Asian, with limited research in the Middle East and none in South America. Known risk factors for OF include extreme poverty, high birth rate, poor access to health care, and high maternal mortality rates. We hypothesized that there are women at risk of OF in countries where prevalence has not been examined. Using data from the World Bank Data Base, we create 'fistula ranges' for the prevalence of each risk factor by calculating the range and standard deviation in the two countries with highest and lowest rates of fistula researched. Then, we compared the prevalence of each risk factor in unresearched countries. Our results indicate that countries where no OF research has been conducted fell within the fistula range for multiple risk factors. This is an alarming indicator that research should be conducted to assess the prevalence of fistula in these regions. This study identifies crucial regions where women may be silently suffering or where an outside factor is successfully combating OF for future study.

A spoonful of bacteria helps the gluten go down: Probing the human oral microbiome for evidence of recent adaptation to host diets enriched in wheat, barley, and rye

CORRIN K. LAPOSKI

Anthropology, University of Connecticut

Despite being a fixture in the modern human diet, gluten is notoriously difficult for many mammalian digestive enzymes to process. Recently it has been shown *Rothia mucilaginosa*, a human oral commensal, secretes enzymes capable of cleaving gluten peptides present in grains. Moreover, these microbial enzymes persist in the upper-gastrointestinal tract of their human hosts and contribute significantly to nutrient extraction. The glaring question is whether these enzymes were recently under selection in *R. mucilaginosa*'s genome as a response to increased host consumption of grains, or if this is an ancestral ability that conferred a side benefit to the host.

This study mines a portion of the *R. mucilaginosa* genome that codes for the S8 peptidase enzyme to look for evidence of recent positive selection. The S8 peptidase amino acid sequence was run through the NCBI's tblastn program to look for homologous sequences, 14 of which were aligned using MUSCLE. Aligned sequences were then submitted to the Datamonkey Adaptive

Evolution Server under the Mixed Effects Model of Evolution (MEME) testing the hypothesis that individual sites in the sequences have been subject to episodic positive or purifying selection. MEME analysis showed 11 sites under positive selection. This is direct evidence that S8 peptidase was under recent positive selection in the human oral cavity. This study illuminates the potential for human dietary preferences to actively shape genetic aspects of the microbiome. Therefore, major human dietary transitions such as the Broad Spectrum and Neolithic Revolution need to be reexamined with the microbiome in mind.

Introduction and Major Findings: The Backbone of Europe: Health, Diet, Work, and Violence over Two Millennia

CLARK S. LARSEN¹, RICHARD H. STECKEL², CHARLOTTE A. ROBERTS³ and JOERG BATEN⁴

¹Anthropology, Ohio State University, ²Economics and Anthropology, Ohio State University,

³Archaeology, University of Durham, ⁴Economic History, University of Tuebingen

This poster summarizes a large collaborative effort by European and American researchers who used the same protocol to record health indicators from the skeletal remains of 15,119 individuals that were buried at 103 localities across the continent of Europe (representing 16 modern European countries) dated from ca. AD 300 to the end of the nineteenth century. We summarized health using an index developed in the Western Hemisphere project.

The analysis shows unexpectedly favorable health situation for people who lived during the early medieval period. Three indicators (femur length, linear enamel hypoplasias, and oral health) document improvement between the pre-medieval and the early medieval period. This was followed by a decline until the industrial period. Only during the late nineteenth century did health and nutritional quality increase to unprecedented levels.

One disadvantage of the early medieval period was the unusually high workload experienced, especially for farmers. Their degenerative joint disease prevalences indicate that they shouldered an enormous work effort, and the high values for osteoperiostitis suggest that farming also took its toll on the lower limb bones.

We observe substantial improvements in social interaction during the early modern and the industrial period witnessed by a decline in violence measured by cranial trauma and weapon wounds. The trends in violence hence differed from that of health and nutritional quality. Overall, the history of European welfare over the past two millennia is multifaceted.

Research supported by U.S. National Science Foundation and The Ohio State University.

ABSTRACTS

Dynamic social networks in the wake of environmental disaster: Hurricane Maria and the Cayo Santiago macaques

SAM M. LARSON¹, CASSANDRE H. KAPLINSKY², ANGELINA RUIZ-LAMBIDES³, MIKE MONTAGUE⁴, NOAH SNYDER-MACKLER⁵, MICHAEL L. PLATT^{4,6,7} and LAUREN J.N. BRENT⁸

¹Department of Anthropology, University of Pennsylvania, ²Centre for Research in Evolutionary, Social and Inter-Disciplinary Anthropology, University of Roehampton, ³Caribbean Primate Research Center, University of Puerto Rico, ⁴Department of Neuroscience, University of Pennsylvania, ⁵Department of Psychology, University of Washington, ⁶Department of Psychology, University of Pennsylvania, ⁷Department of Marketing, University of Pennsylvania, ⁸Centre for Research in Animal Behaviour, University of Exeter

The evolution of complex sociality characteristic of the primate Order must balance the costs and benefits of group-living. Individuals are expected to adjust their social priorities in response to dynamic environments. In late 2017, hurricane Maria made landfall on Puerto Rico, causing wide-spread ecological and structural damage; the offshore primate colony of Cayo Santiago was not exempt from this injury. Using a multi-year data set, we examine how rhesus macaque (*Macaca mulatta*) social behavior might be altered by this environmental disaster. Instantaneous proximity scans were collected in two groups in years prior to and after the hurricane. We used a subsampling routine to generate permuted networks for each group in each year, and from these permutations we estimated several network characteristics like density (the number of unique pairings of individuals), equanimity (how equally involved everyone was), and the frequency with which interactions occur in close kin and same-sex pairs. We find proximity networks were significantly denser after the hurricane and that observed connections were more egalitarian in their distribution with previously socially isolated individuals now becoming more integrated. This is reflected in greater frequencies of male-male proximity scans as well as a relaxing of genetic relatedness in structuring interactions. Far from monolithic, our analysis suggests social tolerance as malleable, with individuals becoming more tolerant in the more challenging post-hurricane landscape.

Research supported by National Institute of Mental Health grants R01-MH089484 and R01-MH096875.

New insights into human hair variation: High-throughput phenotyping paves way for genome-wide association studies and selection screens

TINA LASISI¹, ARSLAN ZAIDI², TIMOTHY H. WEBSTER^{3,4}, NINA G. JABLONSKI¹ and MARK D. SHRIVER¹

¹Department of Anthropology, Pennsylvania State University, ²Department of Biology, Pennsylvania State University, ³Department of Anthropology, University of Utah, ⁴School of Life Sciences, Arizona State University

Human scalp hair morphology is highly variable. However, unlike skin pigmentation, there is no widely used method of quantifying scalp hair variation. Therefore, hair continues to be described by geneticists as 'straight', 'wavy', 'curly' and 'frizzy'. Such oversimplifications of this complex trait, combined with a focus on Eurasian populations, have likely contributed to our lack of knowledge of its genetic basis and evolution in humans. To fill these gaps in our understanding, we developed software to accurately quantify hair fiber morphology and used it to measure hair in a sample of 195 individuals with mixed African and European ancestry. We used these measurements, combined with genomic data, to investigate the effects of ancestry and selection on hair morphology. We found that hair curvature is highly correlated with the percentage of African ancestry ($r = 0.84$, 99% CI [0.80, 0.89]), which is as strong as the correlation between skin pigmentation and African ancestry in the same sample ($r = 0.82$, 99% CI [0.76, 0.87]). To understand the role of selection in shaping hair morphology, we performed tests for selection on genes known to be important in hair biology. One of these, *LPAR6*, exhibits convergent signals of positive selection in both African and Melanesian populations, suggesting that populations with tightly curled scalp hair may have faced similar selective pressures. Our high-throughput and objective phenotyping method has the potential to uncover fine-scale variation therewith improving large-scale gene mapping, as well as, evolutionary and heritability studies of hair morphology.

This work was supported by the Center for Human Evolution and Diversity and the Department of Anthropology at the Pennsylvania State University.

Obstetric constraints in large-brained cebids and modern humans: a comparison of coping mechanisms

NATALIE M. LAUDICINA¹ and MATT CARTMILL^{1,2}
¹Anthropology, Boston University, ²Evolutionary Anthropology, Duke University

Compared to other primates, humans are claimed to have extreme maternal-fetal cephalopelvic disproportion. This claim assumes that other primates, like humans, have a birth canal that is constrained at the pelvic inlet and a vertex presentation of the fetal head as it enters the

birth canal. But these are false assumptions; in non-human primates the inlet is not an area of obstetric constraint, and presentation of the fetal head is generally face-first. Yet even when more realistic assumptions are adopted, the ratio of the effective (coronal) area of the fetal head to that of the bony birth canal at its narrowest point approaches or exceeds the human ratio in some New World monkeys, rising as high as 141% in *Cebus albifrons* and 151% in *Cebus apella* (coronal presentation), compared to a mean of 108% for a vertex presentation in our human sample ($n \geq 10$ for all species). In humans, the disproportion is accommodated through cranial remodeling and relaxation of the pelvic ligaments. But platyrrhine neonates lack large fontanels in the skull roof, and little or no cranial remodeling can occur during delivery. The necessary expansion of the birth canal during labor is produced by extreme pelvic relaxation. Combining published radiographs of *Saimiri* births with 3D animation modeling, we reconstruct the way these primates give birth, compare their birth mechanisms to those known or inferred for humans and apes, and propose functional and evolutionary explanations for the differences.

Wenner-Gren Foundation Dissertation Fieldwork Grant and Boston University Summer Graduate Research Abroad Fellowship

Stabilizing selection on bamboo lemur cyanide-detoxification enzymes suggests regulatory evolution

M. ELISE LAUTERBUR¹, MORGAN E. CHANEY², ANTHONY J. TOSI² and PATRICIA C. WRIGHT³

¹Ecology and Evolution, Stony Brook University, ²Anthropology, Kent State University, ³Anthropology, Stony Brook University

Bamboo lemurs (*Prolemur simus* and *H. spp.*) eat diets that can be rich in cyanide (CN⁻), an antifeedant compound with a low lethal dose (LD) in all mammals in which it has been studied. In the case of *P. simus* and *H. aureus*, reliable estimates of daily CN⁻ intake can exceed the expected LD by 50x, making them some of the few known cyanide-adapted mammals, able to resist cyanide's disparate toxic effects. This allows them to fill a niche rarely exploited by primates: relatively common and fast-growing bamboo forest. One hypothesis for such adaptation predicts that positive selection has acted on genes encoding sulfurtransferase enzymes, which contain catalytic domains that are the primary mediators of CN⁻ detoxification. We show that sulfurtransferases are not under selection in these CN⁻-adapted species, as measured by ratios of non-synonymous to synonymous nucleotide substitutions. However, bamboo lemur thiosulfate sulfurtransferase shows a signal of positive-stabilizing selection in its beta-structure tendency (TreeSAAP, $p = 0.0001$). Therefore, we tested for selection in the regulatory regions of

ABSTRACTS

these genes, and in genes encoding enzymes that create the necessary sulfur donors for enzymatic detoxification. Selection to upregulate the amount of detoxification enzymes, and/or their sulfur donors, could be responsible for increased CN⁻ detoxification and reliance on functional detoxification enzymes in CN⁻-adapted species. Less is known about regulatory evolution than about patterns of coding sequence evolution, despite increasing appreciation of its importance. Our results underscore the importance of investigating beyond protein coding evolution to understand primate adaptations.

American Genetics Association EECG to MEL. Kent State University College of Arts and Sciences.

Talar forces and moments in turning

STEVEN G. LAUTZENHEISER^{1,2}, ADAM D. SYLVESTER³ and PATRICIA A. KRAMER^{1,2}

¹Anthropology, University of Washington, ²Department of Orthopaedics and Sports Medicine, University of Washington, ³Center for Functional Anatomy and Evolution, The Johns Hopkins University School of Medicine

Humans change directions as they move through their environment for a variety of reasons, but how those forces effect ankle morphology remains unclear. We propose that the ground reaction forces associated with a directional change differ from those associated with walking in a straight path, causing differences in joint forces and moments.

Kinematic and kinetic data of 20 individuals were collected using a ten-camera Qualisys system and three Kistler force plates in two conditions: walking unshod in a straight line with and without a 90° turn. Forward (X), side (Y), and vertical (Z) joint forces and moments about the X, Y, and Z axes were calculated at the talar head and analyzed to determine if differences exist during the propulsive phase of stance between turning and straight path walking.

Between straight and turning conditions, vertical joint forces were not significantly different ($p=0.513$), while side ($p<0.01$) and forward ($p<0.01$) forces were different. Joint moments about the Y-axis did not differ ($p=0.48$), but moments about the X- ($p<0.001$) and Z- ($p=0.02$) axes were higher in turns. In both conditions, shearing forces (X and Y) during propulsion result in the moment differences about the X and Z axes.

The ubiquity of directional change combined with our result that turning forces and moments are higher during the propulsive phase of turning than during straight path walking, argue that turning was important in shaping human talar morphology. Further analysis will evaluate other phases in stance and forces and moments in the subtalar joint.

The Epidemiology of Longevity and Behaviour - Evidence from the skeleton and its value in Human Identification

ANNA S. LA VALLEY¹, LAURA MCNERN², STEFFI VASSALLO³ and XENIA PAULA KYRIAKOU^{1,4}

¹Research and Development, Odyssey Fieldschool, ²Archaeology, University of Bournemouth, ³Center for Anatomy and Human Identification, University of Dundee, ⁴Justice Studies, Florida Gulf Coast University

Enthesial changes (EC), osseous modification at ligament and tendon attachment sites, are the result of habitual biomechanical stress (BS) and may indicate behavioural patterns in a population. Physical activity is recognised as a main etiological factor in the development of osteoarthritis (OA). The aim of this study was to examine the relationship between EC and OA in the males and females of a contemporary Greek-Cypriot population. This was achieved by looking at degrees of EC expression on the upper limb and OA severity on the shoulder and elbow joints. A blind analysis was carried out on 51 individuals (25 males; 26 females) from the CRRC. EC was scored using an ordinal scale between 0 and 3; OA severity was based on the number of diagnostic criteria present on/around the joint. It was found that 82.5% of males exhibited severe OA development in the right elbow, 14.3% of which was associated with high EC scores. This suggests that a statistical correlation between EC and OA does exist and that physical activity may be a contributing aetiology to the development of OA. Handedness may be a predisposing factor for left and right differences. However, age may also be a contributing factor as these individuals fell into the 80.4yrs±14.3 category. It is believed that EC development in this population is related to the predominantly rural socio-economic character of Cyprus prior to 1974 whereas OA may be attributed to genetics, environment, age longevity but also behavioural longevity associated with the population's subsistence practices.

Modern evidence of femoroacetabular impingement: implications for interpretations in the archaeological record

AUSTIN B. LAWRENCE¹, SARAH TOWNSLEY², CAROL V. WARD¹, BRETT D. CRIST³ and DANA L. DUREN^{1,3}

¹Department of Pathology and Anatomical Sciences, University of Missouri, ²School of Medicine, University of Missouri, ³Department of Orthopaedic Surgery, University of Missouri

Femoroacetabular impingement (FAI) is an anatomical hip condition common in modern human populations that causes pain and reduced mobility. It is also often identified through nonmetric traits in skeletal remains in archaeological contexts. One form of FAI, the cam-type deformity, is caused by asphericity in the anterior aspect of the femoral head-neck

junction and associated nonmetric traits have been interpreted as indicators of activity (Poirier's facet and plaque). However, relationships between these features, FAI morphology, and FAI symptoms have not been investigated in living patients. In this retrospective study, we investigated the relationship between Poirier's facet and plaque (from reconstructed computed tomography), radiographic signs of FAI (e.g., lateral alpha angle), and FAI symptoms in a clinical sample of 72 living patients treated for FAI or hip/pelvis trauma. Fisher's exact tests were used to determine differences in the frequencies of Poirier's facet and plaque between FAI and non-FAI groups and between symptomatic and asymptomatic FAI groups. Two-sample t-tests were used to assess differences in radiographic measurements between groups with and without Poirier's facet and with and without plaque. The frequencies of Poirier's facet and plaque were not significantly different between symptomatic and asymptomatic FAI groups; however, presence of either Poirier's facet or plaque was associated with an elevated lateral alpha angle. These results suggest that while Poirier's facet and plaque may not be a reliable indicator of pain due to FAI, they likely represent forms of cam-type FAI and may be used as a tool to identify FAI in skeletal remains.

Integration of the canine region within the hominine alveolar arch

JULIE LAWRENCE¹ and WILLIAM H. KIMBEL^{1,2}

¹Institute of Human Origins, Arizona State University, ²School of Human Evolution and Social Change, Arizona State University

How tightly integrated is the canine region within the alveolar arch of hominine species and what insight can this give to the changes in the dental arches in hominin evolution? The early hominin record is characterized by numerous shifts in dental proportions (e.g., canine reduction, megadontia, etc.). Recently, several studies have pointed to strong covariation within the primate postcanine dentition, between the anterior and posterior dental components, and more broadly across both the upper and lower dental arcades. We focused on the understudied and yet crucial morphology of the canine region. We used geometric morphometric methods to delineate the roles of size and shape in the morphological covariation of the canine region with other dental regions. We also examined the influence of allometry and sexual dimorphism on intra- and interspecific patterns of integration. Our sample included modern humans ($n=50$), chimpanzees ($n=33$), gorillas ($n=30$), and *Australopithecus afarensis* ($n=10$). We found that allometry plays a minimal role in explaining the morphology of the canine region. Size sexual dimorphism drives intraspecific patterns of covariation but significant size relationships between dental

ABSTRACTS

regions at the species level diminish when the sexes are examined separately. Intra- and inter-specific shape relationships are consistent in that the canine region shows weak shape covariation with the dentition distal to P3 but strong covariation with the incisors and P3. Our results suggest that low levels of integration between the canine and molar regions facilitated their independent morphological changes across hominin evolution.

A comparative analysis of carpometacarpal joints four and five in various hominoid and cercopithecoid species

HEATHER LAWRENTZ^{1,2}, C. OWEN LOVEJOY¹, RICHARD S. MEINDL¹ and MARY ANN RAGHANTI^{1,2}
¹Department of Anthropology, Kent State University, ²School of Biomedical Sciences, Kent State University

The morphology of joints is largely dependent upon the expression of positional information during ontogeny, but is also subject to potential cartilage modeling imposed by dominant activity patterns. Among joints that might reveal such effects are those between metacarpals four and five and the hamate in knuckle-walking (KW) apes. Because chimpanzees bear little or no weight on their fifth digit during KW we hypothesized that the MC4-hamate joint would be larger than that between MC5 and the hamate (we refer to this as the "facet ratio"). To test our supposition, we collected metrics on articular surface size and shape from humans, chimpanzees, gorillas, orangutans, and baboons. We also defined several shape characters for the two joints and scored them in the five taxa using seriation-scoring. We subjected our shape data to principal components (PCA). When adjusted for body size, group means of hamate facet size ratios differ significantly, although the taxon effect is small. The PCA provided a clear distinction of humans from the other taxa, but failed to differentiate ape species from one another. Moreover, we found *Gorilla* PCA scores to be curiously variable when ranked for overall MC5 mobility, a factor that spanned the entire range of scores separating *Pan* and *Homo*. Our results demonstrate the need to examine a total morphological pattern of potential components of joint patterning within a sample, rather than attempting to classify joints based on single traits.

Correlations between dental wear and oral cavity characteristics: Mandibular torus, palatine torus, and oral exostoses

LOREN R. LEASE

Department of Sociology, Anthropology and Gerontology, Youngstown State University

The etiology of non-metric oral cavity characteristics, mandibular torus (TM), palatine torus (PT) and oral exostosis, is debated. The degree to

which traits' presence and expression is the result of genetic or environmental factors is not fully understood. This study evaluates the correlations among TM, TP, oral exostoses to dental wear/loss and temporomandibular (TMJ) damage.

The sample consists of 504 skulls from the Hamann-Todd Osteological Collection; 223 African-American (103 males, 120 females) and 281 white (151 males, 130 females) aged between 30 and 80. Five age groups were created. Each skull was examined for dental wear/loss, TM, PT, oral exostoses and TMJ damage.

Dental wear/loss was classified into four categories with edentulous or heavy wear/semi-edentulous individuals being the most common (n=336). Wear was statistically significant by age and sex but not ancestry ($p < 0.01$). The maxillary exostoses (n=41) varied significantly by age, ancestry and wear but not sex. The exostoses were more prevalent in young African-Americans with low to heavy wear. MT (N=62) frequencies were significant by wear, sex and ancestry. White males had higher frequencies in the heavy wear/semi-edentulous category and African American males in the heavy wear category. PT (N=85) varied significantly across wear groups, sex and ancestry. PT was more frequent in heavy wear/semi-edentulous and edentulous wear categories; males more commonly having heavy wear, females heavy wear/semi-edentulous to edentulous. More than age, sex or ancestry, the degree of dental wear and tooth loss influences the presence and expression of the oral cavity traits.

Evidence for intestinal parasitic infection from coprolites at the Bronze Age settlement of Must Farm, UK (920-790 BCE)

MARISSA L. LEDGER¹, HELEN WHELTON², RACHEL BALLANTYNE¹, IAN D. BULL², MARK KNIGHT³ and PIERS D. MITCHELL¹

¹Department of Archaeology, University of Cambridge, ²Organic Geochemistry Unit, School of Chemistry, University of Bristol, ³Cambridge Archaeological Unit, University of Cambridge

The Must Farm settlement is a late Bronze Age (920-790 BCE) pile-dwelling located in the east of England, consisting of five stilted timber structures built over a slow-moving water channel. Amongst the remains of the settlement, 15 coprolites were recovered. Lipid biomarker analysis suggested human origin for four coprolites, the remaining 11 could not be determined due to high environmentally-derived background signals. We have very little evidence for human intestinal parasitic infection in the Bronze Age, with only four sites studied in Europe. Thus, this work aimed to provide further evidence for gastrointestinal disease in this understudied time period. Coprolites were rehydrated and processed with microsieves. Subsamples were viewed under a digital light microscope to look

for preserved helminth eggs. Eggs from four different taxa including *Diphyllobothrium* sp. (fish tapeworm), *Echinostoma* sp. (intestinal fluke), *Trichuris* sp. (whipworm) and *Capillaria* sp. were recovered. Both *Echinostoma* sp. and fish tapeworm have aquatic organisms as intermediate hosts, and cause infection in humans when raw or undercooked fish or molluscs are eaten. Their presence in coprolites informs us about diet and culinary practices in Bronze Age Britain. This is the earliest evidence for *Echinostoma* sp. worldwide, and for *Capillaria* sp. and fish tapeworm in Britain. In combination with previous results from our paleoparasitological analysis of occupation sediments at the site, it appears that the marshy freshwater environment of Must Farm put inhabitants at high risk for uncommon zoonotic species that flourish in aquatic environments but protected them from common soil-transmitted species such as roundworm.

This work was funded by a Social Sciences and Humanities Research Council of Canada Doctoral Award (752-2016-2085) and a Cambridge Commonwealth, European, and International Trust Scholarship.

Food mechanical properties and dietary ecology in sympatric *Pithecia* and *Chiropotes* during a period of preferred food scarcity

JUSTIN A. LEDOGAR¹, BARTH W. WRIGHT², MICHAEL C. GRANATOSKY³, MYRA F. LAIRD³, JANINE CHALK-WILAYTO⁴, MARI D. FOGAÇA⁵, ADAM VAN CASTEREN⁶, CALLUM F. ROSS³ and DAVID S. STRAIT⁶

¹Department of Evolutionary Anthropology, Duke University, ²Department of Anatomy, Kansas City University of Medicine and Biosciences, ³Department of Organismal Biology and Anatomy, The University of Chicago, ⁴Department of Biomedical Sciences, Mercer University School of Medicine, ⁵Department of Biodiversity and Conservation, Federal University of Maranhão, ⁶Department of Anthropology, Washington University in St. Louis

Knowledge of the relationship between feeding biomechanics and craniofacial evolution in primates has benefited greatly through the collection of primate food fracture properties in the wild. Much recent work advocates for the use of mechanical properties, including Young's modulus (E , a measure of stiffness) and toughness (R), while other studies employ structural properties, including measures of puncture and crushing resistance. It is therefore a pertinent question as to whether these properties explain differences in feeding ecology equally well. We examine the E and R of fruit tissues eaten by sympatric *Pithecia* and *Chiropotes* at Brownsberg Nature Park and compare our results to previous observations of niche partitioning in these taxa. Specifically, it has been demonstrated that *Chiropotes* breaches unripe fruits with higher puncture resistance, whereas *Pithecia* masticates

ABSTRACTS

seeds with higher crushing resistance. We found that maximum E of fruit exocarp breached was higher in *Chiropotes*, consistent with previous observations of puncture resistance. We revealed even greater differences in exocarp R , suggesting that perhaps toughness is the primary challenge for *Chiropotes* in accessing unripe fruits. *Chiropotes* was also found to prefer larger fruits, which they accessed using more extensive parmastication, including downward pulling to tear open fruit husks. Seeds masticated by *Pithecia* had greater E than in *Chiropotes*, also supporting previous work. Our results are consistent with the hypothesis that sympatric pitheciines diverge dietarily with respect to the intensity of anterior and postcanine tooth use, and suggest that both structural and mechanical properties can be used reliably to quantify primate diets.

This research was supported by funding from Washington University in St. Louis (DSS) and an AAPA Professional Development Grant (JAL).

An automated tool for measuring human limb bones using 2D images

AMANDA B. LEE¹, PENG LI² and DEREK W. HOIEM²

¹Anthropology, University of Illinois at Urbana-Champaign, ²Computer Science, University of Illinois at Urbana-Champaign

Osteometric measurements are necessary for most research involving the analysis of human remains. Currently, the most efficient method for taking linear measurements is by hand, using tools such as sliding calipers and osteometric boards. However, the automation of measurement taking has the potential to enhance data acquisition procedures and improve the quality of research in a broad range of fields.

This study validates new software that automatically records long bone measurements from photographic data. The program uses computer vision to recognize bones, locate landmarks, and take measurements. A total of 12 postcranial measurements on four limb bones were taken from a sample of 37 individual human skeletons. A single observer took pictures and repeated bone measurements using an osteometric board and digital calipers for each element. The pictures were then analyzed with the measurement software. Photographic and traditional measurements were statistically compared in R.

Using the scaled error index to test for accuracy, the software was able to take measurements accurate to one to two millimeters. Calculation of intraclass correlation coefficients and paired t -tests show that this method performs as well as standard manual measurement methods ($p > 0.05$). Mediolateral diameter of the radius and joint measurements had the highest error rates. Conversely, the measurements with the lowest error rates were the maximum lengths of the long bones. This new, highly accessible method has

the potential to facilitate field work by eliminating the need for cumbersome measurement tools, reducing inter-observer error rates, and expediting data collection.

Predicting glenohumeral range of motion from bone geometry *in silico*, with application to fossil hominins

ERIN C.S. LEE¹, NATHAN M. YOUNG² and MICHAEL J. RAINBOW¹

¹Mechanical and Materials Engineering, Queen's University, ²Orthopaedic Surgery, University of California San Francisco

Scapula morphology is thought to reflect locomotor repertoire, and thus serve as indirect evidence for reconstructing forelimb function in fossil taxa. That said, mapping skeletal form to function to identify those activities most relevant to selection remains a challenge, even in living species. Here, we present a quantitative *in silico* "six-degree-of-freedom" shoulder model and demonstrate how it can be used to predict the upper envelope of glenohumeral range-of-motion (ROM) in both living and fossil species. Specifically, we apply an abduction motion to the shoulders of a range of primates including humans and measure the range within which a congruent position is maintained between the humeral head and glenoid. We validate our model by testing whether species with cranially-oriented scapulae and frequent suspensory activity exhibit a ROM spanning high abduction levels, and species with laterally-oriented scapulae and terrestrial activity exhibit a ROM spanning low levels of abduction. Consistent with *a priori* expectations, the chimpanzee and gibbon had ROMs spanning high abduction levels whereas the gorilla ROM spanned lower abduction levels. Interestingly, upper abduction limits of humans were intermediate and increased with cranial orientation. Furthermore, when applied to *Australopithecus sediba*, a fossil hominin that has been suggested to have retained suspensory behavior, the ROM was more similar to humans than arboreal primates. Importantly, our model is extendable to a range of species and motions enabling a more thorough investigation of how shape variation directly influences the shoulder's functional workspace, providing constraints on both evolutionary scenarios and functional explanations for differences in morphology.

Funding Citation: NSERC RGPIN/04688-2015, NSERC USRA

Estrogen, energy, and skeletal biology: Life history approaches to understanding skeletal phenotype in living women of reproductive age

KATHARINE M.N. LEE¹, MARY P. ROGERS², ANDRZEJ GALBARCZYK³, GRAZYNA JASIENSKA³, JOHN D. POLK¹ and KATHRYN B.H. CLANCY¹

¹Department of Anthropology, University of Illinois at Urbana-Champaign, ²Institute for Genomic Biology, University of Illinois at Urbana-Champaign, ³Department of Environmental Health, Faculty of Health Sciences, Jagiellonian University Medical College

Life history theory examines the allocation of limited resources to understand trade-offs between growth, reproduction, and body maintenance. Bone development is sensitive to physical activity and estrogen levels, including the timing of estrogen-mediated life history events. Here we present data about frame size, bone density, childhood experiences, and life history transitions in women of reproductive age from a rural Polish population. In healthy premenopausal women aged 18-46, we found wrist breadth was significantly related to grip strength ($n=46$, $p < 0.001$, adjusted $R^2=0.39$), even when adjusted for overall height ($n=46$, $p=0.004$, adjusted $R^2=0.51$), which is biomechanically reasonable. Current age was not associated with wrist breadth ($n=76$, $p=0.07$), but it was associated with wrist breadth adjusted for height ($n=76$, $p < 0.001$, adj $R^2=0.15$). Wrist breadth was not associated with age at menarche or gynecological age, suggesting that biomechanical pressures may be significant for this phenotype in this population. Bone density at the 1/3 distal point of the radius ($n=44$) was not associated with these factors, childhood farming, or any anthropometric measurements. These Polish women had higher radial bone density than comparative European populations (mean t -score=3.24), and variation in this measurement was not associated with life history events, current or past farmwork, or anthropometric differences. Bone density is often associated with pubertal timing, estrogen exposure, and physical activity. In this sample, bone density was higher than other populations but was not associated with life history events. Follow-up analyses will examine how energy expenditure and more nuanced measures of estrogen exposure may contribute to this phenomenon.

This material is based upon work supported by: NSF GRFP #DGE-1144245, NSF Clancy#1317140, NSF DDRIG Rogers#1650839 and Lee#1732117, Lewis&Clark Fund for Exploration&Field Research, and Wenner-Gren Foundation Dissertation Fieldwork Grants.

High variability and decoupling from phylogenetic effects characterize the human microbiome

STEVEN R. LEIGH^{1,2}, DANIEL MCDONALD³, NATHANIEL J. DOMINY⁴, TONY L. GOLDBERG⁵, JOANNA LAMBERT⁶, JESSICA L. METCALF⁷,

ABSTRACTS

ANDRES GOMEZ², GILLIAN AO. BRITTON⁴, REBECCA M. STUMPF^{2,3}, ROB KNIGHT^{10,11,12,3}, ELIZABETH K. MALLOTT¹³ and KATHERING R. AMATO¹³

¹Anthropology, University of Colorado, Boulder, CO, ²Carl Woese Institute for Genomic Biology, University of Illinois at Urbana-Champaign, Urbana, IL, ³Pediatrics, University of California San Diego, San Diego, CA, ⁴Anthropology, Dartmouth College, Hanover, NH, ⁵Pathobiological Sciences, University of Wisconsin-Madison, Madison, WI, ⁶Environmental Studies Program, University of Colorado, Boulder, CO, ⁷Animal Sciences, Colorado State University, Fort Collins, CO, ⁸Animal Sciences, University of Minnesota, Minneapolis, MN, ⁹Anthropology, University of Illinois at Urbana-Champaign, Urbana, IL, ¹⁰Computer Science and Engineering, University of California San Diego, San Diego, CA, ¹¹Bioengineering, University of California San Diego, San Diego, CA, ¹²Center for Microbiome Innovation, University of California San Diego, San Diego, CA, ¹³Anthropology, Northwestern University, Evanston, IL

The community of microbes residing in the human colon influences host nutritional status, immune function, and even behavior, making an understanding of host-microbe interactions critical to human biology. Increasingly, data from non-human primates are being used to provide evolutionary context. Hominoids have thus far been assumed to be the best comparative system, given their close phylogenetic relationship to humans.

We compare 16S rRNA sequence and Metacyc pathway data from 18 species of wild, nonhuman primates to 14 literature-reported human populations. Human samples include both “industrialized” and “nonindustrialized” populations. Results reveal substantially more variability in gut microbiome composition and function within and among human populations than within and among other primate species. Moreover, the composition and function of the human gut microbiome is more similar to that of Old World monkeys (Family Cercopitheciinae), particularly baboons, than to other hominoids, including great apes. Unlike previous comparisons among nonhuman primate species that reveal close phylogenetic clustering, the human microbiome differs substantially from closely related hominoids.

These findings indicate that apes are insufficient for placing the human microbiome in an evolutionary context, and underscore that host physiology and environment can be as or more important in shaping the primate gut microbiome than host-microbe co-diversification. Compared to that of other primates, the human gut microbiome has followed a unique evolutionary trajectory, which may provide insight into humans’ marked dietary plasticity and widespread geographical distribution. Comparative

studies of the human gut microbiome should further examine the functional convergence between humans and cercopitheciines and its evolutionary implications.

Supported by NSF 0935347

Childhood growth and diet: insights from analysis of deciduous teeth from the Tooth Fairy collection (France)

MONA LE LUYER^{1,2}, MARLON BAS³, PATRICK MAHONEY¹ and PRISCILLA BAYLE²

¹School of Anthropology and Conservation, University of Kent, UK, ²UMR5199 PACEA, University of Bordeaux, France, ³Institute for Oriental and European Archaeology, Austrian Academy of Sciences, Austria

Since 2014, we have collected naturally exfoliated deciduous teeth from French children of known kinship and life-histories. These teeth are part of the Tooth Fairy collection which is composed to date of 882 deciduous teeth from 89 individuals from 36 French families. The life history records include date and place of birth, sex, birth weight and length, weight measurements during the first six months of life, whether the child was premature or a full-term birth, delivery conditions, and dietary information including weaning age. Data collection and exploitation was approved by the French authority Commission Nationale de l'Informatique et des Libertés. Analyses conducted so far have focused on first and second upper deciduous molars. All teeth have been imaged at high-resolution, dental impression have been taken for occlusal microwear texture analysis, and molars have been sectioned for histologic analysis. Our preliminary results show a range of Retzius periodicities between four to 12 days. Females tend to have a higher Retzius periodicity linked to lower birth weight while males exhibit the opposite condition. Microwear measurements vary greatly across the same facet of the same tooth/individual (up to 67% variation). Microwear texture variables were found to correlate with the degree of macrowear and facet shape. By combining macro-, meso- and microstructural analysis, the Tooth Fairy collection will be used to track factors influencing growth and diet around birth and during early postnatal life. This holistic approach will ultimately provide a framework to understand subtle variations in growth and diet in archaeological specimens.

This research was supported by the FYSSSEN foundation, the Région Nouvelle Aquitaine (CHROQUI project n°2014-1R40217), and the European Research Council (VAMOS project n°676828).

Population Variation in the Fusion Sequence of Primary and Secondary Ossification Centers in the Human Skeleton

MAKENNA LENOVER and MAJA SESELJ
Anthropology, Bryn Mawr College

The fusion sequence of primary and secondary ossification centers is a promising, yet under explored, approach to improving estimation of the number of individuals represented in commingled subadult remains. Limiting this approach is the lack of understanding of population variation in this aspect of human development. Furthermore, the existing reference studies are primarily based on samples of European ancestry.

To explore potential variation in fusion patterns within and among populations, we analyzed patterns of fusion of primary and secondary ossification centers in nine globally representative skeletal samples of East Asian, indigenous North American, African, and European ancestry. Forty-three fusion sites, spanning the axial and appendicular skeleton, were cross-tabulated in R software to determine the sequence of beginning and completion of fusion in each geographic group. These data were distilled into modal sequence trajectories documenting the general fusion pattern and population variation around the modal pattern.

We observed population variation within and among all geographic groups, especially in later fusing sites. The East Asian sample was the least variable one, whereas the African sample was most variable. Certain sites (e.g., the acromion) had higher intra- and inter-population variation. The sequence of completing fusion varied less than the beginning fusion sequence, making it of greater practical utility in forensic and bioarchaeological practice. Our results document the most likely sequence of epiphyseal union in diverse populations and will allow biological anthropologists to estimate the number of individuals in a commingled sample with greater certainty.

National Science Foundation DDIG #0925861; Wenner-Gren Foundation; NYU Graduate School of Arts and Science; New York Consortium in Evolutionary Primatology; Frances Velay Women in STEM research grant

Training Graduate Students To Be Effective Instructors: Our Experience With A Student-Led Pedagogy Interest Group

KATE M. LESCIOTTO¹ and KEVIN FLAHERTY²
¹Department of Anthropology, Pennsylvania State University, ²Department of Biology, Augustana College

Despite the fact that nearly 95% of doctoral students teach or mentor undergraduate students during their graduate programs, institutional emphasis remains squarely on research development and productivity, often at the

ABSTRACTS

expense of pedagogical training. We present the framework for a Pedagogy Interest Workgroup (PIW) that graduate students can organize within their departments to provide a background in pedagogical methods. This framework is based on a group created by graduate students in the Department of Anthropology at Pennsylvania State University. The group met weekly for approximately three months in Spring 2018, primarily in a book-club format which served as a springboard for further discussion of the participants' experiences as instructors and teaching assistants.

The PIW was organized by two graduate students who led participants through guided discussions of *How Learning Works* (Ambrose et al., 2010) and *Teach Students How To Learn* (McGuire, 2015). Discussions were supplemented by group activities, demonstrations, and online videos related to weekly topics. At the end of the Spring 2018 PIW, participants reported high rates of satisfaction with their experience and increased confidence in their abilities as an instructor or teaching assistant. Here we present the PIW syllabus and activities, as well as a summary of participants' experiences, for use by other departments to assist graduate students in their pedagogical training.

Evidence of *Macrotermes* termites within the *Zinjanthropus* horizon at Olduvai Gorge, Tanzania

JULIE LESNIK¹, ROBERT O'MALLEY², AUDAX MABULLA³, ENRIQUE BAQUEDANO⁴, MANUEL DOMINGUEZ-RODRIGO⁵ and CLAYTON MAGILL⁶

¹Department of Anthropology, Wayne State University, ²Dialogue on Science, Ethics, and Religion Program, American Association for the Advancement of Science, ³Department of Archaeology and Heritage, University of Dar Es Salaam, ⁴Museo Arqueológico, Regional de Madrid, ⁵Departamento de Prehistoria, Universidad Complutense, ⁶Institute of Life and Earth Sciences, Heriot-Watt University

Termites are an important food resource for a number of living mammalian clades, including primates. Among the termites regularly consumed by chimpanzees and humans are those of the genus *Macrotermes*. Here we report the presence of termite mound-like deposits at the iconic FLK *Zinjanthropus* archaeological (level 22) horizon at Olduvai Gorge, dated to about 1.785 million years ago as well as the results of focused biomarker and isotopic analyses of hydrocarbons extracted from this feature compared to extant termites and recent termitaria.

Biomarker analyses of termite soldiers and termite workers in dominant East African species of *Macrotermes* show indistinguishable intraspecific saturated hydrocarbon distribution patterns dominated by odd, longer chain-length homologues ($n-C_{21}$ to $n-C_{27}$). In contrast, there

are consistent interspecific differences in relative saturated hydrocarbon abundances. Observed biomarker distributions of termite soldiers/workers are also apparent in associated termitarium sediments, and distinctive as compared to surrounding plant tissues or soil. With this in mind, *in situ* termite mound-like sediment features uncovered from around FLK *Zinj* show near-identical hydrocarbon distributions vis-à-vis edible extant *Macrotermes* species. Stable carbon isotopic analyses of termite-associated hydrocarbons extracted from inferred termitaria at Olduvai Gorge show increased $d^{13}C$ values as compared to surrounding plants, which – based on associated $d^{13}C$ values of hominin molars at FLK *Zinj* – is consistent with the incorporation of C_4 plant-like invertebrate resources in our ancestors' diets.

This work has been supported by the Leakey Foundation.

A unique pattern of serotonergic innervation in the human amygdala

CAROLINE H. LEW¹, KIMBERLY M. GROENIGER¹, KARI L. HANSON¹, DEION CUEVAS², DEMI GREINER², BRANKA HRVOJ-MIHIC¹, URSULA BELLUGI³, CYNTHIA M. SCHUMANN⁴ and KATERINA SEMENDEFER¹

¹Anthropology, University of California San Diego, ²Biological Sciences, University of California San Diego, ³Laboratory for Cognitive Neuroscience, Salk Institute, ⁴MIND Institute, University of California Davis

The serotonin system is critically involved in the regulation of socio-emotional behavior. Differences in the quantity of serotonin, and the density and distribution of associated elements have been linked to species-level differences in nonhuman animals, including primates. The amygdala, a key structure involved in social cognition, behavior, and emotion, is heavily innervated by the serotonin system. Postmortem tissue sections containing the rostrocaudal extent of the amygdala from six human individuals were stained for serotonin transporter (SERT) utilizing heat-based antigen retrieval and immunohistochemistry on free-floating sections. SERT-immunoreactive (SERT-ir) axon fiber density in the lateral, basal, accessory basal, and central nuclei of the amygdala was quantified using unbiased stereological methods. Human amygdala results were analyzed with a published data set from a similarly designed study comparing SERT-ir fiber density in chimpanzees and bonobos (Stimpson et al. 2015) utilizing ANOVA with repeated measures and Tukey corrections for multiple comparisons. Significant differences were found between humans and both nonhuman apes in the accessory basal nucleus, and between humans and chimpanzees in the central nucleus, with the human group demonstrating an increase in SERT-ir fiber density in these nuclei. The accessory basal nucleus serves

as an interface between cognitive circuits of the basolateral amygdala and autonomic circuits of the central nucleus and brainstem. The present findings suggest that an increased emphasis on the modulation of amygdaloid neural circuitry between cognitive and autonomic pathways by the serotonergic system may be a human-specific specialization, and could contribute to species-level differences in social cognition and behavior.

This research was supported by the National Institutes of Health P01 NICH033113, 5R03MH103697 and R56MH109587.

Using Elliptical Fourier Analysis to Validate the Use of Upper-Facial Traits in the Construction of the Biological Profile

JORDAN R. LEWMAN, STEPHEN P. NAWROCKI and KRISTA E. LATHAM

Biology, University of Indianapolis

The facial skeleton displays extensive geographic and ancestral variability that may also be affected by sex and age-at-death. As such, a number of ancestry and sex determination methods have been developed for facial traits, typically focusing on the midface. The upper face is less well understood. The current study employs elliptical Fourier analysis (EFA) to identify discrete features of the upper face in the midsagittal plane that may assist in forensic identification.

Photographic, metric, and demographic data were acquired for 795 crania from the US, Portugal, South Africa, Argentina, and Thailand. Photographs were prepared for EFA using PhotoShop® and analyzed using SHAPE and SPSS® software. Seven significant principle components (PCs) were identified, with eigenvalues indicating each specimen's deviation from the size-corrected modal shape. ANCOVA was run on the eigenvalues using sex, ancestry, their interaction, and age as independent variables. All seven PCs varied significantly by ancestry; specimens from Argentina and Thailand tended to fall at the extremes. Sex was relevant for only PC4 and PC5, the interaction was significant for only PC 3, and age affected none of the PCs.

PCs 1 and 2 reflect anterior projection of the upper-face and frontal convexity, respectively. PCs 3 and 4 reflect vertical rhinal positioning and superciliary arch robusticity. PCs 5 and 6 reflect nasal concavity and rhinal projection. PC7 reflects nasal height. These data support the use of various upper-facial traits in ancestry and sex determination and highlight the need for population-specific standards when constructing a biological profile.

ABSTRACTS

Lighten the load: calcanei of leaping galagids have relatively less cortical bone volume than quadrupedal species

KRISTI L. LEWTON^{1,2} and BIREN A. PATEL^{1,2}

¹Integrative Anatomical Sciences, Keck School of Medicine, University of Southern California, ²Human & Evolutionary Biology Section, Department of Biological Sciences, University of Southern California

Because a heavier hindlimb is more energetically costly to swing than a lighter hindlimb (i.e., more effort is needed to accelerate and decelerate the limb), optimizing hindlimb mass is critical to maximize leap performance. Although previous work in leaping primates has examined overall hindlimb mass and hindlimb muscle mass, little is known about hindlimb bone mass, particularly in the distal-most segments. In this study, distal hindlimb bone mass is assessed by quantifying cortical bone volume in the calcaneus and navicular in a sample of 23 individuals of four galagid species that differ in the percentage of time engaged in leaping locomotion (*Euoticus*, *Otolemur*, *Galago*, and *Galagoides*). We predict that habitual leapers should exhibit relatively less cortical bone volume than more quadrupedal species to decrease overall hindlimb mass. From micro-CT scans, cortical bone was isolated from the distal calcaneal and navicular interarticular segments and its volume was calculated; bone volume fraction was determined as the ratio of cortical bone volume to total bone segment volume. Bone volume fraction for each tarsal was analyzed using the Wilcoxon signed rank test with locomotor group as the categorical factor. As predicted, leaping species have less relative cortical bone volume than more quadrupedal species for the calcaneus (Wilcoxon χ^2 : 5.4, $p=0.02$); no significant differences were found in the navicular. These results support the hypothesis that the distal hindlimb of habitual leaping galagids has relatively less bone mass than that of more quadrupedal species, thereby further aiding in lightening the hindlimb to increase leap performance.

This study was funded by the Office of the Provost at the University of Southern California.

Genetic Research of Ancient Human Remains in the Central Plains during Yangshao Period

JIAWEI LI¹, YE ZHANG², HONG ZHU¹ and HUI ZHOU^{1,2}

¹Research Center for Chinese Frontier Archaeology, Jilin University, ²College of Life Science, Jilin University

The Yangshao culture (~5000-3000 BC) was formed in the Neolithic period in central China. And the Central Plains was the important area to study the form of ancient Chinese civilization and the appearance of country. Archaeological discover proved that the Central Plains were the

central area where acted the Chinese nation with the Han nationality as main body from Xia to the Han and Tang dynasties. Therefore, there is no doubt that the deeper research on genetic structure of human remains from Yangshao culture archaeological sites in the Central Plains is very important for us to explore the formation and development of modern Han.

In this research, the mtDNA hypervariable sequence I (HVS-I) was analyzed in 24 human remains from four sites during Yangshao period in the Central Plains, and whole-genome shotgun sequencing were performed on eight of them. The mitochondrial haplogroups of the 24 samples were A, B, D, F, G Z, M*, M10, and N*, which all common haplotypes in East Asia. And nuclear genome analysis showed that the genetic composition of the ancient farming samples was mainly the ancestral component of East Asia, followed by the ancestral components from Siberia. This is similar to the genetic structure of the modern Han, Naxi, Yi and Japanese. These results indicate that the genetic composition of farmers living in the Central Plains, which dominated by East Asian ancestral components, is relatively stable for thousands of years.

Impact of modernization on human gut microbiome diversity on three islands of Vanuatu

MIAN LI¹, KYLE GOWEN², AMANDA ROOME², DAVE JACOBSON³, NISHA PATEL⁴, JEFFREY KOJI. LUM² and KRITHI SANKARANARAYANAN⁴

¹Department of Biological Sciences, Binghamton University, ²Department of Anthropology, Binghamton University, ³Department of Anthropology, University of Oklahoma, ⁴Department of Microbiology, University of Oklahoma

The Republic of Vanuatu is undergoing a rapid health transition from infectious diseases to noncommunicable diseases as a result of modernization. More than 10 years of longitudinal study showed that increasing rates of chronic diseases positively correlated with the modernization level of islands within Vanuatu. Changes in diet and activity patterns are key indicators of modernization. Recent studies have suggested that the gut microbiome plays a critical role in modulating risk of several chronic diseases, and there is great interest in studying microbiome changes associated with diseased states. The islands of Vanuatu, with uneven pace of modernization among inhabited islands, provide an ideal place to investigate how modernization affects the gut microbiome diversity and whether certain chronic disease associate with any microbes. In total, we collected 41 human fecal samples from the island of Efate (n=2), Aneityum (n=33) and Gaua (n=6) during the summer of 2017. Efate is home to the urban capital. Aneityum is a rural island with regular access to tourism. Gaua is rural island with no tourism. 16S rRNA-based

taxonomy profiling shows that the Vanuatu gut microbial community is characterized by high relative abundances of Firmicutes, followed by Bacteroidetes at the phylum level. Interestingly, Cyanobacteria can be detected in almost all participates. Obese individuals have significantly lower α diversity (Faith PD) than normal and overweight people. Currently, there is no detectable difference among three islands in term of α diversity and individuals from different islands are mingled with each other on the PCA plot.

Rethinking the evolution of the plantar aponeurosis and the medial longitudinal arch

DANIEL E. LIEBERMAN¹, NICHOLAS B. HOLOWKA¹ and FREDDY SICHTING²

¹Human Evolutionary Biology, Harvard, ²Human Movement Science and Health, Technische Universität Chemnitz

Despite debate over when the medial longitudinal arch (MLA) evolved, it is generally hypothesized to be an adaptation for bipedal locomotion that functions as a windlass-like mechanism to stiffen the foot during propulsion in walking and running and as a spring-like mechanism during running. A more pronounced plantar aponeurosis is also commonly hypothesized to be a related, human feature underlying both mechanisms, acting either as a stiff or elastic bowstring at the base of the MLA. Here we test these hypotheses using three sets of data. First, we analyzed the evolutionary history of the plantar aponeurosis with cadaveric dissection data from 23 non-human primate species and 4 non-primate outgroups. Second, we measured foot stiffness in vivo during propulsion in chimpanzees kinematically and in humans using inverse dynamics. Third, we measured elastic energy storage in humans with varying intrinsic foot muscle size and MLA height using inverse dynamics and ultrasound. These analyses disprove the hypothesis that the plantar aponeurosis is a derived human feature to stiffen the MLA during propulsion. Instead, the plantar aponeurosis is present in most primates, although with important structural variations. In addition, species such as chimpanzees that lack an MLA are able to stiffen partially their midfoot during propulsion. Finally, we show that variations in arch stiffness during walking are influenced strongly by MLA height and intrinsic foot muscle strength. We apply these results to the fossil record to suggest that the modern MLA evolved to facilitate elastic energy storage during running.

ABSTRACTS

Statistical modeling of diurnal biomarker data: Guidelines, challenges, and future directions

MELISSA A. LIEBERT¹ and SAMUEL S. URLACHER²

¹Department of Anthropology, Northern Arizona University, ²Department of Evolutionary Anthropology, Duke University

Many biological systems in humans and non-human primates are regulated by temporal rhythms that fluctuate over diurnal periods (e.g., hormone production, body temperature, inflammatory processes). Given the oscillating nature of these physiological patterns, repeat collection of multiple biological samples over timed intervals is required to capture the complexities in diurnal activity. Fortunately, recent advancements in minimally-invasive sampling and statistical techniques, including multilevel, mixed-effects models, have provided novel opportunities to assess variation in diurnal biological rhythms in naturalistic settings. These analytical approaches avoid the limitations of simple averages by estimating between- and within-individual variation simultaneously, while also permitting the concurrent modeling of multiple features of the diurnal curve (e.g., waking levels, change in levels across the day, total daily output). Despite these advances, methodological gaps, including variability in collection methods, sampling times, and estimations of diurnal profile parameters, hamper the ability to understand how diurnal rhythms relate to biological and behavioral outcomes. For example, recent studies suggest that forager-horticulturalist populations in Ecuador, Papua New Guinea, and Bolivia have lower salivary diurnal cortisol levels than industrialized societies (Liebert, 2016; Nyberg, 2012; Urlacher et al., 2018); however, direct comparisons of diurnal patterns across population-based studies should be interpreted cautiously due to differences in collection protocols. Considering these limitations, this study seeks to initiate a conversation on the guidelines, challenges, and future directions of modeling diurnal profiles. As anthropologists increasingly study these biological rhythms, it is important that our field contributes to interdisciplinary dialogue on the statistical procedures used to analyze diurnal biomarker data.

Support: Wenner-Gren Foundation for Anthropological Research (#8749, 8476); National Science Foundation (#BCS-1341165, GRF-2011109300); Ryoichi Sasakawa Young Leaders Fellowship Fund; University of Oregon.

Oral and Sinus Infection Among Okhotsk Marine Foragers: Implications for Differential Frailty

ANGELA R. LIEVERSE¹, HAJIME ISHIDA², DAISUKE KUBO³ and MINORU YONEDA⁴

¹Archaeology and Anthropology, University of Saskatchewan, ²Human Biology and Anatomy, University of the Ryukyus, ³Graduate School

of Medicine, Hokkaido University, ⁴Integrated Biosciences, University of Tokyo

Okhotsk foragers occupied northern and eastern Hokkaido (Japan) between the eighth and twelfth centuries AD. While relying heavily on hunting and fishing, particularly of marine resources, their maritime focus intensified as they expanded eastward across Hokkaido, largely in response to changing winter sea ice conditions. Stable isotope analyses suggest that sexual discrepancies in diet may have accompanied the subsistence shift with their eastward expansion. Males from the eastern Hokkaido Okhotsk period site of Moyoro appear to have consumed more variable diets, including more terrestrial foods, than did females, possibly reflecting preferential access to resources. Did these documented dietary discrepancies between the northern and the eastern groups and between males and females differentially affect frailty, that is, susceptibility to illness, disease expression, and death? This paper uses oral and sinus infection data as proxies for frailty in order to compare two Okhotsk period skeletal samples, one from eastern Hokkaido (Moyoro, n=59) and one from the north (Hamanaka 1 on Rebun Island, n=10). Infection data documented include periodontitis, alveolar cavities of pulpal origin, and maxillary sinusitis, all of which have been associated with an increased risk of morbidity and/or mortality. Results reveal that infection prevalence is quite high overall, but there are no considerable differences between the two regions, despite the subsistence shift. Furthermore, while a number of male-female distinctions are present, these appear to change with advancing age and are more likely to reflect sex-related immune responses or gendered activity patterns, rather than differential frailty.

Funding was provided by 1) Social Sciences and Humanities Research Council of Canada and 2) Japanese Society for the Promotion of Science

Patterns of Genetic Coding Variation in a Native American Population before and after European Contact

JOHN LINDO¹, MARY ROGERS², LIZ MALLOTT³, BARBARA PETZELT⁴, JOYCELYNN MITCHELL⁴, DAVID ARCHER⁵, JEROME CYBULSKI⁶, RIPAN MALHI² and MICHAEL DEGIORGIO⁷

¹Anthropology, Emory University, ²Anthropology, University of Illinois at Champaign-Urbana, ³Anthropology, Northwestern University, ⁴Treaty, Metlakatla Treaty Office, ⁵Anthropology, Northwestern Community College, ⁶Anthropology, Canadian Museum of History, ⁷Biology, Pennsylvania State University

The effects of European colonization on the genomes of Native Americans may have produced excesses of potentially deleterious features, mainly due to the severe reductions in population size and corresponding losses of genetic diversity. This assumption, however, neither considers actual genomic patterns that

existed before colonization nor does it adequately capture the effects of admixture. In this study, we analyze the whole-exome sequences of modern and ancient individuals from a Northwest Coast First Nation, with a demographic history similar to other indigenous populations from the Americas. We show that in approximately ten generations from initial European contact, the modern individuals exhibit reduced levels of novel and low-frequency variants, a lower proportion of potentially deleterious alleles, and decreased heterozygosity when compared to their ancestors. This pattern can be explained by a dramatic population decline, resulting in the loss of potentially damaging low-frequency variants, and subsequent admixture. We also find evidence that the indigenous population was on a steady decline in effective population size for several thousand years before contact, which emphasizes regional demography over the common conception of a uniform expansion after entry into the Americas. This study examines the genomic consequences of colonialism on an indigenous group and describes the continuing role of gene flow among modern populations.

This research was funded by the National Science Foundation (BCS-1413551 and BCS-1518026).

Habituation Update on Assirik Chimpanzees at Niokolo-Koba National Park, Senegal

STACY LINDSHIELD¹, PAPA IBNOU NDIAYE², MALLÉ GUEYE³ and STEPHANIE L. BOGART⁴

¹Department of Anthropology, Purdue University, ²Département de Biologie Animale, Univeristé Cheikh Anta Diop, ³Parc National Djoudj, Direction des Parcs Nationaux, ⁴Department of Anthropology, University of Florida

Habituating non-human primates (NHP) facilitates the development of rich behavioral databases and transforms comparative studies in biological anthropology. Bringing habituation to new corners of the NHP world is near essential to the discovery science and longitudinal study of behavior. For instance, habituation of savanna chimpanzees at Fongoli, Senegal led to breakthrough discoveries on their material culture, disrupting the paradigm that humans are unique among the primates by routinely hunting with tools. We build on this tradition by aiming to habituate a western chimpanzee (*Pan troglodytes verus*) community at the Assirik site in Niokolo-Koba National Park. Our protocols maximize neutral encounters with Assirik chimpanzees while following best practice guidelines on habituation and disease transmission prevention. We conducted dry season vigils near surface water and patrolled the community's home range when water was abundant. From June 2017-2018, we completed 41 vigils and 97 patrols, encountering chimpanzees during 25% (N = 34 cases) of scouting exercises. We encountered

ABSTRACTS

parties with an average of 4.5 ± 3.5 individuals (median = 3, range = 1-14). In 62% of cases (N = 21), the majority of individuals within the party did not immediately flee. Instead, they exhibited curiosity or ignored us. The majority of encounters occurred at water sources (65%, N = 22), highlighting the importance of vigils in water-scarce environments. With sustained effort, habituation of the Assirik chimpanzees is likely. We predict that success will yield novel insights into the behavior and ecology of our closest living relatives who inhabit the speciose savannas at Assirik.

This study was supported by the National Science Foundation (BCS-1700313), Primate Conservation, Inc., Purdue University, the USC Jane Goodall Research Center, and the Leakey Foundation.

Professor Erik Trinkaus and paleoanthropological studies in China

WU LIU and XIU JIE WU

Key Laboratory of Vertebrate Evolution and Human Origins of Chinese Academy of Sciences, Institute of Vertebrate Paleontology and Paleoanthropology, Chinese Academy of Science

In recent decades, human fossils collected from more than 70 sites in China have triggered debates on the emergence of early modern humans in East Asia. In a series of studies conducted from 2006 to the present time, Professor Trinkaus has collaborated with IVPP researchers to study some of these fossils. Using AMS ^{14}C dating of bone specimens exhibiting modern human-like mandible and tooth features, Trinkaus and colleagues reliably assigned Tianyuan Cave fossils to early modern humans. In another study, a modern human-like mandible found at the Zhirendong site was dated to 100 ka, providing evidence that modern humans existed in East Asia 60 ka earlier than previously demonstrated. Meanwhile, Trinkaus and Chinese colleagues have expanded their research to other fields of study. Notably, their morphological analysis of a cranial lesion of a Maba human fossil skull dating to 130 ka has provided evidence of antemortem trauma that possibly resulted from violent human activity. Recently, from 2011 to 2015 Trinkaus participated in a series of paleopathological studies of mandible focused on inner ear morphology and rare anomalies of archaic human remains dating to 120 ka from the Xujiayao site. More recently, since 2016 Trinkaus has participated in a study of newly discovered human crania from Xuchang. Such collaborations have greatly promoted the study of human evolution in China and provided new evidence of

early modern emergence, with characterization of individual variations and population dynamics confirming the emergence of early modern humans in East Asia.

The related studies have been supported by the grants from the External Cooperation Program of BIC (132311KYSB20160004) of Chinese Academy of Sciences, National Natural Science Foundation of China (41630102, 41672020).

Mutable Environments and Permeable Human Bodies

MARGARET LOCK

Department of Social Studies of Medicine and Department of Anthropology, McGill University

Geologists have declared an epochal transition to the Anthropocene, thus formally recognizing human activities as the driving force of destructive global change; a distinction can no longer be made between human history and natural history. Certain commentators argue that Capitalocene better characterizes this situation because the effects of planetary decimation are unequally distributed among humans. A second conceptual change has recently taken place, namely that environmental stimuli both external and internal to the human body bring about the creation of genomes; genomes neither initiate life nor drive human development. The resultant burgeoning field of behavioral epigenetics is introduced followed by illustrative examples in which environmentally caused epigenetic changes that negatively impact on health are presented. Epigeneticists limit their attention to detecting objective changes at the molecular level. I argue that, in addition to epigenetic findings, subjective narratives about embodiment of past and present events must be included to effectively situate and account for biological difference historically, ecologically, and politically. A brief discussion of the microbiome provides a cautionary reminder that microbes are the ultimate driving force of health and illness. In conclusion it is argued that the unexamined assumption of an opposition between culture and nature must be dispensed with.

An experimental study of human hand pressures during suspension and implications for fossil hominin locomotion

VICTORIA A. LOCKWOOD^{1,2}, SZU-CHING LU², SAMANTHA WINTER³ and TRACY L. KIVELL^{2,4}

¹Center for the Advanced Study of Human Paleobiology, Department of Anthropology, The George Washington University, Washington, DC, USA, ²Animal Postcranial Evolution (APE) Lab, Skeletal Biology Research Centre, School of Anthropology and Conservation, University of Kent, Marlowe Building, Canterbury, Kent, CT2 7NR, UK, ³School of Sport and Exercise Sciences, The Medway Building, University of Kent, Chatham Maritime, Kent, ME4 3AU, UK, ⁴Department

of Human Evolution, Max Planck Institute for Evolutionary Anthropology, Deutscher Platz 6, Leipzig, 04103, Germany

Studies of the human hand can be useful for furthering our understanding of how fossil hominins interacted with their environments, particularly in relation to hypotheses concerning the significance of arboreal behaviors. Using a custom-built apparatus, we measured hand pressure experienced during dynamic and static suspension in six human participants to determine where load is experienced by the hand during suspension. Participants grasped 45mm, 80mm, and 105mm support diameters and three activity categories were investigated: static suspension with thumb adducted and abducted, and dynamic suspension using participants preferred hand grip. Qualisys® motion capture and Novel Pliance® pressure systems were synchronized to measure 3D hand posture data and the location of peak pressures, normalized by body mass, across the human hand. Peak pressure was typically experienced by the second through fourth digits across all support diameters and activities. Significant differences in the pressure value were found between the 45mm and 105mm diameters for the thumb adducted and abducted categories. In each activity, the 45mm diameter had the greatest normalized peak pressure. The location of peak pressure was observed to move to more distal and proximal areas of the hand as the diameter of the support increased. The distal and proximal locations of peak pressure on the largest diameter are concordant with previous human ergonomic research and captive bonobo hand pressures experienced during arboreal suspension. These results suggest that if fossil hominins still engaged in arboreal suspension, that morphological signals of this behavior may be found in the second through fourth digits.

Funded by ERC Starting Grant 336301 (TLK, S-CL).

Ontogeny of human cranial vault microstructure

DANIELA LOMBARDO¹, HÉLÈNE COQUEUGNIOT^{2,3} and THOMAS COLARD^{1,2}

¹Univ. Lille, EA 4490-PMOI-Physiopathologie des maladies osseuses inflammatoires, Lille, France., University of Lille, ²UMR 5199, PACEA, université de Bordeaux, 33615 Pessac Cedex, France, University of Bordeaux, ³PSL University-Paris – Ecole Pratique des Hautes Etudes, University of Paris

Human cranial vault (HCV) has a major protective role for the brain. It is formed by two dense layers of cortical bone, and a central layer of cancellous bone called the diploe. Growth, development and evolution of HCV have been widely studied by measuring thickness variations, providing strong evidences of a link with the brain and the masticatory muscles. However, little is known about the ontogenetic changes of its microstructure. The recent development of micro-computed

ABSTRACTS

tomography allows an accurate description of cortical and trabecular bone microarchitecture. The main goal of our study is to record the ontogenetic changes in cranial vault microstructure, from birth to 12 years old.

We selected 45 cranial vault samples of 9mm in diameter, in subadults from 3 months to 12 years old, and 5 complete skulls of newborns. Bone samples were imaged with high-resolution MicroCT (Skyscan microCT®, Bruker, Kontich, Belgium), with 5-10 microns resolutions. Applying specific cortical and trabecular thresholds, 2D and 3D microstructural parameters were measured.

We provided a detailed map of the cortical (thickness and porosities) and trabecular (number, thickness and spaces) parameters related to age. The results showed a fast individualization of outer and inner tables after birth, and the formation of an initial well organized trabecular network from 1.5 years, followed by a long period of increase in size.

This study provided new insights into the cranial vault ontogeny that could be relevant to understand the multiple factors involved in the evolution of human skull.

Endurance activity as a driver of morphological thermal adaptation: the energetics of ultramarathons in extreme temperatures

DANIEL P. LONGMAN¹, ALISON MACINTOSH^{1,2}, REBECCA ROBERTS¹, SASKIA OAKLEY¹, JONATHAN CK. WELLS³ and JAY T. STOCK^{1,4,5}

¹Department of Archaeology and Anthropology, University of Cambridge, ²Department of Anthropology, University of Victoria, ³Childhood Nutrition Research Centre, UCL Institute of Child Health, London, ⁴Department of Anthropology, University of Western Ontario, ⁵Department of Archaeology, Max Planck Institute for the Science of Human History

Both extinct and extant hominin populations have been shown to display morphological features consistent with Bergmann's and Allen's Rules. However, the energetic functional implications of the morphologies described by these ecogeographical rules are poorly understood. While previous research has attracted interest in terms of locomotor energetic efficiency, we examined this through the lens of endurance running. Our investigation considered a less-studied dimension of morphological functionality in endurance running – thermoregulation.

The performance of ultramarathon runners competing in hot and cold environments was analysed with reference to expected thermoregulatory energy costs and the optimal morphologies predicted by Bergmann's and Allen's Rules.

Ecogeographical patterning pertaining to both principles was observed in ultra-marathon runners ($n=140$) competing in thermally-challenging

environments. Finishers of hot-condition events had significantly longer legs (male & female), lower body mass and lower BMI (female) than finishers of cold-condition events. Furthermore, hot-condition finishers had significantly longer legs (male), lower body mass, BMI, ponderal indices and torso circumferences (female) than athletes who failed to complete hot-condition events. A degree of niche-picking was evident; athletes may have tailored their event entry choices in accordance with their previous hot/cold race experiences.

Endurance exercise in hot and cold climates imposes significant thermoregulatory demands, providing powerful selective forces which drive the adoption of temperature-adapted morphologies. We propose a novel mechanism whereby the interaction between environment and prolonged physical activity leads to adaptation and the emergence of environmentally appropriate morphologies. Such phenotypes reduce thermoregulatory energetic expenditure, allowing energetic diversion to other processes such as faster running.

The research leading to these results has received funding from the European Research Council under the European Union's Seventh Framework Programme (FP/2007-2013) / ERC Grant Agreement n.617627

The curious case of goldenhar-gorlin syndrome: Identification and skeletal manifestation

DAYANIRA LOPEZ and HEATHER WALSH-HANEY
Justice Studies, Florida Gulf Coast University

Goldenhar-Gorlin Syndrome (GHGS) is a congenital disease characterized by malformations of the axial skeleton. In some cases, there may be complete absence of skeletal elements, as well as poor development of soft tissue processes, such as the ear. Previous research has identified the dysplasia of the first and second branchial arches during development of the jaws in utero, in the expression of this syndrome. Clinical diagnoses range between 1:3500 and 1:5600 live births with a male to female ratio of 3:27. Despite its rarity, skeletal analysts may have encountered the condition, but because of diagenesis and/or lack of knowledge, this condition may have been identified as an axial development defect (ADD).

The role of the forensic anthropologist in death investigations is to build the biological story of an individual via detailed evaluation of skeletal remains. To do so, it is important to identify (and differentiate) antemortem pathologies, such as GHGS, to add strength to the biological story, while assisting in a positive identification.

We present a case study of donated human remains clinically diagnosed with GHGS revealing that 37% of the skeleton was notably affected. However, other postcranial elements also presented with antemortem trauma of unknown

etiology. To distinguish between skeletal anomalies from the disease and those from in-life injuries, an ethnoforensic interview with the family of the decedent was conducted. Coupling the skeletal analysis with the family information provides a special opportunity for the forensic anthropologist, and by extension, inform skeletal analysts about differential diagnosis of GHGS and ADDs.

Synchrotron radiation holographic nanotomography of ancient human hair: Exploring number, distribution and shape of melanin granules, and their implications as to hair colour

KIRSI O. LORENTZ¹, JULIO CESAR. DA SILVA², CHARALAMBOS CHRYSOSTOMOU³, YUKO MIYAUCHI¹, SIMONE LEMMERS¹, MOHAMMAD R. ZARURI⁴, FARZAD FORUZANFAR⁵ and MANSUR SAJJADI⁵

¹Science and Technology in Archaeology Research Center (STARC), The Cyprus Institute, ²Beamline ID16A, European Synchrotron Radiation Facility (ESRF), ³Computation-based Science and Technology Research Center (CaStoRC), The Cyprus Institute, ⁴Golestan Branch, RICCHT, ⁵ICAR, Iranian Center of Archaeological Research

We investigated the number, distribution and shape of melanin granules in 5000-year-old ancient human hair samples (Shahr-i Sokhta, Iran) from five different individuals ($n=5$; two modern controls $n=2$; total $n=7$) using synchrotron radiation holographic nanotomography. Prior, we observed different hair colours under light microscopy, including reddish hues. As melanin pigment granule number and distribution pattern determine the colour of hair, and these can be affected by degradative processes, including photo-degradation and biodegradation, this research aimed to determine whether there are any significant differences between the ancient hair samples, of different preservation status, by tomographically imaging such melanin granules and their distribution within the hair, in nanometer scale. Our hypothesis was that the reddish hues were due to alternations in the melanin granules due to degradative processes.

Since hair absorbs X-rays only weakly, and hair diameter is only c. 80-100 micrometers, we needed synchrotron radiation (SR) phase-contrast holographic tomography to be able to probe the hair at nanometer-scale. The holographic tomography data capture was performed at 17.05 keV at beamline ID16A at ESRF. Our results show postmortem and postdepositional alterations, with colour changes in hairs attributable to a number of factors such as photodegradation of pigment granules in sunlight, and oxidation of melanin pigment granules over millennia. Human scalp hair, when sufficiently preserved, provides crucial information about past human activities and health, and the characterisation of its

ABSTRACTS

preservation status is therefore of importance. To our knowledge, this is the first time holographic nanotomography has been used to analyse ancient human hair.

Beamtime awarded by ESRF (HG-137-Lorentz); research travel funding by LAAAMP enabled pre-beamtime test; The Cyprus Institute research travel funds enabled Lorentz, Miyauchi and Lemmers to travel to ESRF for beamtime.

Its elementary my dear anthropologist: using lead and arsenic concentrations and stable carbon and nitrogen isotope analysis to estimate anthropogenic disturbance among free-ranging vervet monkeys (*Chlorocebus pygerythrus*) in South Africa

JAMES E. LOUDON¹, ALCYIA E. LEWIS², J.P. GROBLER³, TRUDY R. TURNER^{2,3} and MATT SPONHEIMER⁴

¹Anthropology, East Carolina University, ²Anthropology, University of Wisconsin-Milwaukee, ³Genetics, University of the Free State, ⁴Anthropology, University of Colorado, Boulder

This study combines stable carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) isotope values with Lead (Pb) and Arsenic (As) concentrations in the hair of vervet monkeys (*Chlorocebus pygerythrus*) to estimate anthropogenic disturbance. We studied three groups in South Africa with varying degrees of human impact. The Baviaanskloof group inhabits a reserve that strictly prohibits feeding the wildlife. The Soetdoring group lives in at a reserve ~45 km from Bloemfontein and visitors occasionally interact and feed the monkeys. The Parys group lives alongside a city of ~50,000 people. We expected that the Parys group would exhibit the highest $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values given their greater access to crops and processed foods. We also expected elevated concentrations of Pb and As given their higher exposures to these metals. In contrast, we expect the Baviaanskloof would exhibit the lowest $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values and metal concentrations, and intermediate values for the Soetdoring group. Baviaanskloof vervets exhibited the lowest $\delta^{13}\text{C}$ ($-22.4 \pm 0.2\text{‰}$) and $\delta^{15}\text{N}$ values ($6.7 \pm 0.7\text{‰}$) and the lowest concentrations of Pb ($0.61 \pm 0.25\text{ppm}$). However, this group also yielded the highest concentrations of As ($0.22 \pm 0.11\text{ppm}$). Soetdoring vervets yielded intermediate $\delta^{15}\text{N}$ values ($7.6 \pm 0.9\text{‰}$) and Pb concentrations ($0.77 \pm 0.29\text{ppm}$), the highest $\delta^{13}\text{C}$ values ($-19.8 \pm 0.3\text{‰}$) and the lowest As concentrations ($0.16 \pm 0.08\text{ppm}$). Parys vervets had the highest $\delta^{15}\text{N}$ values ($9.7 \pm 0.8\text{‰}$) and Pb concentrations ($1.1 \pm 0.4\text{ppm}$) and intermediate $\delta^{13}\text{C}$ values ($-20.8 \pm 0.3\text{‰}$) and As concentrations ($0.21 \pm 0.11\text{ppm}$). This study demonstrates the limitations of relying solely on elemental analyses to assess anthropogenic disturbance but highlights how these datasets are good supplements for examining human impacts on wildlife.

Climatic variables are strong predictors of allonursing and communal nesting

ALEXANDRA LOUPPOVA¹, JASON M. KAMILAR^{2,3} and ANDREA L. BADEN^{1,4,5}

¹Anthropology, Hunter College of the City University of New York, New York, ²Anthropology, University of Massachusetts, Amherst, ³Graduate Program in Organismic and Evolutionary Biology, University of Massachusetts, Amherst, ⁴PhD program in Anthropology, Graduate Center of the City University of New York, New York, ⁵Physical Anthropology, New York Consortium in Evolutionary Primatology

Allomaternal care (AMC) is widespread throughout the primate order, with nearly 75% of primate taxa exhibiting some form of AMC. Previous studies of primate AMC have primarily focused on the benefits received from it (e.g., increased infant survival, learning to mother, or improved kin relationships). Our study examined how ecology can influence cooperation and whether energetic costs from AMC are outweighed through increased survival in seasonal and unpredictable environments (e.g. low rainfall, high seasonality, or high variability). Therefore, we tested if increased environmental seasonality and stochasticity will drive certain behaviors especially with cooperative behaviors often linked to arid environments.

Here, we used published data from 91 primate species to ask whether specific AMC behaviors were prevalent in more harsh, unpredictable climates. These AMC behaviors included allonursing, communal nesting, provisioning, babysitting, and carrying. Predictor variables included temperature and precipitation (mean, variation, and seasonality), diet, habitat diversity, mating seasonality, and mating style. We used Phylogenetic Generalized Least Squares (PGLS) to assess which environmental factors could predict AMC behaviors. We found that species inhabiting more seasonal and variable environments were significantly associated with communal nesting ($p=0.004$). While species inhabiting areas with low rainfall, high seasonality and low habitat diversity were strongly associated with allonursing ($p=0.014$). Babysitting, provisioning and carrying did not have significant climatic predictors, which was different from our expected results. Therefore, our results suggest that environmental variables are good predictors of allonursing and communal nesting in primates and can impact variation in AMC behaviors.

Gut microbial composition differs based on reproductive state in wild Phayre's leaf monkeys

AMY LU¹, ELIZABETH MALLOTT² and KATHERINE AMATO²

¹Anthropology, Stony Brook University, ²Anthropology, Northwestern University

Recent research in humans and other mammals have found that the composition of the gut microbiome shifts in response to increasing energetic demands, including those associated with costly reproductive states such as gestation and lactation. Such changes often include an increase in Firmicutes and other microbial taxa that provide hosts with energy via the breakdown of plant carbohydrates and/or lipid metabolism. Here, we examine whether similar shifts in gut microbial communities are found during pregnancy and lactation in a wild Colobine: Phayre's leaf monkeys (*Trachypitecus phayrei crepusculus*, Phu Khieo Wildlife Sanctuary, Thailand). Using fecal samples collected from 15 females with known reproductive states, we found that overall gut microbial community composition differed significantly between cycling, pregnant, and lactating females (PERMANOVA, $R^2=0.115$, $p=0.004$). Although the relative abundance of most major phyla, including Firmicutes and Bacteroidetes, did not vary between reproductive states, the relative abundance of Tenericutes was elevated during the first part of lactation compared to all other periods except the 3rd trimester of pregnancy (all $p<0.05$). A similar increase in Tenericutes abundance occurs during the 3rd trimester in humans, and may be associated with high calorie/protein diets and simple sugar metabolism. Further data are required to determine whether Tenericutes facilitate greater energy extraction, or are simply a consequence of energy-rich diets.

Research was supported by the Leakey Foundation, the National Science Foundation, Stony Brook University, and Northwestern University.

Comparison of Play Frequency in Four Sympatric Monkey Species in Kibale National Park, Uganda

SARA G. LUCCI¹ and JESSICA M. ROTHMAN^{1,2}

¹Anthropology, Hunter College, ²City University of New York, The New York Consortium in Evolutionary Primatology

Play during primate development can take different forms such as social play, which includes wrestling and chasing. It is hypothesized that different species will have different frequencies of overall play. In addition, social play is hypothesized to be more frequent in males than females in species where there is generally more aggression over resources in adult males than females. This study sought to determine the differences in play frequency between males and females among four sympatric monkey species in Kibale National Park, Uganda. Data were collected on infant and juvenile individuals of both sexes of red colobus (*Procolobus rufomitratus*), and grey-cheeked mangabeys (*Lophocebus albigena*), which both have more aggression in adult males than females, and black and white colobus (*Colobus guereza*), and redtail monkeys (*Cercopithecus ascanius*), which have little

ABSTRACTS

difference in aggression between males and females. Over 43 days in 2018, monkeys were observed using 20-minute focal observations, and their frequency of overall play and social play were measured. The four species had different overall play frequencies. Red colobus had the greatest play frequency (5.95 \pm 0.13%) of the four species, followed by black and white colobus (2.32 \pm 0.05%), then grey-cheeked mangabeys (0.35 \pm 0.01%), and the redtail monkeys (0.22 \pm 0.004%) ($P=0.00214$). However, males and females did not have different frequencies of social play in red colobus ($P=0.121$), black and white colobus ($P=0.474$), grey-cheeked mangabeys ($P=0.783$), or redtail monkeys ($P=0.334$). Therefore, while there are differences in play frequency among these species, the hypothesis of social play based on adult aggression was not supported.

Department of Anthropology, Hunter College, City University of New York

Black Sea steppe warriors: health status and demographic structure of the Scythians from Moldova (4th-2nd c. BC)

SYLWIA ŁUKASIK¹, JAKUB BIJAK², MARTA KRENZ-NIEDBAŁA¹ and VITALY SINIK³

¹Department of Human Evolutionary Biology, Faculty of Biology, Adam Mickiewicz University in Poznań, ²Department of Social Statistics and Demography, University of Southampton, ³Archaeological Research Laboratory, Taras Shevchenko University in Tiraspol

Scythians were nomads, pastoralists, who inhabited the Black Sea region in the early Iron Age. Historical sources depict them as warriors, unrestrained rulers of the steppes, who in result of numerous wars have occupied vast areas of Eurasia. The aim of this study was to assess health status and demographic structure of a Scythian population from the Black Sea region. We assumed that the Scythians, due to their position and lifestyle, as well as their dominance over large territories, were characterized by relatively good health and high life expectancy compared to neighboring populations. In total, our analyses involved 312 individuals (93 children and 219 adults) excavated in Glinoe (Moldova), dated to the 4th-2nd c. B.C. The health status was assessed based on stress indicators: enamel hypoplasia (EH), cribra orbitalia (CO) and porotic hyperostosis (PH). The demographic structure was reconstructed by using Bayesian methods. In the study group, the following frequencies of stress markers were found: EH=32.5%, CO=26.7%, PH=1.4%. Life expectancy, assuming stationary population, was estimated at 29.2 \pm 4 years (95% intervals) for newborns (e0), and 15.6 \pm 3 years for 20-year-olds (e20). Slightly higher values were obtained under the stable population assumption, while correcting the number of underrepresented infants reduced the e0 by 10

years on average. Scythians were characterized by a relatively high probability of death in early adulthood. Our results suggest that the demographic structure could depend on their lifestyle (conflicts, wars), which contributed to the significant mortality of young adults, despite their relatively good health.

NCN Miniatura 2017/01/X/H53/00234

Treponemal infections: One disease or many?

SHEILA A. LUKEHART¹ and DAVID C. MABEY²

¹Medicine & Global Health, University of Washington, ²Clinical Science, London School of Hygiene & Tropical Medicine

The origin of syphilis has been a topic of speculation and controversy for many years. Is syphilis really a different disease than yaws or bejel? We address this question in the context of new genomic data on the *Treponema pallidum* subspecies and the increasingly frequent recognition of "non-venereal" subspecies causing genital lesions and "venereal" subspecies causing extragenital lesions in children. We propose that the clinical "differences" that have been used traditionally to differentiate the subspecies are in fact due to the serendipity of the route and age of transmission and to variations in host response, rather than reflecting true biological differences in the etiological agents. Each of the *T. pallidum* subspecies is transmitted by direct contact, with the primary lesions developing at the sites of transmission, and each results in disseminated and chronic infections. There is wide variation in the severity of clinical manifestations, including progression (or not) to late disease among individuals infected with the same subspecies. Modern molecular and genomic studies have revolutionized the study of infectious etiology of bone lesions by removing the subjectivity in assigning "cause" using undeniable genetic data. We explore the recent global genomic and molecular data surrounding the *T. pallidum* subspecies and the clinical contexts in which they are found. These data lead us to support the Unitarian hypothesis, which states that syphilis and the non-venereal treponematoses are one disease, the major differences in clinical outcome being due to the route of infection and the age at which it occurs.

National Institutes of Health

Disentangling and Disappropriating Science

JUSTIN LUND and CECIL M. LEWIS, JR.

Anthropology, University of Oklahoma

Decolonizing and indigenizing movements aim to mitigate a history of trauma and oppression that can manifest in unequal representation both in people, and ideas, in leading professional fields.

This scholarship aims to create space within the academic institution for indigenous perspectives and growth. Among the more challenging fields for these endeavors has been the sciences. Scientific practices apply systematic and structured methodologies that have had great impacts in creating useful understandings of the universe, resulting in countless technological advances. The investigation of nature using structured logic and math is key to the identity of science as defined today, and such foundations are also inherent to much of human reasoning; this process is timeless and near-universal, with no rights to ownership of any entity or group. Nevertheless, because of historical narrative driven by a colonial west, the identity of "western science" as "science" remains pervasive. By distinguishing between indigenous knowledge and western knowledge we reinforce a dichotomy where indigenous knowledge is defined in contrast to scientific knowledge; this is an example of a colonial entanglement, and this entanglement fosters the disparities in scientific practice.

Entanglements are described as a complex process of social identity negotiation where individual and national identities are understood within a colonial context. To disentangle, here we argue that much of the scientific methods should be disappropriated from the perceived "Western" paradigm, to foster bidirectional exchange of information between knowledges resulting in reduced bias in the type of hypotheses raised and investigated; thus, maturing the practice of science.

Olfactory system anatomy in *Homunculus* and the ecological importance of olfactory cues among stem platyrrhines

INGRID K. LUNDEEN¹ and RICHARD F. KAY²

¹Department of Anthropology, University of Texas at Austin, ²Department of Evolutionary Anthropology, Duke University

Anthropoid primates are often viewed as having evolved reduced olfactory systems in favor of higher visual acuity and greater reliance on visual signals. Among platyrrhines, there is significant olfactory system anatomical variation, likely reflecting behavioral variation within this clade. However, the timing of changes in the olfactory system among fossil platyrrhines is poorly understood, in part because turbinals, the bony structures of the nose that support olfactory sensory epithelium, rarely fossilize. Here, we report the first known occurrence of well-preserved turbinals in a stem platyrrhine, *Homunculus patagonicus*, found in the late Early Miocene of Patagonia. The specimen examined here (MPM-PV-3502) is a well-preserved skull that was recovered from the Killik Aike Norte locality from the Santa Cruz Formation in Argentina. High-resolution CT scans of this specimen reveal three ethmoturbinals and one partially

ABSTRACTS

preserved maxilloturbinal. This pattern differs from most platyrrhines, which have one or two ethmoturbinals. Turbinal surface area was digitally segmented and quantified, relative to skull geometric mean, for *Homunculus* and representatives of each platyrrhine clade. A phylogenetic generalized least squares regression shows a significant relationship between olfactory turbinal surface area and skull geometric mean among extant taxa. *Homunculus* has relative olfactory turbinal surface area most similar to pitheciids, suggesting similarity in the behavioral importance of olfactory cues. However, where *Homunculus* has three ethmoturbinals, pitheciids have only one, suggesting that similarity in turbinal surface area does not reflect close phylogenetic relatedness. These findings support the hypothesis that *Homunculus* is a stem platyrrhine ecologically convergent with some crown platyrrhines.

Similarities and differences in cranial trauma in high and low status cemeteries in Colonial Mexico City

PAIGE LYNCH¹, CATHERINE WILLERMET², EMILY MOES¹, HEATHER EDGAR¹ and COREY RAGSDALE³
¹Department of Anthropology, University of New Mexico, ²Department of Sociology, Anthropology, and Social Work, Central Michigan University, ³Department of Anthropology, Southern Illinois University Edwardsville

The Colonial Period in Mexico (1521 – 1696) is characterized by a variety of socioeconomic, political, and biological changes associated with the admixture of colonizing Europeans, African, and indigenous peoples. In Mexico City, social stratification is evident between the *Catedral Metropolitano* and *Iglesia de la Soledad* cemeteries. Historically, *Catedral* served individuals from higher socioeconomic status (SES), whereas *Soledad* served individuals of lower SES. Lower SES is often linked to labor-intensive work and physical conflicts. The aim of this study is to assess differences distribution and type of cranial trauma between the two samples. We hypothesize cranial trauma will be: 1) more prevalent among those buried at *Soledad*, and 2) more common among males.

We examined a sample of cranial photographs of 192 individuals (*Catedral* n= 56; *Soledad* n=136) to assess the type (blunt, sharp), location (facial, cranial vault), and timing (antemortem, perimortem) of trauma. There were approximately 100 photos per cranium, showing all views. Chi-squared tests indicated whether significant differences exist between the sites. Eight crania from *Catedral* (14%) and 20 from *Soledad* (15%) exhibited signs of trauma; these frequencies are not significantly different ($\chi^2=0.00$, $p=0.94$). Cranial trauma is more common in males (71%) than in females (29%; $\chi^2=6$, $p=0.44$). Blunt force trauma was more frequent at *Catedral* (78%; $\chi^2=4.4$, $p=0.04$), while at *Soledad*, blunt and sharp

force had the same frequency (40%; $p=0.39$). There were no significant differences in trauma location or timing. While there is no clear SES pattern to trauma, conflict was a factor in individual's lives.

Hyksos in Egypt – utilising biodistance methods to interpret archaeological and textual evidence from Tell el-Dab'a

NINA MAARANEN¹, SONIA R. ZAKRZEWSKI² and HOLGER SCHUTKOWSKI¹

¹Department of Archaeology, Anthropology, and Forensic Science, Bournemouth University, ²Department of Archaeology, University of Southampton.

Archaeological studies regarding the ethnogenetic nature of past communities have gained renewed interest due to advancements in bioarchaeological methods. The inclusion of biological information has not only assisted archaeological interpretations, but also repositioned the role of textual sources in current investigations.

According to contemporary textual sources, a group of Asiatics called the Hyksos decentralised the ancient Egyptian Middle Kingdom (MK) and assumed power, leading to the Second Intermediate Period (SIP, ca 1640-1530 BCE). Excavations at Tell el-Dab'a, the Hyksos capital, have revealed a fluent mixture of both Egyptian and Eastern Mediterranean cultural elements, but the lack of written sources by the settlers themselves has left many open questions regarding social structure and even the nature of immigration.

To explore kinship structures and postmarital residence patterns of the Hyksos, biological information was analysed together with archaeological evidence. Skeletal human remains from Tell el-Dab'a (n=126) were analysed for dental nonmetrics and odontometrics, with rare dental traits used to investigate familial relationships. Data was grouped according to a variety of factors, including sex, phase and spatial organisation.

The results highlight the importance and interwoven relationship of biological and contextual information. Pooled results showed little change in the biological affinities of the Tell el-Dab'a population when transitioning from the end of MK to SIP (MD=0.005 with $\sqrt{\text{var(MMD)}}=0.13$). While this outcome was also supported by archaeological evidence, shedding further light into the socio-political aspects of the written sources, the results also revealed more information of the Tell el-Dab'a people beyond the archaeological record.

This project has received funding from the European Research Council (ERC) under the European Union's Horizon 2020 research and innovation program (grant agreement No 668640).

Changing social relationship among aging male chimpanzees Changing social relationship among aging male chimpanzees

ZARIN MACHANDA¹, ALEXANDRA ROSATI², LINDSEY HAGBERG³, EMILY OTALI⁴, MELISSA EMERY THOMPSON⁵, MARTIN MULLER⁵ and RICHARD WRANGHAM³

¹Anthropology, Tufts University, ²Psychology, University of Michigan, ³Human Evolutionary Biology, Harvard University, ⁴Kibale Chimpanzee Project, ⁵Anthropology, University of New Mexico

Studies of human aging have shown that older individuals report having fewer, but closer and more positive social relationships compared to younger individuals. These studies are grounded in socioemotional selectivity theory (SST) which posits that these changes allow individuals to prioritize emotional regulation as they get older. In this study, we test predictions generated from SST to examine whether wild chimpanzees exhibit similar changes in their social relationships as they age. We used 21 years of data on 20 adult male chimpanzees living in the Kanyawara community in Kibale National Park, Uganda. We found a trend that adult male chimpanzees were less likely to be found in parties with other males as they age ($\chi^2 = 3.24$, $df = 1$, $p = 0.071$). However, when males were in parties with other adult males, they were more likely to be in larger parties ($\chi^2 = 8.17$, $df = 1$, $p = 0.004$) and they were more likely to sit in close proximity to other adult males ($\chi^2 = 17.473$, $df = 1$, $p < 0.0001$). Furthermore, using a measure of within 5m association to categorize male-male dyads as mutual friends, we found that the number of mutual friends increased with age ($\chi^2 = 8.22$, $df = 1$, $p = 0.004$). Overall, male chimpanzees reduced their overall sociality with age but when they were social, they exhibited closer bonds and had more friends. This pattern is consistent with human data and allows us to reevaluate the underlying assumptions of socioemotional selectivity theory.

Funding from Harvard University, University of New Mexico, Leakey Foundation, National Science Foundation (9807448, 0416125, 1355014), the National Institute on Aging and the Office for Research on Women's Health (R01AG04395).

Dental Pathology and Dietary Intake of Inner Asian Steppe Inhabitants during the Historic Mongol Period- Yuan Dynasty (ca. CE 1200-1400)

MICHELLE MACHICEK¹ and JACQUELINE T. ENG²

¹Intercultural and Anthropological Studies, Western Michigan University, ²Biological Sciences, Western Michigan University

The steppe lands of Inner Asia are well known from travelers' tales of the famous Silk Roads, combined with the historic rise of the Mongol Empire and Yuan Dynasty (ca. CE 1200-1400). However, historic accounts rarely focus on aspects of everyday life relating to health and

ABSTRACTS

diet. This study aims to directly contribute to the historical narrative from a biological perspective through the study of dental pathology and dietary intake of inhabitants from this region during this period. Individuals from three sites located in Inner Mongolia, and samples from eastern, central and southwestern Mongolia were analyzed for stable isotope information on dietary trends (n=33), as well as dental pathology (caries, abscesses, ante-mortem tooth loss) and non-specific stress (enamel hypoplasia) (n=58).

Results of stable isotope analyses of carbon and nitrogen are indicative of mixed dietary intake, including some C⁴ input, despite marked differences in environmental settings between site locations (range δC^{13} -18.17 to -13.99; range δN^{15} 13.88 to 10.99). These results may reflect a greater degree of uniformity in dietary regimes in later periods compared with results obtained from earlier Bronze-Iron Age samples (Machicek and Eng 2017). Comparative dental pathology results between sites indicate no significant associations with all conditions that were assessed (X^2 , $p > 0.05$). Overall, these results provide an initial measure for reconsidering the health of steppe communities and suggest a later historic trend to a more homogenous dietary intake, which may be related to wider social processes involving similar access to resources irrespective of site location.

MM funding: Natural Environment Research Council (UK) & Smithsonian NMNH and MCI. JE funding: Fulbright-Hays Doctoral Dissertation Abroad program & University of California Pacific Rim Award.

Great apes and humans evolved from a long-back ancestor

ALLISON L. MACHNICKI¹ and PHILIP L. RENO²
¹Biomedical Sciences, Joan C. Edwards School of Medicine, Marshall University, ²Biomedical Sciences, Philadelphia College of Osteopathic Medicine

There is current debate whether the human/chimpanzee last common ancestor (LCA) had a short, stiff lumbar column like great apes or a longer, flexible column observed in generalized Miocene hominoids. Beyond reduction to four segments, three additional features contribute to lumbar stiffening: the position of the transitional vertebra (TV), orientation of the lumbar spinous processes, and entrapment of lumbar vertebrae between the iliac blades. For great apes, these features would be homologous from a short-back LCA, but likely functionally convergent though dissimilar phenotypes from a long-back LCA. We quantitatively and qualitatively analyzed hominoid, baboon, and colobine thoracic and lumbar vertebrae using 3D surface scanning and osteological measurements to compare spinous process morphology and sacral depth. We also used a large sample of hominoid vertebral counts to assess variation in the position of transitional vertebra and

lumbar boundary. To determine the developmental independence of vertebral characters, we also analyzed thoracolumbar and lumbar transitions in *Hox9* and *Hox11* mutant mice. All extant hominoids modally place the TV at the ultimate thoracic. However, humans and orangutans place the TV at the 19th vertebral segment, while other apes place the TV at the 20th. Furthermore, chimpanzees, gorillas, and orangutans each have distinct patterns of spinous process angulation and morphology associated with lumbar stiffening. Finally, chimpanzees are unique compared to other hominoids with a greater sacral depth facilitating lumbar entrapment. These differences suggest that lumbar stiffening is convergent among great apes and that human bipedalism evolved from a more generalized long-back ancestor.

Wenner-Gren (ALM); NSF GRFP DGE1255832 (ALM), NSF BCS-1650879 (ALM & PLR); NSF IOS-1656315 & BCS-1638812 (PLR)

Relationships between lower limb bone rigidity and whole-limb force and power production: Implications for estimating muscle performance in the past

ALISON A. MACINTOSH^{1,2} and JAY T. STOCK^{2,3}

¹Department of Anthropology, University of Victoria, ²Department of Archaeology, University of Cambridge, ³Department of Anthropology, Western University

Muscle contractions provide one of the main sources of loading on limb bones during movement, and bone structure has demonstrated relationships with muscle size within the limb. However, even in individuals of comparable size, differences in functional strength also have explanatory power, so bone structure may be useful for estimating whole-limb performance from the skeleton. Here we test the extent to which adult female bending/torsional rigidity (J ; mm²) from sections about the knee joint (mid-femur to mid-tibia) predict *i*) thigh and calf muscle cross-sectional area (MCSA; mm²), *ii*) peak power output (Pmax; W) in a counter-movement jump, and *iii*) maximum force production (Fmax; N) during single-leg hopping. Pmax, Fmax, and thigh MCSA all exhibited significant relationships with lower limb J most strongly at the proximal tibia (66% of maximum length; $r=0.608-0.708$; $p<0.001$). This is attributed to the functional relationship between the main thigh muscles, their insertion on the proximal tibia and the high bending moments that they exert about the knee. Regression models predicting Pmax and Fmax were significantly improved by the addition of proximal tibial J to body size variables. Regression models predicting MCSAs were best predicted by tibial J , at the proximal tibia for thigh MCSA ($r=0.478$, $p<0.001$) and at the midshaft tibia for calf MCSA ($r=0.327$, $p<0.001$). Our results indicate that, among adult women,

local tibial cross-sectional geometry can provide useful information about functionally-related lower limb muscle areas, and about whole-limb muscular performance during *in vivo* movement, particularly if body mass can be estimated.

The research leading to these results has received funding from the European Research Council under the European Union's Seventh Framework Programme (FP/2007-2013) / ERC Grant Agreement n.617627 (to JTS)

Toward a volumetric and chronometric measure of tooth wear rates in ovicaprines

RICHARD H. MADDEN¹, JUSTIN LEMBERG¹, JOHN P. PARKES² and BRUCE A. BUCHHOLZ³

¹Organismal Biology & Anatomy, University of Chicago, ²Kurahaupo Consulting, Christchurch, New Zealand, ³Center for Accelerator Mass Spectrometry, Lawrence Livermore National Laboratory

Much of mammalian tooth evolution involves change in the volume of mineral substance delivered to the occlusal table. High-crowned and megadont teeth are often understood as iconic examples of adaptation to an abrasive-rich diet, the implication being that excess tooth wear drives the evolution of tooth shape. Despite the resilience of these icons of adaptation, geographic variation in tooth wear rates is rarely examined in a single species. This is surprising given that current theories about the dominant cause of tooth wear (mechanical properties of plant foods, concentration of silica phytoliths, amount of ingested soil, or features of gross habitat that relate to rainfall) predict geographic variation. Here we report progress toward a volumetric and chronometric measure of tooth wear in ovicaprines. Daily and annual molar wear rates obtained using AMIRAv6 volume segmentation of dentine and enamel in microCT image stacks and registration-subtraction of worn on unworn crowns, coupled with AMS ¹⁴C bomb-spike calibration of enamel mineralization at m1 crown neck (coincident with onset of wear), are applied to goat (*Capra hircus*) and sheep (*Ovis aires*) from islands where they are hunted as pests. On Raoul, Macauley, Arapawa, Campbell and the main islands of New Zealand, professional hunters kill animals, collect mandibles and document sources of ingested mineral particles with rumen and faecal samples. Chronometric calibration of individual daily and annual molar wear rates may resolve the causes of population and geographic differences in rates of linear and volumetric loss of tooth mineral substance and crown functional life.

ABSTRACTS

Improving health care accessibility to research participants through point-of-care technologies

FELICIA C. MADIMENOS^{1,2}, GEETA EICK³ and J. JOSH SNODGRASS³

¹Anthropology, Queens College, CUNY, ²New York Consortium in Evolutionary Primatology, (NYCEP), ³Anthropology, University of Oregon

Delivering diagnostic health information to research participants through point-of-care (PoC) technologies greatly improves healthcare accessibility in field-based settings. Here, we discuss the value of such devices in population-based research and provide specific examples of their extensive application among the Ecuadorian Shuar, an indigenous population from remote Amazonia. Use of central laboratories, which analyze samples at a distance from the field site and may require weeks to generate results, limit the ability to provide diagnostic information to participants; this approach serves to fragment and de-center the participant from the health care experience. While clinical benefits of PoC devices include the potential to improve quality of care and health outcomes by lowering cost and bringing health care closer to the initial point of contact between provider and patient, for health-focused population-based research, benefits can be far greater. Through collaborations with local health care providers, these portable, user-friendly PoC devices, offer rapid and robust health information to participants who typically have limited, if any, access to these tests. Glucose, lipids, and hemoglobin are among the most commonly used analytes and require little more than a drop of blood from a finger-prick. By providing immediate results through minimally invasive means, PoC devices can demystify the health care process and further dialogue about individual-level health. From a researcher standpoint, PoC devices can facilitate conducting large-scale cross-sectional research necessary for addressing questions of evolutionary and biocultural import. Here, we expand this discussion and highlight the ways PoC devices offer widespread benefits at research, participant, and community-levels.

No funding sources.

The effects of chewing time on gonial morphology in the mammalian mandible

SARA M. MAGEE¹, SHAUHN E. ALAVI² and FREDERICK R. FOSTER¹

¹The Center for Human Evolutionary Studies, Department of Anthropology, Rutgers, The State University of New Jersey, ²Department of Anthropology, University of California - Davis

Relationships between masticatory performance and mandibular structure have been well documented, yet few studies have addressed the gonial region of the mandible. Traditionally, the gonial angle has been used to determine sex in

humans, but its broader role in primate feeding behavior remains unclear. This area of the jaw is an anchor for key mastication muscles, suggesting that its morphology is influenced by localized muscular performance. Specifically, the degree of eversion and inversion may be affected by the use of the masseter and medial pterygoid muscles in long bouts of repetitive chewing. To address this, we compared the degree of gonial flare with chew cycle duration in a group of 100 mammalian species, including 45 primate species. Data on chew cycle duration was collected from a literature review, and seven landmark measurements were taken on mandibles from males and females of each species in collections at The American Museum of Natural History (New York City, New York) and The National Museum of Natural History (Washington, D.C.). Multivariate linear regression was used to control for the effects of several confounding variables on chew cycle duration. Phylogenetic generalized least squares (PGLS) regression was used to determine if the flaring of the gonial region was related to chew cycle duration while controlling for species relatedness. The results of our study suggest that the gonial region flaring is more pronounced in species that spend more time chewing, although factors such as food mechanical properties and bite force could also affect morphology in this region.

Work for this study was supported by a Bigel award provided by the Department of Anthropology, Rutgers, The State University of New Jersey.

Morphological characteristics of inter-osteonal transverse connections in human Haversian tissue

ISABEL S. MAGGIANO¹, COREY M. MAGGIANO¹ and DAVID M. COOPER²

¹Department of Anthropology, University of West Georgia, USA, ²Department of Anatomy, Physiology and Pharmacology, University of Saskatchewan, Canada

Nearly a century ago, Richard Volkmann's description of transverse "tunneling" led to the conceptual separation between longitudinal and transverse canals in cortical bone. Still, today, little is known about the basic morphological variability of transverse connections, which impedes understanding their formative processes and functionalities. Modern synchrotron micro-CT imaging permits the 3D reconstruction of Haversian networks, through hand-tracing and computer-aided interpolation. In order to gain a better understanding of transverse connection morphologies in cortical bone, the present study combines the analysis of outlines of osteon segments and associated transverse canal connections. Our results show surprising levels of morphological complexity and suggest three types of transverse connection canals are present: 1) connections developing through BMU-mediated resorption into directly

adjacent previously existing systems, 2) connections perforating reversal lines into previously existing systems, and 3) short, transversely connecting secondary osteons. While the overall frequency of transverse connections emphasizes the importance of inter-system connectivity and communication necessary in a healthy Haversian network, their described morphological diversity suggests there may be multiple mechanisms for their activation and possibly multiple functions, ranging from network drainage, exchange of vessels or nutrients, to osteoclast migration, with important implications regarding bone health and adaptation.

Microscopic markers of an infradian biorhythm in human juvenile ribs

ROSIE PITFIELD¹, JUSTYNA J. MISZKIEWICZ² and PATRICK MAHONEY¹

¹Anthropology and Conservation, University of Kent, ²Archaeology and Anthropology, Australian National University

Recent studies have indicated that an infradian systemic biorhythm may coordinate aspects of human hard tissue growth and adult body size. Here we investigate if evidence of this biorhythm retained in human teeth as the periodicity of Retzius lines (RP) corresponds with the microstructural growth of a non-weight bearing bone, the rib. Using static histomorphometric methods, the RP of permanent first molars was calculated and combined with measures of bone remodeling for ribs from 50 human juvenile skeletons. Results provide the first evidence that the infradian biorhythm is linked to bone remodelling in children. Retzius periodicity was negatively correlated with relative osteon area and Haversian canal size in children aged between eight to 12 years. Results imply that a faster biorhythm (fewer days) relates to increased bone deposition during remodelling leading to larger osteons relative to Haversian canal size in ribs from these children. A faster biorhythm was also correlated with the relative cortical area of their ribs. Relationships between bone remodelling and the biorhythm were much more variable in younger children aged between three to seven years of age. Our results provide the first evidence that an infradian biorhythm is linked to bone remodelling in older children.

Examining the frequency of crenulated premolars and their association with crenulated molars

CHRISTOPHER MAIER¹ and G. RICHARD SCOTT²

¹Department of Anthropology, Eckerd College, ²Department of Anthropology, University of Nevada, Reno

The distribution of crenulated molars has recently been reported for modern human populations, with the highest degrees of expression observed

ABSTRACTS

in African and African American individuals. It was suggested that crenulations might be evident on premolars, particularly in individuals with strongly expressed molar crenulations. Neither the occurrence on premolars nor the association with molars have previously been examined. A sample of African, African American, European American, and Hispanic individuals (n=683) was evaluated for crenulated premolars following a modified version of the scale proposed for scoring molars. Traits scores were examined for significant differences between ancestry groups, as well as a relationship between crenulations on premolars and molars.

Crenulations of third premolars are relatively rare, occurring in only 8%-9% of the overall sample. Fourth premolars are more frequently crenulated than third premolars, regardless of jaw, occurring in 25%-30% in some samples. Additionally, African and African American individuals exhibit premolar crenulations about twice as often as any other group. Bonferroni corrected chi-square tests indicate significantly different frequencies among groups. Furthermore, Fisher's exact test supports the observation that the elevated frequency in the African derived samples is driving the significance of the chi-square tests. Correspondence analysis of crenulation score and group membership further supports that the presence of crenulations is most common among African ancestry. Finally, polychoric correlation coefficients demonstrate a strong positive relationship between premolar crenulations and crenulated molars. Correspondence analysis between premolar and molar scores indicates that crenulated premolars are associated with higher degrees of expression on the molars.

'Basque'ing in Uniqueness: An Examination of Basque Dental Variation

DIANA MALARCHIK¹ and G. RICHARD SCOTT²

¹Anthropology, PAR Environmental Services, Inc.,

²Anthropology, University of Nevada, Reno

The Basque population of northern Spain and southern France has been of interest to anthropologists due to their linguistic, cultural, and biological uniqueness. Multiple studies have focused on language groups, genetic markers, Y chromosome and mtDNA haplogroups, and skeletal morphology. Little attention was paid to Basque dental variation until G. Richard Scott initiated work on Basque dental morphology. Examining eighteen crown traits and six root traits, Scott showed Basques have a classic European dental pattern but remain an outlier in the context of other European populations. To follow up on the study of Basque crown and root morphology, mesiodistal (MD) and buccolingual (BL) crown diameters were obtained for living Basque, Spanish, and Spanish-Basque samples along with medieval and post-medieval samples from Vitoria, Spain. This odontometric analysis of

the Basque dentition once again demonstrated their outlier status among Western Eurasian populations. For genetic markers, blood group genes, and linguistics, Basques are outliers in the context of other Europeans. The same is true for dental morphology, as Basques consistently demonstrate a "Eurodont" dental pattern yet are outliers for multiple traits. For dental metrics, Basques have low total crown areas comparable to other small-toothed populations, including Lapps (Sami), Bushmen (San), and Ainu. While the European characteristics of the Basque dentition are evident, their outlier status is affirmed by dental morphology and tooth size.

Variation in butyrate-production pathways across human and nonhuman primates

ELIZABETH K. MALLOTT and KATHERINE R. AMATO

Department of Anthropology, Northwestern University

Over the course of human evolution, shifts in dietary practices, such as meat-eating and cooking, have resulted in reduced fiber intake, particularly in industrialized populations. This dietary shift has likely had important consequences for host-gut microbe interactions and human nutrition and health, as fiber-degrading microbes produce short-chain fatty acids (SCFA), which are used as host energy sources and mediate host fat deposition and inflammation. Reduced fiber consumption is associated with a loss of gut microbes that degrade fiber, which can be compounded over generations, and may have altered the abundance of SCFA-producing genes in human gut microbiomes, influencing metabolic disease risk in modern humans. To determine if low-fiber diets in humans are associated with changes in butyrate production, one SCFA, we compared the gut microbiomes of humans and non-human primates, examining variation in the presence and relative abundance of four butyrate-producing pathways – 4-aminobutyrate, acetyl-CoA, glutarate, and lysine. Butyrate-producing pathway genes were identified in industrialized human (n=20), non-industrialized human (n=10), ape (n=10), Old World monkey (n=30), New World monkey (n=40), and lemur (n=15) gut metagenomes. Humans had significantly fewer pathways present compared with other phylogenetic groups (humans=1.90±0.88 pathways, apes=3.00±1.41, Old World monkeys=3.03±0.76, New World monkeys=2.70±0.82, lemurs=2.27±0.59) ($F_{4,120}=8.02$, $p<0.001$). Additionally, humans from industrialized populations lacked two pathways – 4-aminobutyrate and glutarate – while non-industrialized humans and all other phylogenetic groups had all four pathways present, albeit at varying frequencies. This marked decrease

in butyrate-producing pathway presence may increase human susceptibility to metabolic disorders, particularly in industrialized populations consuming low-fiber diets.

This study was funded by Northwestern University.

The use of enamel and dentine extension rates to estimate crown and root formation time and examine the M1 eruption process in wild chimpanzees

MAIRE MALONE

Department of Anthropology, University of Michigan

M1 eruption age has been used to estimate life history pace in fossil hominins due to the close correspondence between M1 eruption and life history variables, such as weaning, in primates. However, estimating M1 eruption age has generally only been possible by using the dental remains of juveniles who have died before their teeth finished forming. It has been suggested that the age at peak root extension rate in chimpanzees may correspond with eruption/functional occlusion, providing an additional way to assess the eruption process, and thereby infer aspects of life history pace from teeth of living and fossil primates.

Presented here are crown and root formation times and root extension rates for the M1s of 7 chimpanzees (*Pan troglodytes schweinfurthii*) from Uganda. Ages at peak root extension rate are also compared with those of *Pan* individuals from the literature.

The mean peak root extension rate was 10.6 microns/day and the mean age at peak extension rate was 3.6 years, with the 2 females having the latest peaks. Compared with other studies, these chimpanzees show a higher mean peak extension rate, and a younger age at which this peak rate is reached, though it still falls within the range of chimpanzee M1 eruption age.

These results demonstrate how peak molar root extension rates may be related to the eruption process. This association allows M1 eruption/occlusion age to be estimated even in isolated adult teeth, greatly expanding the possibilities for examining life history parameters in the fossil record.

A Study on Spondyloarthritis of Individuals from Taosi North Cemetery

XINGYU MAN, SUNZIFENG RUAN, PINGYUAN MU and XUEZHU LIAO

School of Archaeology, Jilin University

Spondyloarthritis (SpA) is a chronic inflammatory rheumatic disease as a direct result of spinal compression, which is a common pathological phenomenon among ancient populations. In this research, we studied 13 individuals (10 male and

ABSTRACTS

3 female) from Taosibei Cemetery, located in middle part of China, which was used during a period around 800 BC-200 BC. Our aim is to see whether there's an obvious relationship between age, gender and SpA and whether the distribution on the entire spine is more selective, thus to assess the cause and effect of this disease. We ranked the severity of osteophytes on centrums (from slight osteoproliferation to fuse together), then a computed tomographic scanner (9500 CBCT, KODAK, Japan) was used to diagnose more precisely to be distinguished from DISH.

According to our results, SpA has a close connection both with age and gender. Male individuals seem to have experienced more serious osteophytes, indicating their labor intensity might be greater than that of female. Individuals aged 35-40 must have been more susceptible to SpA, as their severity scores were found to be most serious. No special distribution characteristics of SpA were found, while bamboo spines were usually found between lumbar vertebrae, cervical vertebrae, or the articular part between T12 and L1. This indicates that the Taosibei population might have a large stress on the lumbar and cervical vertebrae due to hard labor. Further studies on the relationship between hereditary and SpA are planned to be conducted.

Modeling *Varecia* current and future habitat in eastern Madagascar

AMANDA N. MANCINI^{1,2}, TONI LYN MORELLI³, ADAM B. SMITH⁴, ELIZABETH BALKO⁵, CORTNI BORGERSON⁶, RAINER DOLCH⁷, ZACHARY FARRIS⁸, SARAH FEDERMAN⁹, SHEILA HOLMES¹⁰, MITCH IRWIN¹¹, RACHEL JACOBS¹², STEIG JOHNSON¹⁰, TONY KING¹³, SHAWN LEHMAN¹⁴, EDWARD LOUIS¹⁵, ASIA MURPHY⁹, TIANASOA H. RATOLOJANAHARY⁷, ONJA RAZAFINDRATSIMA¹⁶ and ANDREA L. BADEN^{1,17,2}

¹Anthropology, Graduate Center- CUNY, ²NYCEP, The New York Consortium in Evolutionary Primatology, ³NE CASC, Northeast Climate Adaptation Science Center, ⁴Center for Conservation and Sustainable Development, Missouri Botanical Garden, ⁵Ecology and Evolutionary Biology, Cornell University, ⁶Anthropology, Montclair State University, ⁷Association Mitsinjo, Association Mitsinjo, ⁸Fish & Wildlife Conservation, Virginia Tech, ⁹Ecology & Evolutionary Biology, Yale University, ¹⁰Anthropology and Archeology, University of Calgary, ¹¹Anthropology, Northern Illinois University, ¹²Anthropology, George Washington University, ¹³Conservation and Reintroduction, The Aspinall Foundation, ¹⁴Anthropology, University of Toronto, ¹⁵Conservation Genetics, Henry Doorly Zoo, ¹⁶Biology, College of Charleston, ¹⁷Anthropology, Hunter College- CUNY

Climate change and habitat modification are increasing threats to global biodiversity. Much of the current conservation paradigm focuses on elucidating environmental drivers of species' distribution, persistence, and connectivity, and projecting how this may change in the future. We

sought to predict the current and future distributions of the Critically Endangered black-and-white ruffed lemur (*Varecia variegata*) and red ruffed lemur (*Varecia rubra*). To achieve this, we obtained over 10,000 presence/absence points from *V. variegata* and over 2,000 points from *V. rubra* across their known range. We assessed these data in relation to climatic, land use, and land cover variables in order to identify drivers of contemporary range occupation. We performed ecological niche modeling using an ensemble prediction from generalized additive models, generalized linear models, and boosted regression trees. Furthermore, we predicted future *Varecia* distributions using available climate change models and projected future forest cover, generated *de novo* based on rates of forest loss between 2000 and 2015. We found that both species occupied the same climate niche space and were therefore modeled as a single genus. Forest cover was the single greatest predictor of *Varecia* presence, with climate having little influence. Future forest loss scenarios resulted in a severely restricted distribution of *Varecia*, with most suitable habitat disappearing by 2070. Together these results highlight the importance of forest cover for *Varecia* persistence and are in line with recent work identifying forest cover as the main driver of functional connectivity.

Demographic reconstruction of health and disease at the St. Lawrence County Poorhouse, Canton, NY

MADELEINE L. MANT¹, MINDY PITRE², CAROLINE MCCARTHY³ and ABBIE HALE²

¹Archaeology, Memorial University, ²Anthropology, St. Lawrence University, ³Museum Studies, New York University

Health and disease across the life course of institutionalized individuals is an area of increasing interest in biological anthropology. Chronic marginalizing pressures such as low socioeconomic status and food insecurity have been identified as having embodied health effects, affecting individuals' blood pressure, fracture healing rates, and mental health. This research presents the first results of the Death in St. Lawrence County Project, drawing upon the intake records of 1777 adult individuals (1095 males and 682 females) from over 20 countries of origin who made use of the St. Lawrence County Poorhouse (Canton, NY) between 1875 and 1920. The records allow for demographic reconstruction of the poorhouse residents over a 45-year period and indicate that males were significantly more likely ($p < 0.05$) to enter the poorhouse due to sickness, mobility loss, and traumatic injuries than women. Females were significantly more likely ($p < 0.05$) to seek admittance due to a diagnosis of insanity or abandonment by their husbands or children. Salvage excavation in 2017 of skeletons from the associated poorhouse

cemetery found evidence of care in burial, including containers, coffin hardware, and burial shrouds. These datasets allow for a biocultural reconstruction of health across the life course of these institutionalized individuals, some of whom made use of the poorhouse multiple times due to both biological and social pressures.

Revisiting the savanna chimpanzee (*Pan troglodytes*) as a referential model for hominin origins: Issa, Tanzania as a case study

LINDA F. MARCHANT¹, ALEXANDER K. PIEL² and FIONA A. STEWART²

¹Anthropology, Miami University, ²School of Natural Sciences and Psychology, Liverpool John Moores University

Nearly six decades have passed since field work on savanna chimpanzees (*Pan troglodytes*) began. Research in west and east Africa revealed these chimpanzees live at lower densities in more open habitats, have larger community ranges, and experience greater seasonality coupled with lower annual rainfall. These attributes led some anthropologists to use these apes as a referential model for the LCA (Moore, 1996; Marchant and McGrew, 2005). New technologies such as GIS, PAM (Passive Acoustic Monitoring), camera traps, weather stations, drones, Landsat and DigitalGlobe satellite imagery have expanded the quality and quantity of research findings and sharpened our understanding of the adaptive flexibility of savanna chimpanzees. In 2008 a permanent research presence was established at the field site of Issa, Tanzania (*Pan troglodytes schweinfurthii*) to further document savanna chimpanzees living in the mosaic habitat of the Greater Mahale Ecosystem Research and Conservation region, GMERC (Stewart *et al.*, 2018). This site has yielded new ethoarchaeological evidence (Hernandez-Aguilar, 2009) and made a persuasive case for niche construction using nest sites, and nest site reuse (Stewart *et al.*, 2011). Results from Issa, and other savanna chimpanzee research sites, continue to strengthen the argument for the value of these apes as a referential model in our efforts to reveal early hominin adaptations.

Investigating human stature variation in prehistory with per-individual ancient DNA and osteological data

STEPHANIE MARCINIAK¹, CHRISTINA M. BERGEY¹, ANA MARIA SILVA², AGATA HALUSZKO^{3,4}, MIROSLAW FURMANEK³, BARBARA VESELKA⁵, PETR VELEMINSKY⁶, GIUSEPPE VERCELLOTTI⁷, JOACHIM WAHL^{8,9}, KRISZTIÁN KISS¹⁰, TAMÁS HAJDU¹⁰, NOREEN VON CRAMON-TAUBADEL¹¹, RON PINHASI¹² and GEORGE PERRY^{1,13,14}

¹Department of Anthropology, Pennsylvania State University, ²Department of Life Sciences, University of Coimbra, ³Institute of Archaeology, University

ABSTRACTS

of Wrocław, ⁴Archeolodzy.org Foundation, ⁵Department of Archaeology, Leiden University, ⁶Department of Anthropology, Prague Natural History Museum, ⁷Department of Anthropology, Ohio State University, ⁸Paleoanthropology, Senckenberg Centre for Human Evolution and Palaeoenvironment, University of Tübingen, ⁹State Office for Cultural Heritage Management Baden-Württemberg, Osteology, ¹⁰Department of Biological Anthropology, Eötvös Loránd University, ¹¹Buffalo Human Evolutionary Morphology Lab, Department of Anthropology, University at Buffalo, ¹²Department of Anthropology, University of Vienna, ¹³Department of Biology, Pennsylvania State University, ¹⁴DFG Center for Advanced Studies, University of Tübingen

In bioarchaeology, achieved adult (skeletal) height is a proxy for childhood health. However, in addition to environmental influences, adult height is also greatly affected by genetic variation. Recent genotype-phenotype association studies conducted with hundreds of thousands of modern individuals in combination with ancient DNA provide an opportunity to quantify the heritable component of height in the skeletal remains of prehistoric individuals, to then facilitate more precise investigations of how environmental factors may have affected achieved adult stature in past communities. We compared 'predicted' genetic height and 'achieved' osteological height on a per-individual basis for 65 ancient individuals from sites in Europe spanning the Upper Paleolithic to Iron Age (33000-1200 BP) by combining published ancient DNA data (>0.7X sequencing depth coverage) with skeletal measurements for each individual. Genotypes were imputed using the Human Genome Diversity Project panels and height genetic scores were estimated using summary statistics from a modern European dataset. We predicted height based on a quality-filtered dataset of 6,864,638 single nucleotide polymorphisms, with 34,000 to 1.18 million SNPs scored per ancient individual (0.8-51% genotype call rate; samples with >99% missingness were excluded). Long bone maximum length measurements were used to estimate osteological stature with a regression-based approach (standard error 1.86-2.73%). Allelic height scores and osteological height were positively correlated ($r^2=0.2025$, $P=0.0017$). By more precisely quantifying per-individual differences between realized osteological and potential genetic heights, our approach can ultimately be used to inform how gene-environment interactions impacted individual growth trajectories in diverse contexts across prehistory.

Diagnosing SAPHO syndrome in human remains

JULIE ANNA MARGOLIS¹, MARK HUBBE¹ and MELISSA M. QUINN²

¹Anthropology, The Ohio State University, ²Division of Anatomy, Department of Biomedical Education

& Anatomy, The Ohio State University College of Medicine

Through gross anatomical dissection, a donor cadaver was discovered to have connective tissue pathologies diagnostic of SAPHO (synovitis, acne, pustulosis, hyperostosis, osteitis) syndrome. SAPHO syndrome is a rare (and possibly undiagnosed) inflammatory condition in which osteitis and hyperostosis typically affect the anterior chest wall, with or without skin manifestations. Pathognomonic for the syndrome is a "bull's head" appearance of the clavicles, manubrium, and first ribs from increased symmetric tracer uptake during bone scintigraphy. This characteristic pattern of pathological bone growth was observed in the donor cadaver associated with other osteoarticular manifestations of the disease. SAPHO syndrome is relevant in the study of past skeletonized remains given the fact that it manifests as a systemic alteration of the skeleton; and can be mistaken as wide-spread, non-specific infectious response in a paleopathological study. However, the inflammatory nature of the syndrome may be indicative of other stress events and have genetic associations. Despite its relevance, pathological diagnosis of SAPHO syndrome has not been previously presented in full body cadaveric material. The only known previous study attributed one manubrium fused with the first ribs from an anatomical bone collection to SAPHO syndrome. In the paleopathological literature, the syndrome has not been described and is very rarely mentioned. We present this case as an initial description of differential diagnosis criteria for paleopathological perspectives and to raise awareness of SAPHO syndrome among biological anthropologists.

Support for this project was provided by The Ohio State University, Division of Anatomy Body Donor Program, with special thanks to the generous donors and their loved ones.

Assessing Fish Consumption in the Ancient Greek World Using Sulphur Stable Isotope Ratios

KATEY MARI¹, LAURIE REITSEMA¹, KATHERINE REINBERGER¹, CHELSEA BATCHELDER¹, STEFANO VASSALLO² and BRITNEY KYLE³

¹Department of Anthropology, University of Georgia, Athens, GA 30602, ²Regional Archaeological Superintendence of Palermo, Italy, ³Department of Anthropology, University of Northern Colorado, Greeley, CO 80639

Carbon and nitrogen isotope ratios from human skeletons, while aptly suited to provide individualized information about past human diets, are imprecise indicators of fish consumption from among other protein-rich resources, due to the fact that carbon and nitrogen isotopic signatures in fish bones may be indistinguishable from those of terrestrial animals. Sulphur stable isotope ratios ($\delta^{34}\text{S}$) more specifically

differentiate between aquatic versus terrestrial foods in human paleodiet. We report and interpret $\delta^{34}\text{S}$ data from human bone collagen of 30 individuals from 6th-5th century BCE graves from the Greek colony of Himera, Sicily to determine if fish were consumed, an idea supported by history and literature, but disputed by previous carbon and nitrogen isotope studies. Humans' $\delta^{34}\text{S}$ values ranged from +0.64‰ to +7.12‰, showing that at Himera, marine fish were not a significant part of people's diets. Despite Himera's location on the coast of the Tyrrhenian Sea and at the mouth of the Himera River, Himieran diet consisted primarily of terrestrial resources, which agrees with previous carbon and nitrogen isotope data. Because there is carbon and nitrogen stable isotope overlap in the values of terrestrial animals and Mediterranean fish (e.g., anchovies, sardines), incorporating $\delta^{34}\text{S}$ data in Mediterranean bioarchaeological research programs is a useful tool for reconstructing human diets. Correctly estimating the role of fishing and fish consumption in ancient Mediterranean cities allows for great gains to be made in understanding ancient colonial economies, lifestyles, and dietary patterns.

This research was funded by National Science Foundation Research Experience for Undergraduates award numbers 1560227 and 1560158, the University of Georgia, and the University of Northern Colorado.

Can the humeri of the *Adapis* group shed new light on the locomotor repertoire of these early primates? New data using 3D Geometric Morphometrics on the distal humerus

JUDIT MARIGÓ^{1,2}, ANNE-CLAIRE FABRE³, NICOLE VERRIÈRE² and MARC GODINOT⁴

¹Institut Català de Paleontologia Miquel Crusafont, Universitat Autònoma de Barcelona, Cerdanyola del Vallès, Barcelona, Spain, ²Centre de Recherches sur la Paléobiodiversité et les Paléoenvironnements (CR2P, UMR 7207), Sorbonne Universités (MNHN, CNRS, UPMC-Paris6), Muséum National d'Histoire Naturelle, Paris, France, ³Life Science Department, Natural History Museum, London, United Kingdom, ⁴Ecole Pratique des Hautes Etudes, PSL, Paris, France

"*Adapis parisiensis*" is an adapiform primate that may be a mix of different species, the *Adapis* group, whose locomotor repertoire has been traditionally analogized with lorises. Twenty humeral remains attributed to this group and recovered from Quercy (France) have been re-analyzed and compared to extinct and extant primates using different techniques. The variance of several linear measurements of their distal articulation was quantified using Levene's tests, and in some of them it exceeded that of living primates of similar size. In addition, several features of the distal articulation were observed in some specimens, even though previous descriptions assured that these traits were not present in "*A. parisiensis*". Moreover, distal articulation proportions do not

ABSTRACTS

overlap with lorisisds whatsoever when linear measurements are used. All these results led to question again if it was a single species, and if the locomotor repertoire assigned to it was correct.

3D geometric morphometrics were used on a broad dataset of primates including fossil adapiforms and omomyids, all extant families of strepsirrhines and platyrrhines, and *Tarsius*. Our results show that the only fossils overlapping with the *Adapis* group morphospace are two specimens of *Protoadapis*. Most *Adapis* group specimens do not overlap with any extant primates, suggesting that there may not be living analogues for them. Two specimens overlap with lorisisds, although they also overlap with galagids, cheirogaleids and lepilemurids. Many other adapiforms and omomyiforms fall close to certain *Adapis* group specimens, confirming that early strepsirrhines and haplorhines are not that easy to differentiate using humeral remains.

Fondation Fyssen; CERCA Programme/Generalitat de Catalunya: 2017 SGR 86 GRC, 2017 BP 00003; Ministerio de Economía, Industria y Competitividad (MINECO)/ FEDER, UE): CGL2017-82654-P, IJCI-2015-26392.

Eating in or dining out: a multiscale (local to global) examination of stable carbon and nitrogen isotope ratios from the Roman period (AD 200-400) community at Oymaağaç, Turkey

KATHRYN E. MARKLEIN

Department of Anthropology, The Ohio State University, Center for Life Sciences Education, The Ohio State University

Bioarchaeological studies have provided novel, complementary, and illuminating perspectives and approaches for gauging and evaluating the extent and pervasiveness of Roman imperialism and colonization into peripheral territories. Previous research in Britain has argued that changes to general dietary patterns, reconstructed through stable isotope ratios, represent possible indirect, biocultural impacts of Roman imperial influence and immigration on local, provincial populaces and lifeways. This study considers dietary discrepancies based on stable carbon and nitrogen isotope values from collagen samples within the rural community of Oymaağaç, in northern Anatolia, a community on the geopolitical margins of the Roman Empire. A multiscale—local (n=44), intraregional (n=94), and interregional (n=892)—examination of $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values from contemporaneous sites within the Roman Empire considers patterns of dietary homogeneity and heterogeneity in Anatolia and across African, British, European, and Italian populations. On an interregional level, ANOVA demonstrate both significantly ($p < 0.05$) enriched $\delta^{13}\text{C}$ values in African, Italian, and Anatolian samples and enriched $\delta^{15}\text{N}$ distributions in African and European samples. Levene's tests indicate greater variance in $\delta^{15}\text{N}$

distributions among African samples than other regional samples. On an intraregional Anatolian level, no significant differences in variances were observed, despite significantly higher $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values in Oymaağaç samples. Finally, on a local level, no differences were observed in sex or age distributions. This global to local perspective of isotopic results indicates that dietary profiles at Oymaağaç, while relatively homogenized within the community, were locally determined and unique, contrasting regionally and internationally with food consumption practices across the Roman Empire.

Proliferative periosteal reactions: assessment of trends in Europe over the past two millennia

CARINA MARQUES^{1,2}, VITOR MATOS¹ and NICHOLAS J. MEINZER³

¹Research Centre for Anthropology and Health (CIAS), Department of Life Sciences, University of Coimbra, Coimbra, Portugal, ²Department of Anthropology, William Paterson University, USA, ³Department of Economic History, University of Tübingen, Germany

A large body of bioarchaeological research has been produced pertaining to long bone proliferative periosteal reactions (PR) and on its role in signaling health changes in populations undergoing major transitions. Exploring the PR profile in the dataset Global History of Health Project-European module (GHHP) potentially elucidates on the role of PR as proxy to health status.

The dichotomous variable presence/absence of PR was scored on long bones of 5336 skeletons (4033 adults, 1303 non-adults; 2403 males, 1693 females, and 1240 undetermined sex) from the GHHP database.

Globally, people living in Europe through the Pre-Medieval to the Industrial periods were moderately affected (22.2%) by PR. A preferential lower limb bilateral distribution in adults (14.1%), a male preponderance (25.2%), and peaking scores in the 30-40 age-at-death category, were the major trends documented. PR did not signal the effect of an "urban penalty", since similar scores were obtained in both rural (25.2%) and urban (20.1%) settlements. The analytical model shows that PR scores were significantly higher in the Early Medieval period ($p=0.02$), characterized by an almost negligible urban component in the European reality. Most other geographic, demographic and spatial variables were non-significant.

The sample's chronological, geographic and sociocultural heterogeneity surely impacted on these results. The usefulness of PR as a marker of major economic, demographic, and societal transitions depends upon local and regional proclivities. Our study emphasizes the problems of taking PR as a monolithic proxy to health status in a given population.

Investigating covariation between cranial vault thickness and brain size

HANNAH E. MARSH

Anthropology, University of Central Missouri

Cranial vault bones grow and shape in response to brain growth and develop; in extreme situations, such as hydrocephaly, the cranial vault bones can become paper thin as the endocranial pressure and volume increase to excess. In less extreme examples of possible co-variation between cranial vault thickness and brain size, Australian Aboriginals have thick vault bones and brains on the small end of human variation, whereas Inuit groups have been found to have thinner vault bones, and have larger brains for recent humans. This suggests that as the brain grows larger during development, the vault bones expand along the sagittal and coronal directions instead of becoming thicker. With smaller brains, the bones are not pushed to grow in the sagittal or coronal, and therefore growth occurs that increases the overall thickness of the bone. To investigate this relationship, this study measures cranial vault thickness and cranial capacity in a geographically diverse sample of recent humans. Larger cranial capacity groups tend to have thinner cranial vaults. This pattern of thickness and cranial capacity may explain cranial vault thickness variation in humans through Bergman's and Allen's rules.

A new method for obtaining tibial torsion in living humans

AUBREE S. MARSHALL¹, MCKENZIE A. SCHRANK¹, JESSICA S. WOLLMANN¹ and LAURA T. GRUSS²

¹Anthropological Sciences, Radford University, ²Biology, Radford University

Tibial torsion, the twisting of the tibia about its longitudinal axis that develops throughout childhood, is relevant to many clinical, biomechanical, and paleoanthropological issues. The most accurate method of measuring tibial torsion is with a CT scan, but this is costly and exposes the subject to ionizing radiation. It is therefore impractical for many researchers, especially those outside of clinical work. Here, a new cheap and reliable method of measuring tibial torsion is introduced. The procedure involves seating a subject on a table, with the thigh parallel to the edge of the table and the knee at its edge at a 90° angle to put the tibial condyles at a baseline 0° (horizontal). The foot is placed in a relaxed position on a clear sheet of plexiglass supported by a wire frame, elevated at an adjustable height so that a photo of the foot can be taken from below. From this photo foot angle and trans-malleolar axis (TMA, between the medial and lateral malleoli), a proxy for tibial torsion, can be measured. TMA and foot angle were measured multiple times on both feet in sixteen subjects by four observers. Test-retest reliability was good,

ABSTRACTS

with a correlation between measures of $r = 0.778$ for TMA and $r = 0.868$ for foot angle. This method should therefore be considered as an accessible new method to replace expensive and potentially harmful CT scans when measuring tibial torsion in living subjects.

Differences in dietary habits between papi- onins and hominins from the Shungura Formation, Ethiopia: evidence from an improved Dental Microwear Texture Analysis based on surface sampling on phases I and II molar facets

FLORIAN MARTIN¹, CHRIS-ALEXANDER
PLASTIRAS^{1,2}, AURIA KALLEND¹, ARTHUR
FRANCISCO³, JEAN-RENAUD BOISSERIE^{1,4} and
GILDAS MERCERON¹

¹PALEVOPRIM, CNRS and University of Poitiers,
France, ²School of Geology, Aristotle University
of Thessaloniki, Greece, ³Institut Prime, CNRS,
Université de Poitiers, ISAE-ENSMA, France, ⁴Centre
Français des Etudes Ethiopiennes (CFEE) – USR
3137, CNRS/Ministère de l'Europe et des Affaires
Etrangères, Ambassade de France en Ethiopie,
ADDIS ABABA, Ethiopia

The fossil record from the Shungura Formation includes several primates with terrestrial habits. By the means of a modified Dental Microwear Texture Analysis, we aim at deciphering at best how papionins and hominins have shared resources.

We here integrate both shearing and crushing facets for every individual and take into account variations for all texture parameters over a given surface. The sampling strategy allows to generate n sub-surfaces and thus n values per surface for each of 17 parameters. From those latter, 16 statistics (mean, quartiles, kurtosis ...) are produced generating thus 272 variables per surface.

From a routine, the most significant statistic per parameter and facet type from a modern Ethiopian monkeys dataset ($n=104$; *Theropithecus gelada*, *Papio hamadryas*, *Chlorocebus aethiops*, *Colobus guereza*) are used to generate a Principal Component Analysis. Height parameters on both crushing and shearing facets explain most of the variance along PC1 (48.2%) and PC2 (13.2%) whereas spatial parameters notably on shearing facets contribute to PC3 (10%) and PC4 (8.3%). Combined with ANOVAs on PC coordinates, this approach discriminates more significantly these monkeys than earlier studies.

Fossil specimens are inserted as supplementary data. The extinct specimens of *Theropithecus* ($N=165$) and *Papio* ($N=65$) plot next to their modern relatives. The three genera of hominins ($N= 32$) plot next to the modern *Theropithecus*, suggesting that contrary to the contemporaneous *Papio*, none of them integrated hard,

but either soft or tough food items. However, *Australopithecus* differs from *Paranthropus* and *Homo* in having more complex texture on crushing facets.

The authors thanks the French National Research Agency, ANR (Projects EVAH, TRIDENT, OLD and DIET-SCRATCHES), French Ministry of Foreign Affairs, Fondation Fyssen, Erasmus+ program, and CNRS-INEE/PALEVOPRIM.

Ecological predictors of allomaternal care across human societies

JORDAN S. MARTIN, ERIK J. RINGEN and ADRIAN
V. JAEGGI

Anthropology, Emory University

Allomaternal care is central to human's life history, which couples short interbirth intervals, fast weaning, and large birth size with highly dependent juvenility. Formal models and previous work in cooperatively breeding animals predict higher levels of alloparental care in harsher environments, suggesting allomaternal care may have evolved in hominins due to increased environmental uncertainty. Although this hypothesis remains difficult to test directly, the relative importance of allomaternal care varies across human societies, providing an opportunity to assess how local ecology influences this behavior. Here we investigate associations among allomaternal infant care and key ecological factors across 141 societies in the Standard Cross-Cultural Sample (SCCS). In addition to environmental harshness, we predicted that reliance on agriculture would enhance allomaternal care due to its positive effects on fertility, while severe rates of starvation would decrease care due to prohibitive energetic costs.

Using measures of temperature, precipitation, and resource availability, we extracted two principal components—environmental harshness and resource abundance—consistent with prior biogeographical research. We fit a Bayesian multilevel phylogenetic regression model to test our hypotheses while controlling for population history. As expected, environmental harshness and agriculture were associated with greater allomaternal infant care, while starvation was associated with lower rates. Overall, most societies in the SCCS exhibited a moderate degree of allomaternal care, underscoring its importance for human life history. These results are consistent with formal models, and demonstrate continuity in the ecological determinants of cooperative breeding across taxa, supporting the hypothesis that environmental uncertainty led to its evolution in hominins.

Mandibular third premolar root morphology in *Rudapithecus hungaricus* and its implications for diet

ROBERT M.G. MARTIN¹, ADELIN LE CABEC²,
DAVID R. BEGUN¹ and KORNELIUS KUPCZIK³

¹Department of Anthropology, University of
Toronto, ²Department of Human Evolution, Max
Planck Institute for Evolutionary Anthropology,
³Max Planck Weizmann Center for Integrative
Archaeology and Anthropology, Max Planck
Institute for Evolutionary Anthropology

Rudapithecus hungaricus is a putative stem hominine known from the late Miocene site of Rudabánya, Hungary (ca. 10 Ma). Previous analyses of its crown morphology and wear are indicative of soft-fruit consumption with specializations in the anterior dentition for processing harder fruit resources. Increased root surface area has been linked to patterns of increased occlusal loading in primates. Using conventional microtomography, we digitally extracted the left P_3 from the female *Rudapithecus hungaricus* mandible RUD 212 along with a comparative mixed-sex sample of extant hominoids. The RUD 212 P_3 has two roots housing two root canals in an oblique mesiobuccal-distolingual configuration, a pattern common in all extant apes. Root dimensions (root surface area, root tissue volumes, root length, buccolingual and mesiodistal diameter of the cervical plane, and cervical plane surface area) of the RUD 212 P_3 fall in the lower to middle range or below that of *Pan troglodytes verus*, which is consistent with other proxies of body mass in this individual. A linear regression of a mixed-sex sample of extant hominids (excluding *Homo*) demonstrates that the RUD 212 P_3 had a generic great ape root surface area relative to its cervical plane surface area (a reasonable proxy for body mass in hominoids). These results therefore neither support nor reject the hypothesis that *Rudapithecus hungaricus* engaged in hard-fruit consumption. As a next step, characterizing the root morphology of the entire dentition to infer an antero-posterior occlusal loading gradient in this species will provide more evidence regarding its diet.

This research was supported by the Natural Sciences and Engineering Research Council of Canada, the Department of Anthropology (University of Toronto), and the Max Planck Society.

What do Denisovans look like? Looking into the Middle and Late Pleistocene hominin fossil record from Asia

MARIA MARTINON-TORRES^{1,2}, BERMÚDEZ DE
CASTRO JOSÉ MARÍA^{1,2}, XING SONG^{3,4}, WU XIUJIE³
and LIU WU³

¹Hominin Palaeobiology, CENIEH (National
Research Center on Human Evolution) Spain,
²Anthropology, University College London, ³Key
Laboratory of Vertebrate Evolution and Human
Origins, Institute of Vertebrate Paleontology and
Paleoanthropology, ⁴CAS Center for Excellence

ABSTRACTS

in Life and Paleoenvironment, CAS Center for Excellence in Life and Paleoenvironment

For many decades, the name *H. erectus* has been used as a blanket term to refer to almost any hominin found in Asia during the Pleistocene until the appearance of *Homo sapiens*. However, recent fossil studies have helped to refine the morphological definition of classic *H. erectus* (Xing et al., 2017). In this context, hominin fossils like those from Zhoukoudian, Hexian and Yiyuan can be assigned to *H. erectus* s.s., whereas the taxonomy of fossil samples from Xujiayao, Xuchang, Maba or Panxian Dadong remain uncertain (e.g., Xing et al., 2015, Liu et al., 2013). These samples become particularly relevant in the light of the Denisovan's discovery (Krause et al., 2010). It is not clear yet whether Denisovans deserve specific distinction or may be represented by some Middle to Late Pleistocene human samples we already know from the Asian fossil record. Here we present an overview of the Chinese record for this period in search of possible candidates to represent the physically "elusive" Denisovans.

Krause, J., Qiaomei, F. et al. 2010. The complete mitochondrial DNA genome of an unknown hominin from southern Siberia. *Nature*, 464 894–97

Xing, S., Martínón-Torres et al. 2018. The fossil teeth of the Peking Man. *Scientific Reports* 8.

Xing, S., Martínón-Torres, M. et al. 2015a. Hominin teeth from the early Late Pleistocene site of Xujiayao, Northern China. *American Journal of Physical Anthropology* 156, 224-240.

Liu, W., Schepartz, L.A. et al. 2013. Late Middle Pleistocene hominin teeth from Panxian Dadong, South China. *Journal of Human Evolution* 64, 337-355.

Chinese Academy of Sciences (XDPB05, 132311KYSB20160004), National Natural Science Foundation of China (41630102, 41672020), Ministerio de Economía y Competitividad (CGL2015-65387-C3-3-P), British Academy (International Partnership and Mobility Scheme PM160019), Leakey Foundation

Finding heterochronic signals through the noise: can statistical reduction of landmark datasets find a heterochronic relationship in the pannins?

JASON S. MASSEY¹ and KIERAN P. MCNULTY²

¹Department of Integrative Biology and Physiology, University of Minnesota Medical School,

²Department of Anthropology, University of Minnesota - Twin Cities

Heterochrony is often used to describe morphological shape change in hominin and pannin evolutionary history. Regarding the latter group, previous studies have investigated the hypothesis that *Pan paniscus* is a paedomorphic version of *P. troglodytes*. These studies have tested this hypothesis globally and regionally (on separate, *a priori* anatomical modules). However, regardless

of the anatomical unit studied, the developmental trajectories of the two species do not overlap in shape space: a necessary criterion for identifying classical, Gouldian heterochrony.

Given the theoretical importance of heterochronic mechanisms in understanding evolutionary change, but failure of current multivariate studies to find consistent examples of them, we designed a process of systematic data reduction in order to limit landmark sets to those most likely to conform to a model of Gouldian heterochrony. Using three separate statistical "filters," we identified landmarks that played significant roles in the divergence of *Pan troglodytes* and *P. paniscus* developmental trajectories. After each round of reducing the landmark set, we tested trajectories to determine whether they overlapped in shape space. Landmark sets with overlapping trajectories would then be further tested for evidence of heterochrony.

None of the study designs resulted in trajectories that overlapped in shape space. Therefore, further investigations of heterochrony in size-shape space was not possible. This is consistent with several previous studies that found neither global nor regional heterochrony reliably explained multivariate shape differences between species of *Pan*. In this case, even deliberate attempts to isolate congruent trajectories failed to yield developmental programs that overlap in shape space.

Public health policies, inequality, and industrialization in 20th century Cleveland health outcomes: a study from the Hamann-Todd Osteological Collection

SARAH A. MATHENA-ALLEN

Anthropology Department, University of Massachusetts Amherst

Within the United States, economic intensification of industrialization, particularly within the Midwest, led to a fundamental shift in labor organization with a highly, mobile wage labor pool flooding industrial cities. Rising populations, urban crowding and inadequate sanitation spurred epidemics of infectious diseases including tuberculosis and influenza, chronic malnutrition, and increased exposure to poor air and water quality. However, public health legislation was characterized by contradictory discourses between conservatives and social reformers regarding the responsibility of the state to care for their populations, and social anxiety regarding the management of the working class women's bodies, particularly for minority women, including increased institutionalization and health inequalities. Specifically, this project seeks to examine the relationship between intersectionality of social identities, particularly race and gender, and its' complex, synergistic relationship to social institutions, such as public health facilities and hygiene legislation, and overall disease

morbidity and mortality in 19th to 20th century Cleveland through an osteological and archival data collection through a life history approach. Results from a preliminary study of the Hamman Todd collection (HTC) (N=57) show high rates of recidivistic trauma, infectious disease, and chronic conditions such as rickets and leukemia compared to the general population of Cleveland. In addition, high rates of oral pathologies (caries and linear enamel hypoplasias) suggests individuals within the HTC have an increased risk of poor later life health outcomes, particularly for women. These results highlight that individuals within the HTC, particularly minority women, had decreased access to health and social institutions than their contemporaries.

Looking for Neandertal derived traits: new data from the Le Moustier 2 Neandertal neonate (Le Moustier, France)

BRUNO MAUREILLE and CAROLINE PARTIOT
UMR PACEA, CNRS

Le Moustier lower Rock-shelter is a well known Prehistoric Mousterian site from Périgord Noir. Discovered in 1907 and excavated first by the Swiss antiquary Otto Hauser, who found Le Moustier 1 juvenile fossil (1908), then by Denis Peyrony who discovered Le Moustier 2 perinate Neandertal (1914), the upper half of its archaeostratigraphy presents a succession of well dated Late Mousterian layers (MIS 3) successfully excavated and studied by Brad Gravina and Emmanuel Discamps since 2014.

Erik Trinkaus is the International Paleoanthropologist who has devoted an important part of his scientific life to the description of Upper Pleistocene human lineage morphological variabilities as well as discussions on the phylogenic interest of Neandertal traits (for example, the Neandertal upper face (Rak 1986 versus Trinkaus 1987)). But, he did not have the opportunity to study the two Le Moustier specimens (even if he recently underlined differences between results obtained on Le Moustier 2 and Mezmaiskaya 1 neonates (Weaver et al., 2016) compared to the ones on Kiik-Koba 2 juvenile Neandertal (Trinkaus et al., 2016)).

With this poster, we produce the first set of cranial and infracranial morphological data on the Le Moustier 2 bones compared to these of an extant human neonate and underline the ones that are architecturally similar to Neandertal adult traits. Then, considering the age at death of the

ABSTRACTS

fossil, we underline the features that we interpret as derived Neandertal, common primitive orthodontic interindividual variability traits (including potential growth and developmental troubles).

This research is supported by the ANR project N mo of the LabEx Sciences arch ologiques de Bordeaux, n  ANR-10-LABX-52 and the project "NATCH" convention 2016-1R40240-00007349-00007350 of the R gion Nouvelle Aquitaine.

Reinterment of the human remains excavated from the Erie County Poorhouse Cemetery: persons never to be forgotten again

MELANIE M. MAYBERRY^{1,2}, JOYCE E. SIRIANNI¹ and DOUGLAS PERRELLI¹

¹Anthropology, University at Buffalo, SUNY,
²Anthropology, SUNY Buffalo State

In 1907, the University at Buffalo purchased land from Erie County that had belonged to the Erie County Poorhouse, including the burial ground associated with the poorhouse and hospital, which functioned there from 1851-1913. Gradually, the university built over the cemetery grounds until the burials and inhabitants were forgotten. Between 2008 and 2012, 392 unidentified individuals were excavated from the Erie County Poorhouse Cemetery during construction. Between 2012 and 2017 extensive research was carried out on the skeletal remains resulting in publications and reported at national conferences. In Spring of 2017, a collaboration was formed between University faculty, administrators, and students, Erie County funeral directors, and local clergy, with the goal of reburying the Erie County Poorhouse individuals with dignity and respect. Cemetery placement was arranged, with additional space set aside for future excavations. Each individual was given their own burial pouch and tag, and all were placed into shared caskets with roughly 50 individuals per casket. Burial permits were written for eight caskets in four cemetery plots in Assumption Cemetery on Grand Island, New York. Finally, a non-denominational service was led by local clergy in a University Catholic Community Center. In a funeral procession led by eight hearses, attendees traveled from Buffalo to Grand Island to lay the inhabitants of the Erie County Poorhouse Cemetery to rest in the safety of cemetery grounds, marked by burial stone and ceremony they likely did not receive in their initial burial.

Preliminary Investigation of Aging Effects on Cross-Sectional Geometric Properties of Adult Ribs in a Medieval Polish and Modern Skeletal Sample

REBECCA C. MAYUS and AMANDA M. AGNEW
Anthropology, Skeletal Biology Research
Laboratory, The Ohio State University

Bone cross-sectional geometry provides a record of bone gain and loss throughout life, with total area of a skeletal cross-section demarcating processes of bone acquisition and cortical area, or quantity of bone, reflecting age-related endocortical bone loss. The goal of this study was to investigate the amount of human variation visible in skeletal cross-sectional geometry, both within and between skeletal samples. To quantify this variation, adult human ribs from a medieval Polish sample (Giecz Collection, site Gz4, 11th-12th c., n=136) and a modern cadaveric sample (n=193) were investigated. As these samples originate from different time periods and geographic locations, cross-sectional properties were expected to vary between the two. Histological rib cross-sections from both collections were taken from ribs 4-7 at approximate midshaft and were categorized according to age at death (young adult, 18-30 years; middle adult, 30-50 years; older adult, 50+ years). Parameters collected for each rib included Total Area (Tt.Ar), Endosteal Area (Es.Ar), Cortical Area (Ct.Ar), and Relative Cortical Area (%Ct.Ar). Cross-sectional geometry for Giecz ribs falls within the range of variation for modern samples. For both samples Tt.Ar remains generally constant across all adult age groups. Es.Ar increases slightly in middle adults and elderly adults, resulting in a decrease in Ct.Ar and %Ct.Ar in these groups. These trends are comparable for both collections. However, within each age category all variables exhibit a wide range of variation. Future research will investigate the sources of variation seen in both modern and medieval ribs.

Identification of Extant Cercopithecoid Isolated Molars using 3D GM

ERIC J. MAZELIS

Department of Anthropology, CUNY, New York Consortium in Evolutionary Primatology (NYCEP), NYCEP Morphometrics Group, Leibniz-Institut f r Evolutions- und Biodiversit tsforschung, Museum f r Naturkunde Berlin, Germany

Many Eurasian and African sites produce sparse numbers of cercopithecoid fossils, which are often poorly preserved. Some sites only yield jaw fragments or isolated teeth. To date it has not been possible to identify most isolated teeth to a level below that of the subfamily. This study is aimed at applying 3D Geometric Morphometrics (GM) to identify the tooth position and genus of isolated molars in extant Cercopithecidae with the goal of building a comparative sample for the analysis of fossil specimens. The results could be utilized in studies of the rise, distribution, and expansion of fossil species. Furthermore the results may be of use in the study of paleoenvironments in which hominin taxa developed and lived.

This study is based on over 1500 molars of over 400 individuals from 38 species and 18 genera spanning both tribes of Cercopithecinae and

the three colobine subclades. Specimens were surface scanned at various institutions, virtually isolated and landmarked (14 landmarks, 168 semi-landmarks on 7 curves) in Landmark Editor (v.3.0.0.6). Semi-landmarks were slid to reduce Procrustes Distance and a Generalized Procrustes Analysis (GPA) and Principal Components Analysis (PCA) were performed with the Geomorph R package. Centroid Size (CS) and the first 30 PC scores were used as variables in a Canonical Variates Analysis (CVA) in PAST (v.3.14). Results show that over 80% of specimens can be assigned to the correct tooth position (LM1-3, UM1-3) and that, on average, about 85% of specimens were identified as the correct genus.

Funded in part by NSF 0966166 (NYCEP IGERT)

Expression of the μ -opioid receptor gene in the frontal cortex of a mouse model for the evolution of human endurance running

NATASHA Y. MAZUMDAR¹, JOHN D. POLK², THEODORE GARLAND, JR.³, LAURA L. SHACKELFORD⁴ and JUSTIN S. RHODES⁵

¹Anthropology, University of Illinois at Urbana Champaign, ²Anthropology, University of Illinois at Urbana Champaign, ³Biology, University of California, Riverside, ⁴Anthropology, University of Illinois at Urbana Champaign, ⁵Psychology, University of Illinois at Urbana Champaign

Many people report feelings of euphoria or improved mood after engaging in endurance running (ER), a phenomenon commonly referred to as the "runner's high". The exact neural origins of the "runners high" remain unknown, but it is speculated that reward mechanisms may have been selected for if ER was beneficial for hunting or foraging behaviors. Here, we examine whether μ -opioid receptor gene expression (*Oprm1*) has changed in a region of the brain involved motivation and reward in response to selection for increased voluntary wheel running in mice. At generation 66 of the experiment, high-runner (HR) mice ran approximately 15 km/day whereas C mice ran 5 km/day. Previous work found increased expression of *Oprm1* in the cerebellum, a region involved in motor coordination, in a sample of the high-runner (HR) versus control (C) lines. Here we extend this analysis to the frontal cortex using all 8 lines. A total of 6 samples from each of the 4 replicate HR lines and 4 replicate C lines from generation 66 of the selective breeding experiment were compared using real time PCR. Significantly elevated *Oprm1* expression in HR relative to C lines provides strong evidence that the difference arose from selection for distance running as opposed to genetic drift. Since the reward circuit is strongly conserved across mammals, these results could be used to infer

ABSTRACTS

that evolution of similar brain reward mechanisms may have been at work in early humans, further supporting selection favoring ER capability in humans.

New cranial capacity estimates for Sts 19 and Sts 25 (*Australopithecus africanus*)

ROBERT C. MCCARTHY

Department of Biological Sciences, Benedictine University

According to previous estimates, Sts 19, and particularly Sts 25, are at the lower end of the range of *A. africanus* cranial capacity variation. Sts 19's 436-cubic centimeter (cc) cranial capacity has been estimated using the partial endocast method by comparing it to endocasts for Taung, Sts 5, OH 5, and SK 1585, a practice which has drawn some criticism. Sts 25 is still partly encased in matrix, and so previous estimates between 350-375 cc based on cranial vault dimensions are rarely cited in studies of *A. africanus* cranial capacity variation.

In this study, I re-estimated cranial capacity in Sts 19 and Sts 25 using regression and multiple regression analyses of linear, angular, and area measurements of the external cranial base in chimpanzee, gorilla, and orangutan ontogenetic comparative samples.

Regression equations with the lowest percent prediction errors for the comparative samples and a "test" sample of other *A. africanus* specimens (Sts 5, MLD 37/38, Taung) produced point estimates between 430-477 cc for Sts 19 and 407-481 cc for Sts 25. New estimates for Sts 19 bracket previous estimates, but estimates for Sts 25 from cranial base dimensions are larger than previous estimates and congruent with a 456-cc estimate produced using multiple regression on parietal dimensions in a mixed australopith/paranthropid sample. New estimates for Sts 19 and Sts 25 clarify variation at the lower end of the range of cranial capacity variation in the *A. africanus* hypodigm and allow more precise estimates of sexual dimorphism and other intraspecific sources of variation.

Methods for the excavation of unmarked burials located beneath an historic structure

BRITTANY S. MCCLAIN¹ and JOSHUA HAEFNER²

¹Archaeology, AmaTerra Environmental, Inc.,

²Archaeology, TRC Companies, Inc.

While restoring the Oakwood Cemetery Chapel—located in the oldest city-owned cemetery within Austin, Texas—Hicks & Company met with the unanticipated discovery of skeletal remains beneath the existing footprint of the chapel. In order to proceed with subsurface construction and resume restoration, the exhumation and relocation of 37 unmarked burials was required.

The purpose of this presentation is to provide the reader with instruction, methodology, and guidance on the most effective and efficient approaches for the exhumation of unmarked burials located beneath a standing historic structure. Space constraints, unforeseeable obstacles, and other variables necessitated that some techniques and recordation be altered. Skeletal preservation strongly correlated with the proximity to the chapel exterior.

As many of the skeletal remains were bisected either parallel or perpendicular to the chapel foundation, excavations required ingenuity and creativity to exhume complete skeletons. This work involved simultaneously conducting exterior and interior excavations, tunneling beneath the chapel foundation for the exhumation of complete skeletal remains, and maneuvering around structural features essential to the integrity of the chapel foundation. Thirty-seven burials were effectively excavated, each utilizing various forms of excavation techniques. In total, four burials required exterior/interior excavations, 10 burials required tunneling, and 23 burials required typical excavation.

Overall, this presentation will serve as a reference or set of guidelines for the methodological excavation and exhumation of historic skeletal remains. This work has further implications in bioarchaeology in the probability that this scenario will occur again during the rehabilitation of similar historical structures.

Identifying Intracranial Complications of Sinusitis From Skeletonized Remains: Forensic and Bioarchaeological Implications

SAMANTHA M. MCCRANE

Anthropology, University of Florida

Sinusitis, or inflammation of the sinuses, is currently one of the most common diseases diagnosed in the United States. Clinically, this diagnosis involves inflammation of one or more sinuses and mucosa. Osteologically, only changes to the bony sinuses can be observed. This means that complications involving the blood vessels, visual complex, brain, dura mater, or other soft tissue structures are often disregarded in osteological investigations.

This project presents four cases originating from the CA Pound Human Identification Laboratory where individuals displaying postmortem indicators of sinusitis exhibit concurrent diploic vascular inflammation on the lateral cranial walls. These vessels can be viewed radiographically, and even macroscopically in one case, but this feature has not been discussed in the anthropological literature. The enlarged diploic vessels indicate vasculitis broadly. Coupled with sinusitis, these cases link observed skeletal indicators of sinusitis (including drainage cloaca(e), osteonecrosis,

or areas of pitting, thinning, or other pathological bone resorption surrounding the sinus(es)) to a class of intracranial complications discussed in the clinical literature. Giant cell arteritis, which can be triggered by infections such as sinusitis, is one such complication that can arise secondary to sinusitis and preserve in the bone. These complications may appear more frequently in individuals from marginalized populations or archaeological specimens due to limited treatment options. This preliminary study develops criteria for identifying such complications, testable in larger samples. As intracranial complications of sinusitis can be life-threatening, developing criteria and methods to positively identify instances osteologically is useful for informing forensic and bioarchaeological investigations.

Keeping their cool: Behavioral thermoregulation and body temperature patterns of wild vervet monkeys

RICHARD MCFARLAND^{1,2}, LOUISE BARRETT^{2,3}, ANDREA FULLER², ROBYN S. HETEM^{2,4}, SHANE K. MALONEY^{2,5}, DUNCAN MITCHELL² and S PETER HENZI^{3,6}

¹Anthropology, University of Wisconsin-Madison, ²Physiology, University of the Witwatersrand, ³Psychology, University of Lethbridge, ⁴Animal, Plant and Environmental Sciences, University of the Witwatersrand, ⁵Anatomy, Physiology and Human Biology, University of Western Australia, ⁶ABEERU, University of South Africa

The impact of climate change on Earth's biodiversity is becoming ever more apparent, and increasing attention is being devoted to identifying the behavioral strategies a species uses to cope with climatic stress. Previous studies have provided useful insights into the relationship between environmental and behavioral variability, but we have little knowledge of the impact these factors have on an animal's thermal physiology. We implanted a subset of wild vervet monkeys (*Chlorocebus pygerythrus*) with temperature-sensitive data loggers (N=19). Vervets in the Eastern Cape, South Africa, are more prone to cold stress than heat stress as reflected in their wide amplitudes of body temperature in the winter, and relatively tight amplitudes in the summer months (Z=17.54, P<0.001). Vervets show remarkable efficiency in keeping their body temperature stable, and avoid significant bouts of hyperthermia, despite ambient temperature regularly exceeding 40°C. In the summer months, ambient temperature had a strong positive effect on average (Z=5.41, P< 0.001) and minimum body temperatures (Z=5.27, P<0.001), but only a weak effect on maximum body temperatures (Z=1.95, P=0.051). Ambient temperatures had a strong positive effect on the time animals spent in the shade (Z=8.99, P< 0.001). Drinking water did not have an effect on body temperature (Z=1.52, P=0.13). Mean body temperatures were lower

ABSTRACTS

after swimming events ($-1.04 \pm 0.47^\circ\text{C}$, $N=9$). Overall, our data support the view that vervet monkeys cope well in the heat, and use behavior as a means to aid thermoregulation.

Claude Leon Fellowship (RM); NSERC Discovery grant (PH and LB); Canada Research Chair funding (LB); NRF grants (SPH and DM); Carnegie grant (AF); Harry Oppenheimer Fellowship (DM).

Skeletal aging in Virunga mountain gorillas (*Gorilla beringei beringei*) from Volcanoes National Park, Rwanda

SHANNON C. MCFARLIN¹, LAURA BAIGES-SOTOS², JORDI GALBANY³, HALSZKA GLOWACKA⁴, JUHO-ANTTI JUNNO⁵, THADÉE MUHIRE⁶, CHRISTOPHER B. RUFF⁷, TIMOTHY G. BROMAGE⁸, MICHAEL R. CRANFIELD⁹, WINNIE ECKARDT⁹, KIRSTEN GILARDI⁹, TARA S. STOINSKI⁶ and ANTOINE MUDAKIKWA¹⁰

¹Center for the Advanced Study of Human Paleobiology, The George Washington University, ²Department of Archaeology, University of Sheffield, ³Department of Social Psychology and Quantitative Psychology, University of Barcelona, ⁴Department of Basic Medical Sciences, University of Arizona College of Medicine-Phoenix, ⁵Department of Archaeology, University of Oulu, ⁶Karisoke Research Center, Dian Fossey Gorilla Fund International, ⁷Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine, ⁸Departments of Biomaterials and Biomimetics, New York University College of Dentistry, ⁹Mountain Gorilla Veterinary Project, University of California at Davis, ¹⁰Department of Tourism and Conservation, Rwanda Development Board

Despite their importance for understanding the evolutionary foundations of modern human senescence, available data on aging processes in nonhuman primates from well-studied natural environments are rare, with notable exceptions. We examined patterns of skeletal aging in Virunga mountain gorillas from Volcanoes National Park, Rwanda. Virunga gorillas are distinctive in their herbivory, increased terrestriality, and accelerated life history compared to other great apes. Data were collected from naturally accumulated skeletons [$N=50$ M, 39 F, 5 Unk], including 53 known-age individuals (0-43 years). Virunga gorillas do not show the dental senescence reported in some other primates. While molar percent dentine exposure significantly increases with age, and occlusal topography metrics significantly decrease with age, 3D relative shearing crest length is maintained, even in heavily worn teeth. Periodontal disease, evidenced by alveolar bone loss, increases significantly with age in molars but not premolars. Degenerative bone changes are also common. Degenerative joint disease (eburnation, osteophytes, porosity) significantly increases with age for all joints (forelimb, hindlimb, vertebrae). However, the strength of correlations differs across body compartments and sexes. Long bone diaphyses show medullary expansion and cortical thinning with age,

and periosteal expansion that preserves bone strength despite endosteal bone loss. Fore-to-hindlimb strength decreases with age in Virunga gorilla females, possibly associated with behavioral changes, but they lack the rapid bone loss characteristic of post-menopausal human females. Skeletal aging processes in Virunga gorillas and other primates may be influenced by local ecology and behavior, and provide insights into the unique features of human aging.

NSF BCS 1316104, 0852866, 0964944, 1520221; Wenner-Gren Foundation 8657; LSB Leakey Foundation; NGS 8486-08; Andrew Sherratt Fund and Petrie Watson Grant; Government of Rwanda and RDB Tourism and Conservation.

Using Novel 3D Techniques to Visualize and Quantify Primate Neck Anatomy

FAYE MCGECHIE¹, SPIRO SULLIVAN¹, KEVIN M. MIDDLETON¹, CASEY M. HOLLIDAY¹, THIERRA K. NALLEY², NEYSA GRIDER-POTTER³ and CAROL V. WARD¹

¹Pathology and Anatomical Sciences, University of Missouri, ²Medical and Anatomical Sciences, Western University, ³School of Human Evolution and Social Change, Arizona State University

The functional anatomy of the neck is an integral part of an animal's postural and locomotor repertoire, yet remains poorly understood in part due to the anatomical complexity of the cervical musculoskeletal system. Here we use a new methodology to visualize and quantify aspects of muscle architecture, as well as to explore 3D muscle mechanics of the head and neck of a Philippine tarsier (*Carlito syrichta*). First, the specimen was contrast stained and microCT-scanned (0.043mm^3 voxels). From these data, individual neck muscles were segmented in Avizo. We tracked individual muscle fascicles based on grayscale values and fascicle diameter in Avizo Xfiber. Outputs from Xfiber (fascicle length, pennation angle, and muscle volume) were used to calculate estimates of physiological cross-sectional area (PCSA) in the intrinsic epaxial neck muscles. We combined PCSA values with resultant muscle force vectors to estimate muscle moments about joints for flexion, extension, lateral flexion and rotation about each cervical intervertebral joint. Results demonstrate that the moment arms for muscles used in head and neck rotation like obliquus capitis inferior are larger in the tarsier relative to body size when compared to humans. This implies that an increase in rotational movements in this species is accomplished by modifying bony morphologies instead of increasing muscle force. This workflow provides a more comprehensive characterization of musculoskeletal functional capacity in a complex system. Not only does it provide novel insight into the neck of this unusual primate, but provides the basis to compare primates with different neck postures and locomotor adaptations.

A Woman's World: Approaches to exploring obstetrical dilemmas in past populations

CANDACE MCGOVERN

Archaeology, University of Reading

Evolutionary changes required to accommodate bipedal movement and a larger brain size, alongside various pathologies and related morphological changes, make humans prone to obstructed labour. Within archaeological populations the high frequency of reproductive age females is often attributed to an obstetrical dilemma, particularly a contracted pelvis. This occurs when the pelvic inlet, mid-plane, or outlet is too small to allow for a viable neonate to pass through the birth canal. However, cases of a contracted pelvis are difficult to establish in past populations as full-term neonates are rarely found within the pelvic cavity.

To ascertain the likelihood of a contracted pelvis, measurements at the pelvic inlet, mid-plane and outlet, alongside pathological and morphological data, were collected from 402 Romano-British females between 13 and 45 years at death. Metric data was compared with current and pre-caesarean section medical policies to determine when a successful natural birth would be possible. Pelvic measurements below the viable fetal minimums were considered 'high risk' while those below the modern clinical minimums labelled 'at risk'. Within the sample, 34% ($n=89$) had at least one pelvic measurement considered to be contracted, 9.6% ($n=25$) fell into the 'high risk' category while 24% ($n=63$) were 'at risk'. All females under the age of 14 years had a contracted pelvis and would have found natural birth hazardous. Additionally, 37.6% ($n=151$) displayed pathological or morphological changes which can influence birth success. Overall, this comparative analysis can provide a better understanding of the birthing process and childbirth hazards among archaeological populations.

Enamel growth variation corresponds with LEH defect depth in great apes

KATE MCGRATH^{1,2}, DONALD J. REID¹, DEBBIE GUATELLI-STEINBERG³, KEELY ARBENZ-SMITH¹, SIREEN EL-ZAATARI⁴, LAWRENCE M. FATICA¹, MICHAEL R. CRANFIELD⁵, TARA S. STOINSKI⁶, TIMOTHY G. BROMAGE⁷, ANTOINE MUDAKIKWA⁸ and SHANNON C. MCFARLIN^{1,9}

¹Center for the Advanced Study of Human Paleobiology, The George Washington University, ²PACEA, Université de Bordeaux, ³Department of Anthropology, The Ohio State University, ⁴Paleoanthropology, Senckenberg Center for Human Evolution and Paleoenvironment, Universität Tübingen, ⁵Mountain Gorilla Veterinary Project, Baltimore Zoo, ⁶Dian Fossey Gorilla Fund International, Zoo Atlanta, ⁷Department of Biomaterials and Biomimetics, New York University College of Dentistry, ⁸Department of Tourism and Conservation, Rwanda Development Board,

ABSTRACTS

⁹Division of Mammals, National Museum of Natural History, Smithsonian Institution

Linear enamel hypoplasia (LEH) appears as pronounced horizontal grooves on the outer surface of teeth. LEH defects are understood to represent episodes of nonspecific stress in early life, but little is known about their etiology in nonhuman primates. Researchers have suggested that more severe stressors result in deeper LEH defects, while others argue that depth is related to enamel geometry, i.e., larger or smaller striae angles, reflecting differences in growth rates. Here we ask whether inter- and intraspecific variation in enamel growth corresponds with documented differences in defect depth among great apes. Enamel extension rate (EER), or the rate at which teeth grow in height, was assessed using histological methods in canines of four taxa (*Gorilla beringei*, *Gorilla gorilla*, *Pan troglodytes*, *Pongo* sp., N=16). While sample sizes are too small for statistical comparisons, mountain gorillas have faster EER, and show no overlap with other taxa in the middle 3/5^{ths} of crown height, where LEH defects most commonly occur. This matches our previously reported pattern of defect depth, with mountain gorillas having shallower defects than other taxa in the same crown region. In general, males have faster extension rates than females, but there is some overlap, particularly outside the midcrown. We found that EER is negatively correlated with defect depth ($r^2=0.66$, $p<0.001$). These results suggest that enamel growth variation influences LEH defect morphology, with faster-growing crowns having shallower defects. However, stress severity may also play an important role in defect formation and help to explain the appearance of particularly deep defects.

NSF (IGERT 0801634, BCS 0852866, 0964944, 1520221, 1613626); Leakey Foundation; National Geographic Society Committee for Research and Exploration (8486-08); Ministerium für Wissenschaft, Forschung und Kunst Baden-Württemberg; Lewis N. Cotlow Award.

Living in Dust and Smog: Identity, Inequality, and Mortality During England's Industrial Revolution

SARA A. MCGUIRE

Department of Anthropology, The Ohio State University

The consequences of industrialization in England include an increase in social inequality and the deterioration of urban environments. As such, the environments in which individuals lived and worked varied as a consequence of region and biosocial identity (age, sex, and socioeconomic status - SES). This study examines subsets of two historic English populations (rural Barton-upon-Humber, n = 40; urban South Shields, n = 60) from the Industrial period to determine how identity and the inequality inherent in England's class system during this period caused differences in

individual mortality and stature, which is used as a proxy for health. Specifically, the correlation between age at death and stature with sex and SES is explored, as well as differences between rural and urban environments. Standard bioarchaeological methods and transition analysis were used to estimate age and sex, and long bone measurements were used to estimate stature. T-tests, one-way ANOVAs, and correlations were used to explore the relationships between age, sex, stature, environment, and SES. No significant differences were observed in age or stature by environment, or by low status working class versus mixed SES individuals. However, low SES females in this study had significantly higher ages at death compared to low SES males ($p = 0.050$). As such, there is some evidence of differences in individuals' life experiences as correlated with aspects of identity. This study forms the preliminary analyses of a dissertation that will further evaluate inequality via pollutant exposure during Industrial England.

This research was funded by OSU's Department of Women's, Gender and Sexuality Studies Coca-Cola Critical Difference for Women Research Grant and OSU's Alumni Grant for Graduate Research and Scholarship.

Microbial mismatch: The evolution of the primate microbiome

ERIN A. MCKENNEY and MEGAN S. THOEMMES
Department of Applied Ecology, North Carolina State University

The primate microbiome, and therefore primate health, is strongly influenced by the species that live around and within bodies. However, with a transition to modern western lifestyles, we have created novel environments that select for less diverse associate communities, which are often dominated by a few taxa. This loss in diversity occurs in two ways: the architecture of modern homes limits our exposure to environmental microbes, and changes in our diet affect which taxa are found in primate guts. Traditional human homes, like those of Himba pastoralists, harbor microbial communities that bear similarity to the surrounding environment (average richness outside: 1056 OTUs, inside: 1015 OTUs; $\chi^2 = 1.148$, $P = 0.284$). By contrast, enclosed structures (e.g., North American homes and, more extremely, the International Space Station) harbor communities with a high relative abundance of body-associated taxa (approximately 27% of total sequence reads; e.g., *Staphylococcus* and *Streptococcus*), which are also known to contain some common pathogenic lineages. In addition, modern diets that include processed foods and are high in sugar and fat have altered our internal microbiomes. Western human cultures and captive primate populations now host fewer, but more potentially pathogenic, types of gut microbes compared to humans that live more traditional lifestyles (e.g., the Hadza, Malawian,

and Amerindian peoples) or wild nonhuman primates. Together, these microbial shifts may underlie the epidemiological transition to degenerative diseases that result from evolutionary mismatch.

This work was funded by UCSD/ Salk Center for Academic Research, Training in Anthropogeny (CARTA), NSF Career grant no. 0953390, NSF STEM-C MSP grant no. 1319293, NSF DDIG grant no. 1455848.

Spatial differences in Late Neolithic to Early Bronze Age hunter-fisher-gatherer diet in Lake Baikal's Little Sea micro-region, Siberia

HUGH G. MCKENZIE¹, ANGELA R. LIEVERSE², ALEXEI G. NOVIKOV⁴, OLGA I. GORIUNOVA⁴ and ANDREA L. WATERS-RIST³

¹Department of Anthropology, MacEwan University, ²Department of Archaeology and Anthropology, University of Saskatchewan, ³Department of Anthropology, Western Ontario, ⁴Laboratory of Archaeology and Paleoecology, Institute of Archaeology and Ethnography, Siberian Branch of Russian Academy of Science, Irkutsk State University

Extensive stable carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) isotope and AMS radiocarbon research of prehistoric hunter-fisher-gatherers from the Cis-Baikal region of Siberia has permitted temporally refined dietary reconstructions. Within this area, the Little Sea micro-region contains two ecological zones, Ol'khon Island and the shore of the Mainland, each containing cemeteries spanning the Late Neolithic (LN) (~5570–4600 calBP) to Early Bronze Age (EBA) (~4600–3730 calBP). This research (a) presents new isotope and AMS data for LN and EBA cemeteries from the Little Sea micro-region, and (b) demonstrates a spatiotemporal dietary shift based on the new data that is maintained when combined with previously published isotope data from additional sites. In the LN, individuals buried on the Island have significantly higher $\delta^{15}\text{N}$ and lower $\delta^{13}\text{C}$ means (16.3‰, -18.4‰) than individuals from the Mainland (15.6‰, -17.6‰; $U=47.5$, $p=0.02$; $U=38.0$, $p=0.006$). This suggests the Island individuals consumed more freshwater seal and/or fewer littoral fish. In the EBA, there is no longer a difference in $\delta^{13}\text{C}$ between Island vs. Mainland burials (-18.6‰ vs. -18.3‰), but the extent of the $\delta^{15}\text{N}$ difference increases (15.4‰ vs. 14.2‰), suggesting the amount of littoral fish consumption became similar, and that Island individuals continued to consume more seal. These unexpected spatial differences in resource consumption may imply a degree of territoriality, for example semi-exclusive seasonal rounds,

ABSTRACTS

existed within the Little Sea populations, within which temporal changes in resource availability, trading patterns, group affiliation, and/or social structures caused diachronic changes in diet.

The authors gratefully acknowledge support from the Social Sciences and Humanities Research Council of Canada (Insight Development Grant 430-3013-743), as well as from University of Saskatchewan, and MacEwan University

Media interpretations of “Palaeo-diets” for pregnant women, babies, and toddlers: Relationships to anthropological evidence and public health guidelines

LUSEADRA J. MCKERRACHER^{1,2}, TINA MOFFAT¹, MARY E. BARKER³ and DEBORAH M. SLOBODA^{2,4,5,6}

¹Anthropology, McMaster University, ²Biochemistry and Biomedical Sciences, McMaster University, ³MRC Lifecourse Epidemiology Unit, Southampton University, ⁴Paediatrics, McMaster University, ⁵Obstetrics, McMaster University, ⁶Farncombe Institute for Digestive Health, McMaster University

“Palaeo-diets” are contemporary diets based loosely on bioarchaeological/ethnohistoric reconstructions of pre-Holocene foodways. Some writers and marketers have recently developed Palaeo-dietary guidelines for pregnant women, babies, and toddlers. These guidelines require scrutiny because nutrition during the earliest life stages affects health for the entire life course. Yet, to date, the composition, evidentiary bases, and public health implications of Palaeo-pregnancy and infant/toddler diets remain uninvestigated.

To address this, we reviewed core themes emerging from 25 high-traffic websites outlining Palaeo-diets for pregnant women and babies. We discuss each theme in relation to both bioarchaeological/ethnohistoric evidence and global public health recommendations. The themes include: 1) pregnancy food selection/preparation, 2) pregnancy symptom management, 3) initiation/length/intensity of breastfeeding exclusivity, 4) “ancient” baby formula, 5) infant transitional foods selection/baby-led weaning, 6) seasoning infant foods, and 7) breastfeeding cessation.

Biases in the archaeological, ethnographic, and ethnohistoric records present significant challenges to interpreting pre-Holocene, early-life diets, but it is clear that successful ancient diets varied substantially among populations. So, the anthropological evidence underlying the “Palaeo” guidelines appears un-straightforward. Nonetheless, most Palaeo-inspired pregnancy/infancy diet recommendations – emphasizing consumption of whole, micronutrient-dense foods for everyone, and extended, intensive breastfeeding for babies – align with those of public health institutions. A critical caveat concerns make-it-yourself infant formulas, which cannot safely be substituted for breastmilk or regulated formula.

The complexity of the evidence on ancient maternal and infant diets is not translating into their popular interpretations. While most recommendations from Palaeo-diets are unlikely to harm mothers or babies, much of Palaeo-marketing appears unjustified.

Identifying a new dwarf lemur (*Cheirogaleus*) species from southern Madagascar

ADAM T. MCLAIN¹, RUNHUA LEI², CYNTHIA L. FRASIER², JUSTIN M. TAYLOR², CAROLYN A. BAILEY², SHANNON E. ENGBERG², RUSSELL A. MITTERMEIER³, RICHARD RANDRIAMAMPIONONA⁴ and EDWARD E. LOUIS, JR.^{2,4}

¹Biology and Chemistry, SUNY Polytechnic Institute, ²Grewcock Center for Conservation and Research, Omaha’s Henry Doorly Zoo and Aquarium, ³Global Wildlife Conservation, ⁴Madagascar Biodiversity Partnership

Several individuals of the lemur genus *Cheirogaleus* (previously identified as the species *C. major*) from localities in south-eastern Madagascar (Ambatotsirongorongo, Ampasimena, Andohavondro, Farafara, Ivorona, Manantantely, Mandena, Manombo, Midongy du Sud) were suspected to be a new species due to genetic analyses. Samples were taken in the field for later evaluation. Subsequent analyses of these samples were conducted via a combination of wet bench and computational techniques, and included analyses of nuclear (FIBA, vWF, CFTR-PAIRB) and mitochondrial (cytb, COII, COIII, D-loop, ND3, ND4L, ND4, several tRNA genes, and the PAST fragment) loci. Results were analyzed phylogenetically via maximum likelihood (ML) and Bayesian methods. Our overall dataset consisted of *Cheirogaleus* individuals from across Madagascar and representative of all known and suspected species in that genus, as well as several outgroup taxa. Phylogenetic trees constructed via these analyses were then used to examine genetic divergence between lineages. Briefly, we observed that this lineage formed a distinct clade with high support values (ML= 99; Bayesian= 1.00) and notable genetic divergence across all tested loci. The full cytb locus, for example, displayed genetic distances of 3.2-3.6% between this new species and all other *C. major* group individuals surveyed, and 12.7%±0.009% divergence from the geographically close *C. lava-soensis* (part of the *C. crossleyi* species group) lineage. Based on the genetic evidence we have elevated this lineage to species status as *C. sp. nov. 3*, with a taxonomic name to be released in a forthcoming publication.

Wild platyrrhine quadrupedal kinematics on multiple and inconsistent substrates

ALLISON MCNAMARA¹, NOAH T. DUNHAM², JESSE W. YOUNG² and LIZA J. SHAPIRO¹

¹Anthropology, University of Texas at Austin, ²Anatomy and Neurobiology, Northeast Ohio Medical University

Wild primates navigate complex arboreal habitats that include multiple, inconsistent substrates with diverse characteristics. However, our understanding of quadrupedal gait kinematics is limited to mostly laboratory data on single substrate use. We present an analysis of wild platyrrhine quadrupedal gait on multiple substrates to quantify gait flexibility and further understand the adaptive context in which primate quadrupedalism evolved. We collected high-speed video data on platyrrhines in lowland Amazonian Ecuador and quantified kinematic adjustments to substrate inconsistencies that could disrupt continuous gait. We analyzed quadrupedal locomotor bouts of *Saimiri sciureus* (n=35 bouts, 121 strides) containing >1 stride on >1 substrate and categorized each substrate inconsistency as a “challenge” (e.g., gap, obstacle). We digitized footfall events, categorized substrate characteristics, and calculated kinematic variables for each stride within bouts. Asymmetrical walking gaits were used significantly more than symmetrical walking gaits. Within symmetrical gaits, diagonal sequence was used significantly more than lateral sequence. Change in footfall order occurred significantly more frequently in strides with a challenge. Time lags between touchdowns of paired forelimbs and ipsilaterally paired fore and hindlimbs both significantly increased in strides with challenges compared to strides without challenges while controlling for speed. Increasing time lags between paired limbs due to the presence of challenges may indicate that forelimbs are used to test the stability of upcoming substrates. Our results demonstrate that quadrupedal walking is diverse and flexible across various substrate disruptions, and future analysis will reveal whether this is consistent across taxa.

Funding provided by National Science Foundation Grants BCS-1640552, BCS-1640453

Taxonomic variation in the large catarrhines from Rusinga and Mfangano Islands

KIERAN P. MCNULTY

Anthropology, University of Minnesota

Fossil apes from Rusinga and Mfangano play an important role in documenting the early diversification of Hominoidea. Nevertheless, there is controversy over the taxonomy and phylogeny of the largest to these. Whereas most researchers concur that *Ekembo* is represented by two species, there is less agreement about

ABSTRACTS

anatomical diagnoses and specimen attributions. Recent discoveries and new geochronological results further complicate this: fossils attributed to *Ekembo* span greater anatomical and temporal ranges than previously thought.

Re-analysis of the *Ekembo* hypodigm suggests that older specimens are more primitive than their younger counterparts in features that distinguish *Ekembo* from *Proconsul*. They lack *Proconsul* synapomorphies, but nevertheless appear less derived than the mostly-younger *Ekembo* sample. In the context of recent geochronological results, this is not surprising: specimens from the Wayando Formation may be 2 My older than those from the Hiwegi Formation.

The 2018 discovery of two canines from the Wayando Formation confirms taxonomic variation among large catarrhines. The male canine is poorly preserved but exhibits root anatomy that diverges from *Ekembo*; the female canine preserves a complete root and nearly unworn crown, and is distinct from both *Ekembo* and *Proconsul*. Although this material is insufficient to name a new taxon, identifying the presence of another catarrhine calls into question the attribution of all large primates to *Ekembo*. Furthermore, the existence of this taxon suggests the possibility – should the species prove closely related to *Ekembo* – that future discoveries will help document change over time in the large apes of Rusinga and Mfangano.

This work was funded by grants from the National Science Foundation (BCS #1241807), Leakey Foundation, and the University of Minnesota.

Identifying plantigrade adaptations in Miocene hominoids with implications for hominin bipedalism

ELLISON J. MCNUTT

Ecology, Evolution, Ecosystems, and Society Graduate Program, Dartmouth College, Anthropology, Dartmouth College

It is generally accepted that plantigrady (i.e., heel-striking) is an important precursor to stable, striding bipedalism. However, little is currently known about the evolution of plantigrady within hominoids. In this study, a multifaceted approach was used to examine foot posture in Miocene hominoids and test hypotheses about the locomotor pattern that preceded bipedalism. A high-resolution plantar pressure mat (Tekscan mobile MatScan) was used to identify where the foot contacts the ground in semi-wild mammals classified as digitigrade (wolves), semi-digitigrade (baboons), and plantigrade (bears and humans). These data were used to guide 3D geometric morphometric analyses of 407 calcanei from 20 mammalian taxa to identify anatomical markers of plantigrade locomotion. Among other differences, calcanei from plantigrade apes and bears possess a relatively wide plantar aspect of the

proximal calcaneal tuber; semi-digitigrade and digitigrade mammals have a narrow proximal calcaneal tuber, but a wide plantar surface distally. 3D surface scans of original fossil calcanei (n=15) from Miocene hominoids, including *Proconsul*, *Ekembo*, *Dendropithecus*, *Limnopithecus*, *Rangwapithecus*, and *Oreopithecus* were entered into these analyses. In the Miocene, there were two calcaneal morphs: (1) those displaying similarities to calcanei from semi-digitigrade monkeys (e.g., *Limnopithecus*, *Dendropithecus*); and (2) those displaying similarities to calcanei from primates practicing semi-plantigrade arboreality, including *Ateles*, *Hylobates*, and *Pongo* (e.g., *Proconsul*, *Ekembo*, *Oreopithecus*). No known Miocene calcanei show the same adaptations for terrestrial plantigrady found in African apes and humans.

This research was supported by the National Science Foundation, grant number 1730822.

Untangling the Osteological Paradox: Using Discordance in Dental and Skeletal Age Estimates to Identify Periods of Heightened Biosocial Stress

CAIT B. MCPHERSON¹ and JAMES T. WATSON^{1,2}

¹School of Anthropology, University of Arizona,

²Arizona State Museum, University of Arizona

La Playa, an Early Agricultural Period (EAP) (3,600 – 1,800 BP) site located in Northern Sonora, Mexico provides an extensive record of human physiological adaptation to an arid environment and is an ideal population for examining the role played by agricultural intensification in shaping patterns of skeletal growth and development. However, the juvenile sample (n=56) from La Playa has yet to be systematically assessed for skeletal evidence of biosocial stress. Significant discordances in dental and long bone age estimates indicate that a high proportion of subadults (40%) suffered from suboptimal linear growth. Moreover, moderate rates of anemia-linked skeletal biomarkers (30%) and enamel defects (50%) traditionally attributed to nutritional or immunological disruptions were documented in the sample. These results indicate that La Playa juveniles were exposed to both chronic and acute biosocial stressors that constrained somatic growth. In addition, age-related disparities in standard height-for-age measures and stress biomarker prevalence suggest that patterns of juvenile morbidity and mortality were products of heterogeneous frailty, with individuals under heightened disease and nutritional stress during sensitive developmental periods disproportionately impacted. The results of this study further suggest that using degree of discordance between estimated dental and skeletal ages is a viable method for identifying periods of heightened biosocial stress during skeletal growth and development in archaeological populations. Applying this methodology to the La Playa

skeletal sample indicates that individual heterogeneity in immunological susceptibility likely influenced demographic patterns observed in the death assemblage.

Incorporating Histological Methods to Examine the Response to Famine in Mid-19th-Century Ireland

LAUREN A. MECKEL, HALLIE R. BUCKLEY and JONNY GEBER

Anatomy, University of Otago

In 2005, a mass burial ground was discovered during a redevelopment project adjacent to a former union workhouse in Kilkenny City, Ireland. The burials, which date between 1847 and 1851, contained the remains of at least 970 individuals who died as a consequence of the Great Irish Famine. The skeletal assemblage is unique in the field of bioarchaeology as it can be contextualized to the most well-recorded historical famine in the world, an aspect that allows researchers to examine the effect of poverty, starvation, and disease on the skeleton from a biocultural perspective. For example, archival records from this time describe attempts by the British government to relieve the poor of starvation by distributing 'Indian meal' (maize, a C4 plant) imported from North America. Since bone is a dynamic tissue that changes in response to factors like diet, activity, and disease, this research seeks to observe the impact of maize on the rib bone microstructure of these skeletons. In a preliminary analysis, carbon and nitrogen isotope values, which would have been influenced by a C4 component in the diet, were compared to histomorphometric features. The results suggest that $\delta^{13}C$ may have had an influence on the rate of remodeling in the microstructure of the ribs. Future analysis will further explore the effect of relief food on the bone health of famine victims, the distribution of resources and conditions within the workhouse, and the overall impact of structural violence in 19th century Ireland.

This research is funded in part by the Royal Irish Academy and the National Monuments Service

Living with a permeable body: corporeal plasticity and its politics from ancient medicine to epigenetics

MAURIZIO MELONI

Alfred Deakin Institute, Deakin University

Emerging postgenomic disciplines like epigenetics and microbiomics are contributing today to a rewriting of the human body as profoundly permeable to its surroundings and extensively shaped by environmental factors. These views of biological plasticity represent an important discontinuity with the bounded body of twentieth century biomedicine and genetics. In my paper, I offer an archaeology of the plastic body that is emerging in contemporary postgenomic

ABSTRACTS

disciplines. I investigate a longer history of the beliefs about the plasticity of human biology starting with ancient and early modern medicine, mostly humoralism, and analyse the biopolitical techniques required to govern such permeability. I focus in particular on the way in which notions of corporeal plasticity have been connected with profoundly racialized and gendered discourses in ancient and early modern times. I also highlight how a longer history of plasticity may help problematize contemporary identification of plasticity with openness, unlimited potentialities and change. Finally, I interpret the complex sociological and biopolitical implications of emerging notions of plasticity in contemporary epigenetics in the light of this past and often forgotten history. I present evidence about a longer and more complex history of corporeal plasticity and its implications for contemporary notions of vulnerability, risk and intervention.

Sexual Dimorphism of Cranial Fluctuating Asymmetry in a Historic Hispanic Population

RAPHAELA M. MELORO¹, JOSEPH T. HEFNER², MICHAEL HEILEN³ and VALERIE B. DELEON¹

¹Anthropology, University of Florida, ²Anthropology, Michigan State University, ³Center for the Study of Cultural Landscapes, Statistical Research, Inc.

Physiological stress is affected by numerous biocultural factors and has a high impact on developmental stability, producing biomarkers such as fluctuating asymmetry. Analyzing differences in the pattern and degree of stress markers in a population can yield information about the overall health of a population and differences in exposure among subgroups. Generally, females are expected to have a lower degree of fluctuating asymmetry than males due to genetic buffering during development.

This study analyzed three-dimensional landmark coordinate data collected from ectocranial surface scans of Hispanic adult male and female crania (n=22, n=22) from the mid-19th century Alameda-Stone cemetery in Tucson, Arizona to examine sex-based differences in fluctuating asymmetry in individuals from the same ancestral group. Thirty landmarks were collected in multiple replicates for each specimen to capture shape of the face and neurocranium. Additional landmarks from the cranial base were omitted due to damage on most of the crania. Data collection and analysis of asymmetry were conducted in R statistical software using the Geomorph package.

Surprisingly, the level of fluctuating asymmetry found in females was greater than that found in males. Patterns of directional asymmetry were comparable between the sexes. It is possible that the low sample sizes in this study were unable to fully capture the degree of fluctuating asymmetry

in the population. Taphonomic distortion is another likely confounding factor. Geometric morphometric methods using semi-landmarks to define curves may better capture variations in symmetry in these groups, and future work will include these approaches.

10,000 years of mandibular evolution in southern South America: Implications for morphological diversification

LUMILA P. MENENDEZ¹, MARINA L. SARDI², NAHUEL A. SCHEIFLER³, MARIELA E. GONZALEZ³, PABLO MESSINEO³ and GUSTAVO G. POLITIS³

¹Evolutionary Anthropology, Konrad Lorenz Institute, ²CONICET-División Antropología, Universidad Nacional de La Plata, ³INCUAPA-CONICET, Universidad Nacional del Centro de la Provincia de Buenos Aires

South America (SA) was the last continent to be colonized by modern humans. One of the relevant research questions that still remain to be addressed is how SA populations became differentiated. Previous studies that pointed to tackle this question analyzed molecular, cranial, dental, and postcranial variation. However, there are no studies so far analyzing mandibular variation with a wide temporal-spatial coverage in SA, what might be biasing current interpretations. Mandibular variation in modern humans has been described by a reduction pattern across time, which was interpreted either as a result of evolutionary history and/or the differential impact of diverse subsistence strategies. The aim of this study is to evaluate morphometric changes in southern SA mandibles for discussing which evolutionary processes were involved during human diversification. For this, a total of 28 3D landmarks were registered in a sample that includes 6 early-middle Holocene specimens (EMH) from the Argentinean Pampas and 10 late Holocene populations (LH) from SA (N~200). Results of the PCA and CVA showed that the EMH specimens are primarily differentiated from the LH ones, and secondarily associated to the southern samples. Shape and size variation shows that more robust mandibles with a larger body and ramus characterize EMH. Additionally, the spatial regressions performed show that diet contributes to explain 40% of mandible shape variation. Overall, such patterns could be interpreted either as the result of population diversification driven by selection and/or genetic drift. A discussion considering previous studies in the area and alternative explanations will be presented.

This research and presentation was possible thanks to a fellowship from the Konrad Lorenz Institute for Evolution and Cognition Research.

The Influence of Breeding System and Group Size on the Probability of Extinction in Diurnal Lemurs

FERNANDO M. MERCADO MALABET^{1,2}, LUDMILA T. KUMPAN^{1,2} and SHAWN M. LEHMAN¹

¹Department of Anthropology, University of Toronto, ²School of the Environment, University of Toronto

Despite decades of research on the conservation biology and population dynamics of endangered species, there is limited understanding of the socioecological mechanisms that drive some species to have a higher probability of extinction. We address this knowledge gap by modelling how variations in the breeding systems and group sizes of three diurnal lemurs (*Eulemur mongoz*, Critically Endangered; *E. fulvus*, Near Threatened; *Propithecus coquereli*; Endangered) predicted extinction risk. These three species are largely sympatric throughout their geographic range yet differ in their social structure and each suffers from varying extinction probabilities. We hypothesized that the capacity of these lemurs to persist in disturbed environments rests on the reorganizational flexibility of their social structure. We used population viability analysis (PVA) to model how variations of these parameters affect the time in which a population crashes. We modeled a series of mock-populations that simulated variations in the breeding systems and group sizes of the three lemur species. PVA models for both species were developed in Vortex 10 (ver. 10.3.3.0) and analyzed using the *vortexR* package (ver. 1.1.5). Our models show that mock-populations that exhibited a pair-bonded breeding system or small social groups had a higher probability of extinction (Pr. E.= 0.84 and 0.76, T = 100 years) than species living in polygynous groups or large populations (Pr. E.= 0.01 and 0.16, T = 100 years). The results of this research provide a theoretical framework to refine and explore the varying causalities associated with differential extinction probabilities in rare lemurs.

Financial support for this work was provided by the School for the Environment at the University of Toronto, the Ontario Government, and the Natural Science and Engineering Research Council.

Diet, Grit and Dental Microwear Textures: the facts

GILDAS MERCERON¹, LARISA DESANTIS² and PETER S. UNGAR³

¹PALEVOPRIM, CNRS and University of Poitiers, ²Department of Earth & Environmental Sciences, Vanderbilt University, ³Department of Anthropology, University of Arkansas

Dental Microwear has long been used as a dietary proxy to explore differences in feeding behaviors among extinct species of mammals. Modern species stored in museums or wild populations with associated dietary metadata have provided robust baselines to interpret results for extinct taxa. For more than 35 years, researchers

ABSTRACTS

have debated the etiology of microwear, with some arguing that grit/dust, rather than food type per se, is responsible for distinctive microwear patterning.

We here review analyses of dental microwear of several modern taxa to demonstrate empirically that, while dust/grit likely plays a role, patterns reflect differences in food fracture properties.

For instance, koalas consume almost exclusively silica-free eucalyptus leaves, yet demonstrate dental microwear indicative of consumption of tough leaves, suggesting that dust/grit on leaves (abundant in arid habitats) does not obfuscate the expected dietary signal.

Studies of terrestrial primate species, such as *Theropithecus gelada* and *Cercocebus atys*, show markedly different microwear textures consistent with hardness and toughness of reported diet. Likewise, studies of more arboreal primates, such as *Trachypithecus cristatus* and *Macaca fascicularis*, differ in microwear as expected given differences in their diets. Within-population studies of primates and ruminants have also shown that dental microwear tracks both seasonal availabilities and differing energy requirements between sexes.

Finally, controlled food testing demonstrates that there is no need to invoke dust/grit to generate differences in dental microwear between grass- and browse-fed sheep. When dust in levels simulating natural concentrations is added to these two fodders, dental microwear still mirrors diets.

The authors thanks NSF FAIN 1455198 (to DeSantis), the French National Research Agency ANR (Project TRIDENT ANR-13-JSV7-0008-01 to Merceron) and NSF SBR 0315157/0948283 and the LSB Leakey Foundation (to Ungar).

4.2 Ma *Australopithecus anamensis* axial remains: the oldest australopithecine vertebrae in the fossil record

MARC R. MEYER¹ and SCOTT A. WILLIAMS^{2,3}

¹Department of Anthropology, Chaffey College,

²Center for the Study of Human Origins, Department of Anthropology, New York University,

³New York Consortium in Evolutionary Primatology

Seven *A. anamensis* vertebral fossils from the Assa Isse locality in Ethiopia's Middle Awash area dated to ~4.2 Ma constitute the oldest known australopithecine axial remains. Because the spine is the interface between major body segments, these fossils can be informative on the behavior and evolution of the first australopithecines.

Two C1 vertebrae are similar in size and morphology to *H. sapiens*, with synapomorphies signifying that like humans, *A. anamensis* lacked the atlantoocclusal muscle, reducing their capacity for climbing relative to the great apes. The retroflexed C2 dens and very long C6

spinous process likely reciprocate the facial prognathism, long clivus and retroflexed foramen magnum of australopithecines, rather than reflecting locomotor or postural behaviors. Two thoracic vertebrae are similar to *Homo* in shape and size with an enlarged endplate surface associated with mitigating high vertical loads. The full costal facet of the T1 vertebra is unlike the extant great ape demifacet pattern and represents the oldest evidence for the derived univertebral pattern in hominins.

Most other *A. anamensis* fossils demonstrate that cranially and postcranially the taxon was more primitive than its evolutionary successor *A. afarensis*. However, here we find many aspects of vertebral morphology independent of allometry are more derived in *A. anamensis* than its putative descendant *A. afarensis*. These fossils offer evidence indicating habitual bipedality in *A. anamensis* despite some plesiomorphic features related to craniofacial morphology and further our understanding of the adaptation and evolutionary significance of *A. anamensis*.

Severe skeletal lesions associated with a documented case of juvenile leukemia

JULIA MEYERS¹, ELLIE GOODERHAM¹, LUÍSA MARINHO¹, HARMAN NAHAL¹, KATHERINE NICHOLS^{1,2}, DEREK O'NEILL¹, LAURE SPAKE¹ and HUGO F.V. CARDOSO¹

¹Archaeology, Simon Fraser University, ²First Nation Studies, Simon Fraser University

There are a noticeable and distinctly small amount of leukemia cases reported in the archaeological literature, even more so among juveniles, with only two published accounts of juvenile leukemia (Klaus 2016, Molto and Sheldrick 2018). Osteological manifestations of leukemia are rarely reported even in the clinical literature, and include one case of juvenile leukemia reported by Rothschild et al. (1997). Opportunities to study historically diagnosed cases of juvenile leukemia provide insight and inform researchers of potential skeletal morphology when examining archaeological cases. This report describes the skeletal lesions observed during the examination of the remains of a 10-year-old girl, who died in 1965 in Lisbon, Portugal, and whose cause of death was diagnosed as leukemia. This individual belongs to the skeletal reference collection housed at the National Museum of Natural History and Science, Lisbon. These remains show a variety of lesions, mostly localized lytic, on the sacrum, hip bones, the proximal epiphyses and metaphyses of the tibiae, and the distal epiphyses and metaphyses of the femora. Lytic lesions have caused the near complete destruction of the left ilium, and partial destruction of the left ischium and the pubis. This clinically diagnosed case is one of the few examples of confirmed juvenile leukemia. As such, it

provides a reference for the skeletal lesions which may be expected to be present in archaeological leukemia cases, thus aiding with differential diagnosis.

Covariation across the thoracolumbar vertebral column in hominoids

EMILY R. MIDDLETON

Anthropology, University of Wisconsin-Milwaukee

Previous research suggests spinal musculature and function are key determinants of torso shape in anthropoids, and supports a hypothesis of strong integration within the thoracolumbar vertebral column. An assumption of strong integration also underlies the observation that hominoids, compared to monkeys, exhibit a number of shared characteristics related to stiffening and shortening the spine to aid in below-branch suspensory locomotor behaviors. Here I investigate patterns of covariation across the thoracolumbar vertebrae in three hominoid taxa (*Homo*, n=317; *Pan*, n=87; *Hylobates*, n=67) using linear metrics to test the assumption of a strong, shared pattern of vertebral integration across extant apes. Using the R statistical computing environment, I calculated a set of evolvability statistics based on an application of Lande's multivariate response to selection equation. Confidence intervals based on the bootstrapped standard error of each index were used to evaluate differences among taxa. All taxa exhibit markedly weaker integration at the cranial end of the thoracolumbar column (T1-T3) than in the more caudal thoracics or lumbar, which corroborates previous research noting weaker integration in the cranial ribs compared to the more caudal ribs. Notable differences among taxa include the overall weaker vertebral integration in humans compared to the nonhuman apes as well as the relatively stronger integration across the lumbar region in *Hylobates* compared to *Pan* and *Homo*. Thus, contrary to expectations of a shared pattern, results indicate that variation in patterns and magnitudes of covariation across hominoid taxa exist and are potentially reflective of different locomotor and obstetric selective pressures.

Grant support for data collection was provided by the Wenner-Gren Foundation, the Leakey Foundation, and New York University.

Conservation to Coexist: Participatory Action Research for Wildlife Conservation, Economic Development, and Biological Anthropology Research

KRISTA M. MILICH¹, KAYCE SORBELLO¹, JILLIAN MCCARTEN¹, LAUREN WISEMAN-JONES², RICHARD BUSOBOZI³ and MOSES KUGONZA³

¹Anthropology, Washington University in St. Louis,

²Department of Life Sciences, Imperial College

London, ³Makerere University Biological Field Station, Makerere University

ABSTRACTS

Human-wildlife conflict is one of the greatest threats to biodiversity conservation. A main source of this conflict is crop raiding – when wild animals destroy the crops in agricultural fields causing subsistence farmers to suffer extreme losses. Animals are killed during crop raiding events, and communities develop negative feelings about conservation. We developed a community project to assess the impact of human-wildlife conflict on conservation around Kibale National Park, Uganda, and to implement changes to mitigate this conflict. During our initial survey, we found that over 90% of the people living in the areas where we work are subsistence farmers with no other source of income. All respondents felt that crop raiding was the biggest problem with living near the park. They had strong negative feelings about the park and the animals, including the 13 species of primates that live there and have contributed a wealth of knowledge to studies in biological anthropology. Thus, we worked with project participants to establish the following land-use changes: 1) planting garlic as a cash crop, 2) planting tea as a buffer crop, 3) building bee fences, and 4) maintaining a trench around the boundary of the park. Through monthly surveys, we assessed the success of these changes on reducing crop raiding and improving conservation initiatives. Compliance with land-use changes was significantly associated with a reduction in crop raiding events, an increase in economic stability, and an improved attitude about conservation. This project provides guidelines for sustainable interventions to human-wildlife conflict and primate conservation.

Funding was provided by the The Nacey Maggioncalda Foundation Goldberg Conservation Grant, American Society of Primatologists Conservation Grant, The Rufford Foundation, and International Primatological Society Conservation Grant.

Landscape Survey of Potential Combustion Features at FxJj20 Site Complex in Koobi Fora, Kenya

CATHERINE K. MILLER¹, RUSSELL CUTTS², DAVID BRAUN³ and J.W.K. HARRIS⁴

¹Ecology, Evolution, Ecosystems, and Society, Dartmouth College, ²Anthropology, University of Georgia - Athens, ³Anthropology, The George Washington University, ⁴Anthropology, Rutgers University

This study focuses on a preliminary landscape survey of the archaeological site FxJj20 in Area 131 found within the Koobi Fora Formation in Northern Kenya. This survey targeted the frequency and distribution of potential combustion features. These potential features were found eroding out of the Okote Member of the geologic Koobi Fora Formation, which dates between 1.5 and 1.64 mya. Similar features in other archaeological sites have previously been identified with associations of material that exhibit evidence

of exposure to high temperatures. Twenty-five potential combustion features were found with the current survey. Twelve of these features were recorded with associations of artifacts and fossils. The spatial distribution of the potential features suggests a possible environmental influence on their location and clustering.

Sex-specific cervical vertebral growth in height & depth: A study using computed tomography

COURTNEY A. MILLER¹, SEONG JAE HWANG², MEGHAN M. COTTER³ and HOURI K. VORPERIAN¹

¹Vocal Tract Development Lab, Waisman Center, University of Wisconsin-Madison, ²Computer Sciences, University of Wisconsin-Madison, ³Anatomy, Academic Affairs, School of Medicine and Public Health, University of Wisconsin-Madison

Cervical vertebral morphology changes during human development such that clinicians and researchers commonly determine skeletal maturation using a standardized cervical vertebral maturation index (CVMI), which identifies six morphological developmental stages that transform the vertebral body from an anterior wedge shape to a vertical rectangle. However, CVMI has poor reproducibility given its qualitative nature; furthermore, it does not account for sexual dimorphism. Therefore, using CT scans from 122 (79M; 43F) modern typically developing individuals between the ages of 6 months to 20 years, this study quantified sex-specific normative growth at the midsagittal plane by placing 3D landmarks at the vertebral boundaries to calculate the Euclidean distance in anterior height, posterior height, superior depth, and inferior depth of each cervical vertebral body of C2 to C7. Sex-specific growth trends were identified for each height and depth measure. Findings revealed height growth trends, except for C2, had the expected two periods of accelerated skeletal growth during early childhood and adolescent years, while all depth growth trends obtained the majority of their adult size during early childhood. In C3-C7, anterior heights were smaller than posterior heights until between 13-15 years while inferior depths were larger than superior depths at all stages of development. Additionally, male heights became larger than females after the age of 16 years however, females had smaller depths than males at all ages. These findings provide normative growth trends for comparative purposes, supports the morphological developmental stages of CVMI, and emphasizes the need to consider sexual dimorphism when assessing skeletal maturation.

National Institutes of Health, National Institute on Deafness and Other Communicative Disorders grant (R01 DC6282) and National Institute of Child Health and Human Development core grant (P30 HD03352, U54 HD090256).

Refining our understanding of human diets: Using bulk and compound-specific amino acid stable isotope data to investigate pre-Columbian dietary practices of Lake Titicaca, Bolivia inhabitants (1500 BC – AD 1100)

MELANIE J. MILLER^{1,2}, IAIN KENDALL³, SIAN HALCROW¹, RICHARD P. EVERSHERD³ and CHRISTINE A. HASTORF^{2,4}

¹Anatomy, University of Otago, New Zealand, ²Archaeological Research Facility, University of California, Berkeley, ³Organic Geochemistry Unit, University of Bristol, ⁴Anthropology, University of California, Berkeley

Stable isotope analysis of human skeletal tissues is now commonly used in bioarchaeological research to establish dietary patterns in ancient populations. Although bulk isotope data (primarily bone collagen carbon and nitrogen isotope data) can be informative of general dietary practices, the nuances of specific dietary components are often difficult to resolve using these bulk data sets. Compound-specific amino acid stable isotope analysis is able to provide a further level of detail to dietary studies, allowing identification of particular food groups, such as distinguishing between terrestrial, freshwater, and marine food sources. This is the first study to combine both of these isotopic methods to investigate dietary patterns of a pre-Columbian population from South America, specifically focusing on the inhabitants of the Taraco Peninsula, Lake Titicaca, Bolivia (1500BC – AD1100). Previous research has demonstrated a confounding issue of isotopic overlap between two potential dietary resources: maize, a C₄-plant, and fish from Lake Titicaca, which have enriched $\delta^{13}\text{C}$ values overlapping the range of terrestrial maize. We combined multiple isotopic analyses of teeth (enamel and dentin) including bulk carbon and nitrogen isotope data, and compound-specific amino acid carbon isotope data. The isotopic data show increases in the $\delta^{13}\text{C}$ values of Taraco inhabitants through time, and demonstrate that these changes are being driven by increasing consumption of terrestrial C₄ food sources (likely maize), and not from increasing consumption of fish from Lake Titicaca. This work highlights the importance of using multiple isotopic data sets to reach more conclusive evidence about dietary practices in human history.

Miller was supported by a grant from the European Association of Organic Geochemists.

An Intra-site Biodistance Analysis of the Maya: Dental Evidence for Urbanism at Copan

KATHERINE MILLER WOLF

Department of Sociology, Anthropology, and Geography, Indiana University East

ABSTRACTS

Research focused on the largest collection of human skeletal remains yet recovered in Mesoamerica from the site of Copan, Honduras. Eight-hundred Late Classic (AD 600-820) burials from twenty-two patio groups within eight neighborhoods around the site center were analyzed to assess the degree of biological kinship and migration of the ancient population. The results of the analysis of dental metric data show statistically significant differences between and within neighborhoods and patios across the site. Contextualized with strontium isotope data that suggest 10-40% in-migration during the Late Classic period, these results highlight Copan's complex social system that was influenced by various forms of kinship and migration. As such, the validity of the lineage and ethnic barrio models of ancient Maya social organization are not supported for archaeological reconstructions of Copan.

Funding was provided by the National Science Foundation BCS-1207533 and Arizona State University.

Skeletal microstructure growth dynamics in ancient humans and fossil rats from Indonesian islands

JUSTYNA J. MISZKIEWICZ¹, PATRICK MAHONEY², JULIEN LOUYS³, SUE O'CONNOR⁴, CHELSEA MORGAN¹, BRONWYN WYATT¹ and PETER BELLWOOD¹

¹School of Archaeology & Anthropology, Australian National University, ²School of Anthropology & Conservation, University of Kent, ³Australian Centre for Human Evolution, Griffith University, ⁴Archaeology & Natural History, Australian National University

Substantial evidence exists for insularity manifesting in living populations, but little is known about its effect on skeletal growth dynamics in prehistoric humans and other animals. Here, we reconstruct: 1) femur bone metabolism in ten Timor Island giant and small fossil (late Quaternary ca. 5-18 ka) rats, 2) human femur and occipital bone, and tooth enamel growth links in three adult males of 152.9-164 cm stature, recovered from the Maluku Islands (BCE/CE junction Morotai, 2314-1415 cal. BP Gebe). Osteocyte lacunae density (Ot.Dn) and secondary osteon parameters were recorded in midshaft femur and nuchal crest occipital bone histological sections. Lateral enamel daily secretion (DSR) and root extension rates were calculated from upper first and second human molar histology. Results reveal significant ($p < 0.001$) and negative relationships between Ot.Dn and rat body size, with giant specimens showing low Ot.Dn (Rho min. = -0.891, max. = -0.976). The DSR of 3.9 μm (mid-enamel) to 4.6 μm (outer enamel) for the human crowns is similar to modern day molars, but the daily extension rate of 7.61 μm over the first 2 mm of root growth is faster than the rate roots form over this distance in modern clinical samples. Remodelling data indicate increased

bone deposition (21.18-27.86 $\mu\text{m}/\text{mm}^2$) despite the short adult stature. Findings from our ancient human and rat model experiment suggest that island living may affect internal dynamics of skeletal growth. Giant rats may have slowed down their bone metabolism, whereas short humans increased their growth rates to facilitate a physiological adaptation to island environments.

Tracing Racial Formations: Camper's, Blumenbach's, and Morton's Skulls and the Construction of Race in Anthropology

PAUL WOLFF MITCHELL

Anthropology, University of Pennsylvania

The study of the human skeleton has always been a visual science, requiring the exclusive use of illustration for depiction until the end of the 19th century. Such illustrations, particularly of skulls, were once the primary basis for scientific knowledge about race, but closer examination of canonical illustrations from early cranial race science reveals how visual idealization and distortion were constitutive in the scientific construction of race. Skulls from three major collections in the history of cranial racial science from about 1790-1850 were considered here: 1) those of Petrus Camper (1722-1789), in Groningen, the Netherlands, who was the first to systematically measure racial differences in the human skull; 2) those of Johann Friedrich Blumenbach (1752-1840), in Göttingen, Germany, responsible for a cranial-racial typology and racial labels which have persisted for centuries; 3) those of Samuel George Morton (1799-1851), in Philadelphia, Pennsylvania, USA, who was the first to measure large samples of human skulls for racial comparisons. Crania in these collections were 3D-laser scanned and compared with the illustrations made and published of them by their collectors. Quantitative and qualitative analyses of these comparisons show that aesthetic considerations, exaggeration, and bias played an important role in forming the image of race. Moreover, reconstructing the rationale by which certain skulls were selected over others from the same collection to serve as racial exemplars, as well as considering osteobiographical and biohistorical analyses of these crania, can reveal new insights into the historical process whereby the anthropological race concept was constructed.

This research was funded by the Wenner-Gren Foundation and the Deutscher Akademischer Austauschdienst (DAAD).

A 3D analysis of sacroiliac joint surface topography among primates

PENPICHAYA MIYAN¹, SARAH T. MINCER^{1,2} and GABRIELLE A. RUSSO¹

¹Anthropology, Stony Brook University, ²Interdepartmental Doctoral Program in Anthropological Sciences, Stony Brook University

As part of both the pelvis and the vertebral column, the sacrum is a keystone of the locomotor skeleton. The sacroiliac joint (SIJ) in particular is responsible for transmitting weight received from the torso to the hindlimbs, and withstanding forces associated with tail-assisted suspension in prehensile-tailed primates. Previous studies demonstrate that dimensions of the SIJ reflect differences in positional behaviors and tail morphology among primates. Here, we apply recently-developed 3D methods to quantify the complex topography of the SIJ and assess if it differs among primates grouped by positional behavior and tail length/ability. Data were collected from high-resolution computed tomography scans of >24 sacra from a broad sample of extant primates ranging in tail length/ability and positional behaviors. The joint surface was isolated, smoothed with a mesh polygonal surface, and processed in MorphoTester to calculate 4 topographic features: Dirichlet Normal Energy (DNE), Relief Index (RFI), Orientation Patch Count Rotation (OPCR), and size-adjusted surface area (SA). Preliminary results for Mann-Whitney U Tests between primates grouped by tail length/ability show that prehensile-tailed primates have higher OPCR and SA values than nonprehensile-tailed primates, indicating increased complexity and relative size of the SIJ. Among nonprehensile-tailed primates, shorter-tailed primates have higher OPCR and SA values than longer-tailed primates. Surface bending (DNE) and surface relief (RFI) were statistically similar among tail length/ability categories. We additionally discuss differences in SIJ topography among primates grouped by positional behavior, and evaluate the utility of this method for making inferences about primate behavior in the fossil record.

Stony Brook University Undergraduate Research and Creative Activities Summer Research Program (PM); NSF DDIG BCS-1156016 (GAR), Leakey Foundation General Research Grant 7169524 (GAR).

Contribution of tree-fall canopy gaps to variation in nitrogen content of fruits and leaves from *Varecia* and *Eulemur* food trees in northeastern Madagascar

MONICA MOGILEWSKY¹, NATALIE VASEY^{1,2}, MC ANTONIN ANDRIAMAHAIHAVANA³, ZAFIMAHERY RAKOTOMALALA³ and TIMOTHY M. EPPLEY⁴

¹School of the Environment, Portland State University, ²Department of Anthropology, Portland State University, ³Department of Animal Biology, University of Antananarivo, ⁴Institute for Conservation Research, San Diego Zoo Global

Madagascar's fruits provide significantly less protein than fruits from other tropical regions, posing a challenge for frugivorous lemurs such as *Varecia* and *Eulemur* to consume enough protein. To compensate, these species may preferentially select fruits with greater nitrogen content. Several studies have found greater nitrogen

ABSTRACTS

content in plant parts in the canopy and on forest edges. This phenomenon may also occur in tree-fall canopy gaps. To test this, we collected 35 samples of ripe fruit and young leaves from trees located at or near a gap and 20 samples from trees under closed canopy at Masoala National Park, Madagascar from December 2017 through February 2018. During this time, fruits are abundant, and female lemurs are nursing young. Despite high abundance overall, we had difficulty locating ripe fruit on closed canopy trees. All samples were processed to mimic consumer processing, dried on site, then analyzed at the University of Hamburg. We found that samples from gaps had greater percent nitrogen content (mean= 0.66% +/- 0.33) than closed canopy (mean=0.51% +/- 0.14). While the trend was not statistically significant, further investigation is worthwhile given the small sample size and limited sample availability under closed canopy. *Varecia rubra* were observed closer to gaps than expected at random. *Varecia* may have greater protein requirements than *Eulemur* during this season to nurse their multiple, rapidly growing young with high-fat, high-protein milk on schedule. Lemur-gap interactions could be key to understanding how *Varecia* meet protein requirements for successful reproduction.

This research was funded by San Diego Zoo Global; Primate Conservation, Inc; the Edward D. and Olive C. Bushby Scholarship, and Scion Natural Science Association.

Exploring sources of variation in inter-observer reliability scoring of facial expressions using the ChimpFACS

ALEXANDRA K. MOLINA, BRITTANY N. FLORKIEWICZ and ERICA A. CARTMILL

Anthropology, University of California, Los Angeles

The Facial Action Coding System (FACS) is currently the most popular systematic and standardized method of studying facial expressions in mammals. Since its original release for humans, the FACS has expanded to include primates such as chimpanzees. The FACS trains its users to analyze facial expressions by identifying individual muscle movements (called action units or AUs) that are combined to create facial expressions (or AU combinations). All researchers must pass a species-specific certification test and are then considered reliable coders. After certification, interobserver reliability is rarely performed. However, reliability may be affected by variables like video length, apex identification, AU combination composition, and sociality effects. We analyzed the effects of these variables on reliability and propose that researchers should predetermine action units of interest for apex choice to reduce variation between observers. Two ChimpFACS certified researchers independently coded facial expressions from 30 hours of video of 17 chimpanzees (*Pan troglodytes*)

housed at the Los Angeles Zoo. Coding reliability was then evaluated using Wexler's ratio (the method of calculating FACS inter-observer reliability on the certification test). Preliminary results indicate that AU combination composition and sociality effects could have significant effects on coding reliability. We argue that researchers should predetermine which AUs to code as notable to facial expressions of interest and only code one individual during a time of high sociality to improve reliability in studies involving FACS coding. Employing these additional steps would improve replicability in facial expression studies, thereby strengthening research on the evolution of facial communication in primates.

This research was supported by the National Institute of General Medical Sciences of the National Institute of Health under award number R25GM055052 awarded to T. Hasson.

Unexcused abscesses: the unexpected demographics of dental abscesses at Ancón, Peru

CAITLIN MONESMITH, BRITTANY GREEN and SLOAN R. WILLIAMS

Anthropology, University of Illinois at Chicago

Dental abscesses represent a serious health risk in ancient populations; outcomes include chronic pain, further infections, and occasionally lethality. This project examines dental abscesses within a skeletal population from the site of Ancón, Peru, and spans the period from the Middle Horizon (AD 600-1000) to the Late Intermediate Period (AD 1000-1476). My earlier work on this population found that neither age nor sex were correlated with the site's high caries prevalence (60%), and that more severe oral diseases were common. Abscesses, which usually form over long periods, are generally considered a hallmark of elderly populations and have been correlated with old age and high carious lesion prevalence in other Andean contexts (Turner 2015, Gheggi et al. 2017). Surprisingly, this expectation proved not the case at Ancón. Out of a sample of 76 adults, 27 individuals (36%) had abscesses. Less than 15% were individuals over the age of 50 (N=4). Abscesses were much more common in adults under the age of 50 (41% vs 19% in the 21 adults over 50). Crosstab statistical analysis (SPSS) showed a two-sided p-value of 0.047. This high prevalence and age pattern is not observed at other Andean sites. Ancón demonstrates an unusual abundance of dental abscesses and an inversion of the expected demography. While abundance may be linked to the abrasiveness of a coastal diet, this does not explain the age discrepancy, which requires further research to better understand the effects of dietary change on the health of this population.

Photogrammetry in the field: Visualizing pathological lesions in a case of metastatic carcinoma from Antiochia ad Cragum, Turkey

MEGAN K. MOORE¹, EMILY HAMMERL², BEN KREIMER³ and MICHAEL HOFF⁴

¹Sociology, Anthropology & Criminology, Eastern Michigan University, ²Department of Anthropology, University of Nebraska-Lincoln, ³Independent Emerging Media Technologist for the Antiochia ad Cragum Archaeological Research Project, ⁴School of Art, Art History & Design, University of Nebraska-Lincoln

Photogrammetry is the process of measuring objects and features on photographs to generate uniformly scaled two-dimensional images and three-dimensional models. Here, we present an argument for on-site utilization of this technique to assist in visualization and preservation of pathological lesions in order to document a case of metastatic cancer in a skeleton from a Roman-era site in south coastal Turkey. The skeletal remains consist of a middle-aged adult male between 40 and 55 years at the time of death, based on auricular surface and tooth wear. There is a notable absence of osteoarthritis and osteophytosis of the vertebrae, but Schmorl's nodes are beginning to develop on T8-T12, L1-L3, and L5. Multiple lytic lesions are present across the skeleton that destroy the trabecular bone and present with no new bone growth. The subperiosteal surface of the lesions is much smaller than the underlying cavernous lesion. Documenting the shapes of the "punched out" lesions occurring throughout the skeleton is significantly aided by a photogrammetrically reconstructed three-dimensional model of the skeleton, produced from 1,556 images captured with a Panasonic Lumix G7 camera, 20mm lens, and processed in RealityCapture software. The arranged skeletal remains were photographed atop a white sheet. The differential diagnosis considered caries sicca from syphilis, multiple myeloma, subchondral bone cysts, and multiple endochondromas. Based on the older age of the individual, the absence of any healing, and the diffuse distribution across the trabecular bone, metastatic carcinoma is the most likely diagnosis.

The impact of environmental grit on dental wear at Tell el-Amarna, Egypt: Investigating the windblown sand theory

ERIKA L. MOREY

Anthropology, University of Arkansas

Exogenous environmental dust and grit play an important role in paleoecological studies of dental microwear and are often mentioned as the main or contributing source of dental macrowear in the anthropological literature. In numerous studies of ancient Egyptian teeth "windblown sand" is often cited as both the primary source of environmental grit in the diet and the primary

ABSTRACTS

source of dental macrowear. No previous studies, however, have sought to empirically test the volume of exogenous grit that could enter into the diet, impacting attrition of the occlusal surface of the teeth.

In order to investigate the impact to dental macrowear of "windblown sand" in the ancient Egyptian diet, two environmental dust collection towers were erected at the Amarna Project's dig house near El-Hagg Quandil, Egypt during June 2017. Four collection surfaces per tower were located at 0.5m, 1m, 1.5m, and 2m above ground level. The towers collected dust, grit, and other airborne materials for 21 days with collection intervals ranging from 1 hour to 21 days. Of the particulates collected at all heights and across all intervals, most are macroscopic organic materials such as light, fibrous plant matter. Comparatively few inorganic silicates (sand) were collected, even over the longest intervals.

The results of this study suggest that windblown, exogenous environmental grit does not play a large role in the acceleration of dental wear at Tell el-Amarna, a finding which is in opposition to oft-repeated theories of dental wear and its sources amongst the ancient Egyptians.

Funding for this study was provided by the King Fahd Center for Middle East Studies.

Similarities and differences of femoral diaphyseal ontogeny in modern humans and Neanderthals

NAOKI MORIMOTO¹, MARCIA PONCE DE LEÓN², LUBOV GOLOVANOVA³, VLADIMIR DORONICHEV³, TAKERU AKAZAWA⁴, OSAMU KONDO⁵ and CHRISTOPH ZOLLIKOFER²

¹Laboratory of Physical Anthropology, Kyoto University, ²Anthropological Institute and Museum, University of Zurich, ³Laboratory of Prehistory, St. Petersburg, Laboratory of Prehistory, St. Petersburg, ⁴Research Center, Kochi University of Technology, ⁵Department of Biological Sciences, Graduate School of Science, University of Tokyo

The differences of the skeletal features between modern humans and Neanderthals, our closest extinct relatives, have been well documented. However, it still remains largely unexplored how the Neanderthal-like features of the postcranial skeleton are brought about by development. The relative contribution of the prenatal versus postnatal development, and that of genes and environment to determine the skeletal features thus remain unknown. Here we investigate the development of the femoral diaphysis, a fundamental locomotor element, in Neanderthals and modern humans from neonatal to adult stages using methods of morphometric mapping. The modern human sample includes hunter-gatherer and modern urban populations that have different activity levels. Our data show that the femoral diaphyseal morphology of Neanderthals and modern humans is relatively similar at birth

but becomes distinct from each other toward adulthood. Our data also show that the femoral diaphysis considerably changes its morphology even after the age of maturation, and that Neanderthal femoral morphology exhibits a similar pattern of variation indicating similar aging patterns in both taxa.

Financial support was provided by JSPS with Grants-in-Aid for Young Scientists (A) to NM (no. 15H05609).

Metameric variation of upper molars in extant hominoids

WATARU MORITA^{1,2}, NAOKI MORIMOTO³, REIKO T. KONO⁴ and GEN SUWA⁵

¹Institute of Biotechnology, University of Helsinki, ²Faculty of Dental Medicine, Hokkaido University, ³Graduate School of Science, Kyoto University, ⁴Faculty of Letters, Keio University, ⁵The University Museum, The University of Tokyo

Metameric variation of the molar size is generally associated with dietary adaptations in mammals and thought to be yielded by slight alterations of the developmental processes. Humans and great apes show conspicuous variation of tooth morphology both between taxa and tooth types, but it is largely unknown how the metameric variation of the molar is brought about during evolution and development in these taxa. The present study compares enamel-dentine junction (EDJ) of upper molars with humans and extant hominoids [chimpanzees, bonobos, gorillas, orangutans, and hylobates (N=192 in total)]. EDJ highly correlates with outer-enamel surface morphology and is not subject to dental wear. We use methods of morphometric mapping which permit to quantify and visualize the metameric variation of 3D dental morphology.

Results showed that [1] hominoids share a common pattern of metameric variation, that is, linear change in morphospace which indicates simple gradual degradation of molar shape; [2] phylogenetic signal becomes weaker from mesial to distal molars; [3] humans are distinct from the common pattern. Only humans exhibit non-linear shape change in the morphospace, and show typical between-molar similarity pattern. Degradation of shape and phylogenetic signal from mesial to distal molars is consistent with the concept of key tooth. The common metameric pattern among extant hominoids may reflect phyletic inertia. On the other hand, humans show a specific pattern, which suggests considerable developmental modification was introduced in human lineage.

Financial support was provided by JSPS with Grants-in-Aid for Young Scientists (B) to WM (no. 17K15202).

Junk DNE: How Surface Simplification and Scanning Resolution Affect Measures of Dental Crown Sharpness

PAUL E. MORSE¹, JAMES D. PAMPUSH^{2,3} and RICHARD F. KAY¹

¹Evolutionary Anthropology, Duke University, ²Exercise Science, High Point University, ³Physician Assistant Studies, High Point University

Studies of dental functional morphology have been strengthened in recent years by the innovation of methods analyzing the continuous surface topography of digitized tooth crowns. One such method, Dirichlet normal energy (DNE), expresses the relative sharpness of a surface and effectively discriminates among unworn and worn molars of primate taxa with differing diets. However, scanning resolution and subsequent down-sampling may influence a surface's DNE, potentially inflating it at higher resolution as microscopic features are incorporated into the measurement. Here we test how scan resolution and simplification affect DNE. We scanned an upper molar of *Pan troglodytes* at three cubic voxel resolutions (9, 18, and 36 μm), and processed them under otherwise identical procedures. The 18 and 36 μm /voxel scans were simplified to produce series of surfaces representing 10%, 20% ... 90% of the original face counts and DNE was calculated. In both cases, DNE increased linearly with face count ($r^2 = 0.998$). The surfaces of all three scans were simplified to identical face counts, mirroring studies that combine specimens scanned at various resolutions. At lower face counts, DNE was consistent among the three simplified surfaces, but above 15k faces the DNE of the high resolution (9 μm) surface began to diverge from the medium and low resolution scans. Both initial scanning resolution and surface simplification need to be controlled when calculating DNE. With higher scan resolution and less simplification, particles, surface defects, and voxel dimensions will affect results, though they may have little or no relevance for tooth function.

Bite Force Analysis of the Human Mandible: Assessing Jaw Capabilities of Human Ancestors

HARRISON J. MOSES and BARBARA J. WELKER
Anthropology, SUNY Geneseo

Describing the capabilities and limitations of jaw morphology throughout evolutionary history provides a clear picture of what human ancestors were capable of eating and how they processed their food. The chewing and maximum biting capabilities of 17 individuals were assessed with a bite force pressure gauge. Known skeletal correlates of bite force, including length of the ramus and body of the mandible, the magnitude of the gonial angle, and occlusal surface area of the lower dentition were also measured. These data were compared with corresponding skeletal measurements taken from casts of A.

ABSTRACTS

afarensis, H. neanderthalensis, and H. heidelbergensis to approximate their maximum bite force and chewing capabilities. The correlations found between maximum bite force, the gonial angle, and occlusal surface area were significantly stronger than those found for the chewing force. This study evaluates the usefulness of considering both maximal bite force and chewing force in dietary research methods. Further, implications of the data are considered in terms of food choice throughout evolutionary history.

Population diversity, diet and epigenetics

MJ MOSHER^{1,2} and CHAD GERHOLD²

¹Department of Anthropology, Western Washington University, ²Laboratory of Biological Anthropology, University of Kansas

Population comparisons reveal genetic adaptations driven by primary dietary substrates and identify genes crucial to metabolic processes as evolutionary change agents. Studies examine enzymes vital to metabolism of lactose and starches, modulation of metabolic pathways to high protein intake, and opposing eicosanoid signals from essential fatty acid ratios. The epigenome, interpreted as a series of complex and interacting mechanisms capable of archiving nutritional cues, is hypothesized to mediate intermediate levels of human adaptation to environmental stressors without altering gene sequencing. Dietary effects (age and sex-specific) begin *in utero* and continue through the vulnerable window of neonatal growth and development. Metabolic genes appear vulnerable to nutritional programming over the life cycle.

Arctic populations exhibit higher basal metabolism rates (BMR) in their adaptation to harsh, cold environments. Traditional dietary explanations for these elevated BMRs focused on the influence of high protein intake, however, recent research challenges that hypothesis and suggests a developmental or genetic mechanism. We examined sex-stratified data (M21/F31) of epigenetic markers, BMR, and fat patterning from a Siberian population. Using R package CpGassoc: Fixed-effect ANOVA models were constructed, and False Discovery Rate calculated using Benjamini-Hochberg formula to minimize Type-I error in multiple testing. Findings suggest a sex-specific epigenetic response modified by protein/ carbohydrate, but not protein/fat intake ratios, consistent with the sexual dimorphism of cold adaptation: females increasing insulation by adipose stores and males adopting a metabolic response. These responses are most likely mediated by dietary and leptin effects on the sympathetic nervous system and influenced by sex steroids.

Allostatic load predicts chronic disease in New Mexicans of Spanish-speaking descent

CARMEN MOSLEY, MEGHAN HEALY, KATELYN RUSK, KEITH HUNLEY and HEATHER EDGAR

Anthropology, University of New Mexico

Allostatic load (AL), a cumulative measure of exposure to repeated external and internal stressors, is often used to identify the social, demographic, and biological factors that contribute to racial differences in health risk. However, AL has yet to be widely used to explore causes of poorer health outcomes in U.S. populations of Hispanic, Latino, or Spanish origin (HLS). Here, we examine the association of AL with six chronic health conditions (abdominal obesity, hypertension, diabetes, cardiovascular disease, cancer, and gallbladder disease) in a sample of 439 New Mexicans of Spanish-speaking descent. Summary AL scores were calculated from nine biomarkers across physiological systems relevant to disease risk. AL scores were then grouped into five categories (0+1, 2, 3, 4, and ≥ 5). Using logistic regression models fitted to estimate odds ratios (OR) and 95% confidence intervals, we evaluated the association of each health condition with AL, controlling for age, sex, and current smoking status.

AL scores of 3 (4.17) and ≥ 5 (8.42) were significantly associated ($p < 0.05$) with gallbladder disease compared to participants with 0 or 1 AL scores (reference group). Individuals with AL scores of 2 (2.24), 3 (3.13), 4 (5.19) and ≥ 5 (4.59) were significantly more likely to have abdominal obesity than those in the reference group. AL score was not significantly associated with any other chronic conditions. This is one of few studies to demonstrate a direct relationship between AL and chronic disease.

National Science Foundation (BCS 0962825) and the University of New Mexico Graduate Research Development Grant.

Was *Homo heidelbergensis* in Africa?

AURÉLIEN MOUNIER^{1,2} and MARTA MIRAZÓN LAHR^{2,3}

¹UMR7194 HNHP, Musée de l'Homme, CNRS-MNHN, ²LCHES, Department of Archaeology, University of Cambridge, ³Turkana Basin Institute, Kenya

Homo heidelbergensis was invented in 1908 by Otto Schoetensack, following the discovery and description of the hominin mandible from Mauer. Schoetensack considered the specimen to differ from the hominin remains known at the time – humans, Neanderthals and *Homo erectus* – and hence, named a new taxon. While *Homo heidelbergensis* was forgotten for most of the 20th century, it became, in the past thirty years, the focus of every debate regarding the common origin of Neanderthals and modern humans.

Advances in genomics and in palaeoanthropology have now brought a consensus regarding the African common origin of both lineages in the early Middle Pleistocene, within the period 700,000 to 500,000 years ago, and this ancestor is generally referred to as *Homo heidelbergensis*. To use this species name a direct taxonomical link between its holotype, the Mauer mandible, and the specimens lumped into the taxon must be demonstrated.

Therefore, the first part of this study re-states the taxonomic link between Mauer and some of the Afro-European Middle Pleistocene fossil record, using an innovative methodology (phylogenetic modelling) to compute the possible mandibular morphology of an ancestor to modern humans and Neanderthals. The results of these analyses strongly suggest that the ancestor, *Homo heidelbergensis*, was an African taxon. Using evolutionary scenarios drawn from the available genomic evidence, we explore the question of how to draw the boundaries between palaeo-species along evolving lineages by focusing on the Middle and Upper Pleistocene fossils of *Homo sapiens* and *Homo neanderthalensis*, or to their last common ancestor, *Homo heidelbergensis*.

Differential adaptation of cortical and trabecular bone to mechanical loading and its dependence on age

BRAM MULDER¹, JAY T. STOCK^{1,2}, SARAH A. INSKIP¹, CRAIG C. CESSFORD¹ and JOHN E. ROBB¹

¹Department of Archaeology, University of Cambridge, United Kingdom, ²Department of Anthropology, University of Western Ontario, Canada

In adults, bone adapts its structure to mechanical loading mainly through remodeling. Its large surface-to-volume ratio makes trabecular morphology adapt more rapidly than compact bone. We hypothesize that variation in cortical bone cross-sectional geometry will show stronger correlation with loading history during development and early adulthood, while trabecular bone corresponds with loading later in life. Cortical geometry is thus expected to stay relatively constant with age, and its correlation with trabecular architecture is expected to be stronger in young adults.

Femora and tibiae from 100 individuals from medieval Cambridge, UK, were microCT-scanned. For trabecular volumes in the four epiphyses, bone volume fraction (BV/TV) and anisotropy were quantified. Torsional rigidity (J) and relative cortical area (%CA) were computed at 1% increments along the diaphysis.

Relative CA and BV/TV were positively correlated and exhibited an age-related decrease, which was significant in female %CA. Torsional rigidity did not correlate with trabecular parameters in either sex and was the same between age groups.

ABSTRACTS

That J does not change with age is consistent with our hypothesis. However, in young adults we did not find the expected correlation between J and trabecular parameters. Trabecular values did correlate with %CA, but this correlation did not change with age. These results imply that both tissues continue to change throughout life, and that their morphological adaptations do not distinguish between activity in adulthood and childhood as clearly as hypothesized. These findings contribute to a better understanding of bone functional adaptation and the effects of age on bone structural integrity.

The After the Plague project is funded by the Wellcome Trust

Creating opportunities for K-12 outreach with undergraduate mentors

DAWN M. MULHERN, NADIA C. NEFF, HEATHER BROOKSHIER and MICHAELA WILSON

Anthropology, Fort Lewis College

Fort Lewis College is a public liberal arts college in Durango, Colorado with a student body of about 3300. Since most programs do not offer graduate degrees, undergraduate students who excel in the classroom and are interested in teaching have the opportunity to gain experience as undergraduate mentors, providing tutoring or assistance both in and outside the classroom or lab. Faculty in biological anthropology have developed teaching materials and initiated engagement in K-12 outreach with these undergraduate mentors. In this presentation, we discuss three examples of such outreach involving biological anthropology including topics ranging from primates to human evolution and forensic anthropology: 1.) hands-on lab sessions for local middle school students aligned with state science standards, 2.) modules for a week-long summer science camp held at Fort Lewis College geared toward elementary school students and 3.) an activity for elementary school students enrolled in "Forensic Detectives" Discovery Camp at the Powerhouse Science Center in Durango, Colorado. Benefits of these activities include strengthening connections between the college and the community, providing a varied teaching experience for undergraduate mentors where they can learn how to present content to different educational levels, and generating public awareness and interest in anthropology.

Countering the Invisibility of Disability in Bioarchaeology

JENNIFER L. MULLER

Anthropology, Ithaca College

Since its inception, bioarchaeology has included analysis of impairments as represented by traces of morbidities, physical injuries, and intentional modifications in human skeletal remains. However, a paucity of publications in

the bioarchaeological literature examine the lived experiences of disabled people in the past. The invisibility of disability in the bioarchaeological record may stem from exclusion of individual skeletons with particular impairments, seen as outliers to population-based approaches. Yet, more often, invisibility is created via omissions in historical narrations that fail to explore the agency and heterogeneous experiences of disabled people in the past. Recent theoretical developments and multiscale approaches have countered such erasures. Bioarchaeology embraces an interdisciplinary approach that acknowledges the impacts of physical impairment, but also interrogates the social, historical, and relational body represented by skeletal remains. Bioarchaeological narrations of the disabled emerge from the integration of biological, ethnographic, archaeological, and historical data from a variety of sources. Disability is discussed here as a social construction; one that is associated with societal ideologies regarding the medical, economic, political, legal, and moral. Explorations of disability are discussed via examples from the historical past, including institutionalized children from the Erie County Poorhouse in Buffalo, New York. The stories that emerge from this bioarchaeological analysis include disability as a biopolitical strategy designed to determine worthiness of citizenry, but also demonstrate the multiple movements and identities of disabled children. This intervention aims to move away from hegemonic interpretations of impaired bodies and lived experiences of disability.

Aggression, coalition formation, and aging in wild chimpanzees

MARTIN N. MULLER¹, MELISSA EMERY THOMPSON¹, DREW K. ENIG¹, LINDSEY HAGBERG², ZARIN P. MACHANDA³, KRISTIN SABBI¹ and RICHARD W. WRANGHAM²

¹Anthropology, University of New Mexico,

²Human Evolutionary Biology, Harvard University,

³Anthropology, Tufts University

Male chimpanzees engage in costly forms of status competition that include elaborate threat displays and fierce contact aggression. Consequently, high-ranking males often exhibit decreased energy status and elevated stress levels compared to low-ranking males, and adult male mortality exceeds adult female mortality. Senescence should render older males less able to meet the physical demands of reproductive competition. We used long-term data on wild chimpanzees to investigate how males adjust their competitive behaviors to accommodate the aging process. We specifically tested the hypothesis that past-prime males rely more on coalitions to maintain access to reproductive opportunities. Our dataset included >40,000 incidents of male aggression observed between

2005 and 2016 in the Kanyawara community of Kibale National Park, Uganda. Average male rank peaked at age 25, after which it showed a decline with age. Rates of male aggression similarly peaked at 25-26. Subsequently overall aggression declined, but the rate of energetically costly threat displays showed a sharper decline than did contact aggression. As a result, when older males were aggressive, this was more likely to take the form of actual violence. A larger proportion of aggression among past-prime males also involved coalitions, primarily in which these males reinforced the existing dominance hierarchy by supporting the alpha male. Older males who supported the alpha in this way enjoyed relatively high rates of both mating success and conception for their age. Supporting the alpha male appears to represent a low-cost tactic for older males to maintain some reproductive access, despite declining competitive ability.

This research was supported by National Science Foundation grants BCS-0849380, BCS 1355014 and IOS-LTREB1052693, NIH grant AI058715, Harvard University, University of New Mexico, and the Leakey Foundation.

Epigenetics, gene expression, and stress in mothers and offspring in the Democratic Republic of Congo: A biocultural investigation of the intergenerational effects of stress

CONNIE J. MULLIGAN^{1,2}, FELICIEN M. MAISHA^{1,2}, CHRISTOPHER J. CLUKAY^{1,2}, CHU HSIAO^{1,2}, PETER REJ³, NICOLE ESCOFFIER², EDWARD QUINN^{1,2}, LISA NEVELL^{1,2} and DARLENE A. KERTES⁴

¹Anthropology, University of Florida, ²Genetics Institute, University of Florida, ³Anthropology, University of Washington, ⁴Psychology, University of Florida

The field of social and behavioral epigenetics examines how social and behavioral experiences can cause epigenetically-driven changes in gene expression that in turn influence health and well-being. We work in the eastern Democratic Republic of Congo, where 20 years of conflict and post-conflict violence have subjected women to extreme stress and sexual violence.

We collected blood samples from mothers and their offspring at birth, plus follow-up samples from offspring up to five years of age, in three cohorts (2010 cohort, n=25; 2013 cohort, n=103; 2015 cohort, n=77). Using DNA extracted from blood and placental samples, we assayed methylation using Illumina's 450K and EPIC chips, telomere length, and gene expression using the ClariomS chip. We also collected ethnographic and survey data on maternal stress, newborn health outcomes, and cortisol from offspring saliva and hair samples. Using these data, we tested for associations among maternal stress, DNA methylation, gene expression, and offspring health outcomes.

ABSTRACTS

We find that epigenetic aging is accelerated in mothers relative to chronological age, but newborn epigenetic age appears unchanged. In contrast, telomere length is significantly shorter in offspring born to mothers with high levels of war stress, but this effect only emerges after birth. Analyses of epigenome and gene expression data are ongoing. Our study takes a biocultural perspective to understand the molecular, biological, and health effects of stress and violence, particularly from an intergenerational perspective.

Research was supported by NSF BCS-1231264, BCS-1540372 and BCS-1719866, University of Florida (UF) College of Liberal Arts and Sciences, UF Clinical and Translational Science Institute, and UF Research Opportunity Seed Fund.

Comparison of two Alaskan cultural groups during the 1918-19 influenza pandemic using social network modeling

MEGAN MURRAY and LISA SATTENSPIEL
Anthropology, University of Missouri

The spread of infectious disease among human populations is heavily influenced by interactions between humans and how they live and move across the landscape. We address the role of spatial proximity, the strength of kinship ties, and residence patterns in determining differential rates of mortality among the Inupiaq and Yup'ik Inuit in Western Alaska during the 1918-19 influenza pandemic. Despite similar environmental conditions, subsistence, and levels of Western contact, the severity of the pandemic varied markedly between these groups. Kinship studies and ethnographic research among the Inupiaq of the Seward Peninsula show that village life was highly interactive, with strong kinship relationships between most village members, and co-habitation of multiple groups to create a familial unit. Similar studies among the Yup'ik depict a less integrated village population, with sex-based labor and residence patterns. This information is used to construct a social network model that allows examination of factors such as who is interacting with whom and in what context, as well as the frequency and strength of such interactions on epidemic severity. We hypothesize that the more intimate nature of social life as well as the stronger kin-based network connections within the Inupiaq may help to explain their increased influenza mortality rates when compared to the Yup'ik. Results from this analysis have implications for the predicted impact of infectious disease spread among global populations where residence patterns and village social structure are highly interconnected and may help to suggest more effective solutions for reducing mortality among such groups.

The ontogeny of termite gathering among chimpanzees in the Goulougo Triangle, Republic of Congo

STEPHANIE MUSGRAVE¹, ELIZABETH LONSDORF², DAVID MORGAN^{3,4} and CRICKETTE SANZ^{1,4}

¹Department of Anthropology, Washington University in Saint Louis, ²Department of Psychology, Franklin and Marshall College, ³Lester E. Fisher Center for the Study and Conservation of Apes, Lincoln Park Zoo, ⁴Congo Program, Wildlife Conservation Society

The acquisition of tool-assisted foraging skills has the potential to improve diet and increase fitness. Chimpanzees of the Congo Basin (*Pan troglodytes troglodytes*) possess a unique, complex tool repertoire including the use of tool sets and brush-tipped fishing probes to gather termites from above-ground and subterranean nests. We investigated the ontogeny of termite gathering in chimpanzees of the Goulougo Triangle, Republic of Congo and compared it to the development of termite fishing among chimpanzees at Gombe, Tanzania. We hypothesized that tool use would be acquired before tool manufacture, and that the use of tool sets would occur later than use of single tools. Using a longitudinal approach, we screened 15 years of remote video footage and coded developmental milestones of termite gathering for 26 immature chimpanzees. All offspring at Goulougo insert probes by 2.7 years, but they do not manufacture brush-tipped fishing probes until an average age of 4.1 years. This differs from Gombe, where chimpanzees make fishing probes before or during the year when they first insert them, between ages 1.5-3.5. Chimpanzees at Goulougo begin using perforating tool sets between ages four and ten, and only subadults over age 11 can independently puncture subterranean nests. Differences between sites could reflect the design complexity and material selectivity of tools, sequential tool use, and strength demands of termite gathering at Goulougo. These results improve models of the pedagogical settings characterizing tool behavior of early hominins, who likely used complex, perishable technologies.

The Wenner-Gren Foundation, The National Science Foundation, The Leakey Foundation, Lambda Alpha

Evaluating the evidence of treponemal disease from India

VEENA MUSHRIF-TRIPATHY
Department of Archaeology, Deccan College Post Graduate and Research Institute

The spread of treponemal disease throughout the world is the most debated topic in palaeopathology. Skeletal evidence from India has contributed little to this debate to date. Only one documented but questionable case from Megalithic Agripalli has been published. Here, I report three other cases from three different regions and temporal frames based on the

macroscopic examination of skeletal remains. Standardized, empirical, and established diagnostic criteria were used. Possible treponemal infection was identified on one male skeleton from Rakhigarhi, Hissar District, Haryana dated to c. 995 A.D. (AMS, Beta Analytic, Florida), one male individual from Kaothe from Maharashtra, dated around 1600 A.D. (AMS, Klaus-Tschira laboratory, Germany), and one female from Jotsoma, Nagaland, radiocarbon-dated to c. 17th-century A.D.

The Rakhigarhi individual exhibits discrete focal superficial cranial lesions, circumvallate cavitation, stellate scarring, and the contiguous series of lesions identified as caries sicca. Stellate scarring is also seen on both zygomatic bones and nasal bridge. Bone remodeling and superficial cavitation is seen on the preserved femur. The Kaothe individual has stellate scars and nodes/expansion with striation on the ulna and hand phalanx. The female from Nagaland shows caries sicca on the frontal and other cranial fragments and changes consistent with treponemal infection on postcranial bones.

One of these cases predates the Columbian voyages and challenges the dominant theory of its spread from the New to Old World just before A.D. 1500. Bone samples from Rakhigarhi and Kaothe individuals have been sent to the Max Planck Institute, Jena, for possible *Treponema pallidum* extraction.

Estimation of archaic hominin haplotype frequencies in contemporary Aleuts

JOSIE M. MUSKRAT^{1,2}, TARA N. MARRIAGE², KRISTINE BEATY¹, LYDIA SYKORA¹, SARAH ALDEN¹, CHRISTOPHER BARRETT¹, MICHAEL CRAWFORD¹, DENNIS O'ROURKE¹ and JENNIFER RAFF¹

¹Anthropology, University of Kansas, ²Natural Sciences, Haskell Indian Nations University

Recent analyses in genomics have shown archaic hominins to have admixed with our species in regions where the populations overlapped. These studies have also shown that certain haplotypes characteristic of these extinct hominins have introgressed into modern human populations over time. Certain contemporary human populations exhibit greater levels of introgressed archaic hominin alleles than others, and interestingly, Native Americans are among those who show greater levels of introgression. The objective of this study is to re-evaluate the findings of these studies in contemporary Aleuts, a group not previously assessed for these archaic hominin haplotypes, and specifically look for haplotypes shown to be associated with lipid metabolism, *SLC16A11*, and cold adaptation, *TBX15/WARS2*. We used a combination of SNP data arrays and targeted PCR approaches to calculate the frequencies of SNPs associated with these respective haplotypes. We found the introgressed variant of *SLC16A11* to be present at

ABSTRACTS

a significantly higher frequency in contemporary Aleuts than in other Native American populations, and *TBX15* to be present at lower frequency than in other Native American populations. We discuss the implications of our results in the context of Aleut pre- and post-European contact population history and what they might mean for adaptation to Arctic environments.

Funding for this research is provided by the National Institute of General Medical Sciences (NIH NIGMS), grant number R25GM060182.

Exploring adaptive functions of geophagy across non-human primates: Considering the role of sexual selection

BRE N. MYERS and CAITLYN D. PLACEK

Anthropology, Ball State University

Evolutionary theory predicts that non-immunological defenses against pathogens and toxins evolved as counter-measures to protect non-human primates (NHP) during sensitive periods of development. The current study focuses on one type of non-immunological defense, geophagy, the consumption of soil. According to life history theory, pregnant females and juvenile NHP might be at heightened risk for the effects of specific infections and toxins due to immunological constraints. This study therefore predicted that geophagy would be observed more in pregnant and juvenile NHP. Data were collected by scanning databases: Agricola, Google Scholar, Web of Science, PubMed, and JSTOR. The search was initiated by searching for the keyword "geophagy" and scanning for entries related directly to that defense. Both authors created a codebook and B.M. coded for age, sex, and reported function of geophagy. Findings suggest that the primary purpose for geophagy is detoxification and digestion. The secondary purpose being nutrition, and the third reported purpose being sexual selection. Contrary to the hypothesis and current findings in humans, adult males were reported to have slightly more observations of geophagy. However, the sex difference may be biased given the difficult nature of determining sex and age through scan sampling. Researchers suggest that if adult males are consuming more soil, sexual selection might play a role, such that male-male competition may lead injured adult males to engage in geophagy as a method to boost iron levels or ward off parasitic infections from wounds. Future research should consider this understudied role of geophagy and other non-immunological defenses.

The blood must flow: vertebral artery size relative to transverse foramen size in the tarsier cervical spine

THIERRA K. NALLEY¹, PAMELA AMIN¹, NEYSA GRIDER-POTTER², FAYE MCGECHIE³ and JASON M. ORGAN⁴

¹Department of Medical Anatomical Sciences, Western University of Health Sciences, ²School of Human Evolution and Social Change, Institute of Human Origins, Arizona State University, ³Department of Pathology and Anatomical Sciences, University of Missouri, ⁴Department of Anatomy and Cell Biology, Indiana University School of Medicine

Tarsiers regularly rotate their heads 180 degrees from the forward-facing position. Previous work indicates that there is a functional relationship between extreme head rotation and the morphology of the cervical vertebrae, but the effects of extreme rotation on related soft-tissue structures have not been investigated. The vertebral arteries travel through the transverse foramina of the cervical vertebrae and are therefore in danger of occlusion or impingement during head rotation. In this study, we evaluate whether tarsiers have adaptations for preventing such injuries. Specifically, we predicted that there will be a large disparity in the size of the vertebral artery relative to the size of the cervical transverse foramina to accommodate artery movement and to reduce the probability of impingement. We measured relative vertebral-artery size as a ratio of artery area to transverse-foramen area for C3–C6 from a contrast-enhanced microCT scan of a single wild-caught Philippine tarsier (*Carlito syrichta*). We compared these values to those reported for humans in the biomedical literature. Humans have a mean ratio of 0.43 and a wide range of variation: 0.18–1.00. The mean value for C3–C6 in the tarsier is 0.22, with a range of 0.13–0.29. Thus, the tarsier falls at the extreme end of the human range of variation. Although preliminary, our results are consistent with functional expectations and suggest that tarsiers have features that facilitate rotational movements while reducing the risk of injury to the vertebral artery, an important component of the brain's vascular supply.

Preliminary insights into human femoral bone remodelling at Late Bronze Age multiple burials from Iran

REZA NASERI¹, JUSTYNA J. MISZKIEWICZ², TAHLIA J. STEWART² and ARKADIUSZ SOŁTYSIAK³

¹Department of Archaeology, University of Zabol, ²School of Archaeology and Anthropology, Australian National University, ³Department of Bioarchaeology, University of Warsaw

Femur anatomical characteristics are routinely used in bioarchaeology to make inferences about ancient human behaviour. However, in cases of multiple burials, interpretations based on bone

macroscopic data can be challenging due to the commingled and often fragmentary nature of bones representing different individuals. Here, we use histological methods to investigate the extent to which adult femora recovered from multiple burial contexts show corresponding macro- and microstructural biomechanical signatures. Midshaft segment circumference (M.Cm), anterior-posterior diameter (AP.Dm), and anterior (A.Ct.Th) and posterior (P.Ct.Th) cortical thickness were measured in seven adult femora representing individuals from a Late Bronze Age site in Deh Dumen, Iran. Osteon population density (OPD) and Haversian canal density (HCD) were estimated from anterior and posterior cortical strips measuring ~4.82 mm². No statistically significant relationships between the micro- and macroscopic measures of bone functional adaptation were observed ($p > 0.05$, 20/24 Spearman's Rho tests), except when anterior OPD was correlated with AP.Dm and A.Ct.Th ($p = 0.005$, Rho = 0.975), and when anterior (Rho = 0.829, $p = 0.042$) and individual HCD (Rho = 0.886, $p = 0.019$) were tested against P.Ct.Th. Our results indicate inconsistent links between femur size and its underlying bone remodelling signature, though we cannot rule out the effect of age, sex, and other factors underlying the complexity of adult bone metabolic processes. We suggest that, where possible, a complementary analysis of femur micro- and macrostructure may aid in separating multiple leg bones into behavioural categories.

Quantifying growth faltering across the first year of life in rural Gambian infants

DANIEL J. NAUMENKO^{1,2}, JAMES DYKES², G. KESLER O'CONNOR³, ZOFIA STANLEY³, NABEEL AFFARA⁴, DAVID B. DUNGER⁵, KEN K. ONG^{5,6}, ANDREW M. PRENTICE⁷, SOPHIE E. MOORE^{7,8} and ROBIN M. BERNSTEIN^{1,2}

¹Department of Anthropology, University of Colorado Boulder, ²Institute of Behavioral Science, University of Colorado Boulder, ³Department of Applied Mathematics, University of Colorado Boulder, ⁴Department of Pathology, University of Cambridge, ⁵Department of Paediatrics, University of Cambridge School of Clinical Medicine, ⁶MRC Epidemiology Unit, University of Cambridge School of Clinical Medicine, ⁷MRC Unit The Gambia, London School of Hygiene and Tropical Medicine, ⁸Department of Women and Children's Health, King's College, London

Stunting in childhood is thought to be linked in part to repeated and severe episodes of shorter-term growth faltering (e.g., weight loss, or stasis in linear growth) with varied etiology. Most frequently, faltering is described or identified by centile crossing and changes in Z scores across consecutive time points. Here, we present a novel approach for quantifying growth faltering through the identification of specific parameters of individual faltering episodes that can

ABSTRACTS

then be modeled with additional variables. The HERO-G (Hormonal and Epigenetic Regulators Of Growth) study tracked alternate-day growth of rural Gambian infants across the first year of life; here we analyze weight, crown-heel length, and head circumference from a subset of individuals (N=69 (F=36, M=33)). We calculated the first derivative of a 25-knot cubic spline fit to growth data, and identified the initiation, duration, and depth (difference in growth rate from initiation to trough) of faltering events using the 'find_peaks' function in R. Infants had an average of 2-4 faltering episodes in their first year of life, and spent 21-26% of their first year of life in faltering. We built models to assess the contribution of sex, season of birth and conception, and maternal parity to the number of faltering events, the average falter depth, and the proportion of time spent in faltering per individual. None of these variables showed a significant effect on faltering metrics, suggesting complex relationships underlying variation in the causes and consequences of faltering in these infants.

Funded by the Bill and Melinda Gates Foundation (OPP1066932)

Developing a Rapid Technique for Identifying Human Bone in Bioarchaeological and Forensic Contexts: ZooMS and the Battle of Towton

NADIA NEFF^{1,2}, MATTHEW COLLINS² and TIM SUTHERLAND²

¹Department of Anthropology, Fort Lewis College, ²Department of Archaeology, University of York

This study focused on testing and applying the biomolecular protein analysis method Zooarchaeology by Mass Spectrometry (ZooMS) to distinguish human vs nonhuman bone fragments in bioarchaeological and forensic contexts. The research goal was to develop a rapid methodology combining ZooMS and conventional field methods with other sources of information such as geophysical survey and desk-based assessment in order to create human bone fragment scatters that can be used to identify concentrations of human bone to aid in the detection and location of potential unknown human graves and sites of conflict. The site of the Battle of Towton (1461) (the bloodiest battle in English history) was chosen as a case study for the development of this method due to its status of having several undiscovered mass graves discussed in historical documents. This study was accomplished through the testing of lab based collagen extraction methods in application to ZooMS, the systematic collection, documentation and lab based analysis of 80 bone and tooth fragments in order to determine those of human origin. Of the 80 fragments we were able to give 72 a determination of human/nonhuman. A total of 19 were determined to be human. During collection each fragment was assigned a GPS

coordinate. By combining the GPS coordinates with the ZooMS results, human bone fragment distribution scatters were created and superimposed onto GPR data highlighting at least one previously unknown putative mass grave. The applications of this methodology to the fields of forensic anthropology and bioarchaeology are significant and widespread.

Woody cover in modern African ecosystems: Implications for hominin landscape dynamics

ENQUYE W. NEGASH¹, JONATHAN WYNN² and RENÉ BOBE³

¹CASHP, The George Washington University, ²Division of Earth Sciences, National Science Foundation, ³Department of Anthropology, University of Chile

Understanding vegetation structure in modern ecosystems is crucial in inferring ecological conditions that prevailed in the past. This in turn will help us better understand the changing ecological conditions in the Pliocene and the Pleistocene that might have contributed to the course of human evolution. Although global and regional scale environmental and ecological studies have been conducted previously, local scale studies with a high spatial resolution that look at habitat level differences are currently underrepresented. As soils may often be preserved in the fossil record, a detailed study of modern soils is important to establish a good reference for interpreting paleosols, their associated vegetation cover and structure. We present stable carbon isotopic composition of soil organic matter collected from 8 national parks in eastern and southern Africa. Surface soil samples were collected from various habitat types including, rainforests, riparian forest, woodlands, bushlands, shrublands, wooded grasslands and grasslands. Samples were analyzed by EA-IRMS and the associated fraction of woody cover was calculated from aerial imagery. Results of the $\delta^{13}\text{C}$ values show that there are significant differences (One way Anova, $P < 0.05$) in the isotopic composition of soil organic matter from the different habitat types across several parks. Also, an approximately linear relationship is observed between the $\delta^{13}\text{C}$ of soil organic matter and the associated fraction of woody cover. This high spatial resolution dataset can provide a local framework that can be used in making more refined interpretations of woody cover and hominin ecospace when using paleosols from hominin bearing sites.

Home range and territoriality suggest that venom as a weapon in slow lorises

ANNA I. NEKARIS¹, MARCO CAMPARA¹, STEPHANIE POINDEXTER¹, THAIS QUEIROZ¹,

ARIANA WELDON¹, VINCENT NIJMAN¹ and MUHAMMAD A. IMRON²

¹Nocturnal Primate Research Group, Oxford Brookes University, ²Faculty of Forestry, University of Gadjah Mada

Few mammals are venomous, including slow lorises (*Nycticebus*). We examined the role of venom as a territorial weapon in wild *N. javanicus* from West Java, Indonesia. We hand-caught 82 wild animals 290 times (range:1-12) and scored them for wounds, venom production and aggression. We applied GAMLSS models to understand the influence of sex, body weight, presence of wounds, venom secretion and number of recaptures on the level of aggressiveness. Using radio collars, we conducted follows from 1700h to 0600h of 19 adults (9 males, 10 females) from 2012-2017, taking GPS locations every 15 minutes. We calculated a utilization distribution (UD) for each individual and year using the kernel method with fixed smoothing factor. We defined home range as the area of the 90% contour of the kernels and core area as the 50% contour. To examine whether animals used the same space, we measured the proportion of home range and core area overlap (HR) and the utilization distribution overlap (UDO). We found that younger males were the most aggressive, but that aggressive animals had fewer wounds ($\Delta\text{AIC} 2.87$). We found overlap between home ranges of males and females from the same pair: $\text{HR}_{90} = 70\%$; $\text{HR}_{50} = 59.5\%$; $\text{UDO}_{90} = 0.73$ and $\text{UDO}_{50} = 0.16$. Although males had a slight UDO with other males $\text{UDO}_{50} = 0.008$ (range = 0-0.18), females did not exhibit any. Range fidelity was high for settled pairs. Our results are consistent with the hypothesis that venom is a weapon used by lorises to gain territories during dispersal and to maintain them during adulthood.

The Leverhulme Trust, Cleveland Zoo and Zoo Society, People's Trust for Endangered Species, Columbus Zoo, Disney Conservation Fund, Primate Action Fund, Margot Marsh Biodiversity Fund, Augsburg Zoo, Henry Doorly Zoo

Do teeth forming in different early life periods show differential discrepancy with known age?

JENNIFER S. NELSON¹, LESLEY HARRINGTON¹, EMILY HOLLAND² and HUGO F.V. CARDOSO³

¹Department of Anthropology, University of Alberta, ²Department of Anthropology, Brandon University, ³Department of Archaeology, Simon Fraser University

Although it has been established that teeth are more resilient to environmental influences than skeletal elements, their development can be adversely affected by an individual's socio-economic conditions. This study explores differential growth discrepancies in children from the Certosa collection, a 19th century skeletal assemblage representing impoverished Italian

ABSTRACTS

children. Length measurements of developing teeth (deciduous and permanent) were taken from juveniles of known age and sex (n=61). Discrepancies between age estimates based on developing tooth length and true chronological age were calculated, comparing the age prediction accuracy of earlier forming teeth with that of later forming teeth.

Results indicate that deciduous teeth produce more precise dental age estimates (absolute mean difference = 0.19), while discrepancies between chronological age and age based on developing permanent dentition are larger (absolute mean difference = 0.43). The difference between these discrepancies in age estimate is significant ($p=0.013$) and indicates that age based on permanent dentition is a worse predictor of chronological age than age based on deciduous dentition. This reflects increased variation of growth indicators with age and may indicate that the early life experiences of children shelter them from stress factors that can impact dental formation. Conversely, the increased discrepancy between dental age and chronological age observed in later developing dentition may be a result of the disadvantageous conditions experienced by older children. By exploring the cause behind these observed growth discrepancies, the potential to interpret sociocultural circumstances from teeth is greatly increased, as is the accuracy of age estimations based on tooth length.

Funding for this project was provided by SSHRC - Social Sciences and Humanities Research Council of Canada

The Science of Biomarkers and the Nuance and Noise in Biocultural Data

ROBIN G. NELSON

Anthropology, Santa Clara University

The collection methods for and analytical science behind minimally invasive biomarkers are evolving rapidly. However, it is not always clear how to effectively merge these techniques with ethnographic inquiry. Using findings from original data gathered in Jamaica and insights from new research in Canada, I will identify the methodological parameters of using minimally-invasive biomarkers, specifically salivary analytes, to investigate biocultural questions of individual decision making in light of persistent economic insecurity. Research amongst children living in different residential care settings in Jamaica reveals greater variability in immunocompetence experienced by children with seemingly more reliable received economic investment. This group also has increased variability in body composition. Ethnographic data describing the kind of care received by these children makes sense of these findings. The instruments we use to assess economic insecurity, and our ability to properly understand familial dynamics in light of financial uncertainty, should influence what biomarkers

take prominence in our studies. By also highlighting methodological choices from new research in Canada, this poster presents a framework in which ethnographic inquiry precedes the selection of appropriate biomarkers.

This research was funded by The Wenner Gren Foundation (Gr.8349) and Santa Clara University

Particle Based Modeling (PBM) Geometric Morphometric Analysis of the basioccipital bone in *Pax7*-deficient mice

LISA NEVELL^{1,2,3,4}, JOSHUA CATES⁵, SURESH PRAJAPATI⁴, LAURA D. NELON⁴, JERRY CHANG⁴, MATTHEW E. RANDOLPH^{6,7}, BERNARD WOOD³, CHARLES KELLER^{4,6,7} and ROSS T. WHITAKER⁵

¹Anthropology, University of Florida, ²Anthropology, Boston University, ³Center for the Advanced Study of Human Paleobiology, The George Washington University, ⁴Greenlee Children's Cancer Research Institute, University of Texas Health Science Center, ⁵Scientific Computing and Imaging Institute, University of Utah, ⁶Department of Pediatrics, Children's Cancer Therapy Development Institute, ⁷Department of Pediatrics, Albert Einstein College of Medicine

This paper tests the role of *Pax7* in the development of the basioccipital bone. The basioccipital bone contributes to the midline cranial base and forms the anterior portion of the foramen magnum. Basioccipital shapes are compared using a computational shape modeling technique called particle-based modeling (PBM). Particle-based modeling (PBM) has potential advantages for measuring subtle shape variation over existing shape analysis methods, which include manual landmarking, sliding landmarks, and image warping comparisons. PBM also allows hypothesis testing between groups of forms, and indicates which aspects of shape change best differentiate groups of forms. The *Pax7* cell lineage contributes to the basioccipital bone and the *Pax7* lineage location correlates with the morphology most effected by *Pax7* deficiency. The basioccipital bone is broader and shows an antero-inferior inflection of its posterior edge in the *Pax7*-deficient mice. This result supports that argument that the cranial neural crest contributes some cells to the posterior cranial base. The *Pax7*-deficient mouse may be a suitable model for investigating the developmental genetics influencing basioccipital breadth, and the location and orientation of the foramen magnum.

This work was supported by an award to the Center for Integrative Biomedical Computing (NIH/NCRR 5P41RR012553) an NSF IGERT grant (0801634), and a George Washington University Selective Excellence Program award.

A Forensic Anthropological Perspective on Latin American Genetic Diversity

BRIANA T. NEW¹, KATE SPRADLEY² and LARS FEHREN-SCHMITZ³

¹Defense POW/MIA Accounting Agency, SNA International, ²Anthropology, Texas State University, ³Anthropology, University of California, Santa Cruz

Exploring Latin American genetic diversity from an anthropological perspective provides an opportunity to better understand the origin of Texas-Mexico border migrants and improve the identification of unidentified skeletal remains. These migrants originate from a variety of Central American regions, particularly El Salvador, Guatemala, Honduras, and Mexico. Whether these region of origin trends are reflected in genetic data has yet to be explored. The present study compares genetic data from 33 Texas-Mexico border migrants collected by Operation Identification (*OpID*), a Texas-based migrant remains identification effort, with previously published genetic data from 27 Latin American groups. Allele frequencies for 15 short tandem repeat (STR) loci were used to calculate genetic distances. A multidimensional scaling (MDS) plot was generated and tests of significance were run to assess the strength of these population relationships. Results indicate the *OpID* sample has the strongest correlation (>90%) with mestizo groups from South Central Mexico, El Salvador, Guatemala, Nicaragua, and an Amerindian group from Northeast Mexico. Additionally, there are statistically significant differences ($p<0.01$) between mestizo and Amerindian groups. Utilizing genetic data from Latin American populations, the results of this study provide validation for identification methods of skeletal remains and highlight the utility of population differentiation methods from STR data towards identification of Texas-Mexico border migrants.

The authors would like to thank the Grady Early Foundation for their contribution to this research.

Effectively teaching primary literature comprehension in bioanthropology

SAVANNAH NEWELL

Anthropology, Indiana University

Today many classrooms are turning away from traditional textbooks in favor of assigning scientific literature. For most undergraduate students this is their first time reading primary literature. This project assesses the effectiveness of using guiding questions to provide students with a framework for understanding and contextualizing primary scientific literature. This project looks at students (n=18) in a bioanthropology lab methods course during spring 2018 semester. Students were given guiding questions to help them understand related articles. Students were assigned articles covering a variety of bioanthropology topics throughout the semester and were

ABSTRACTS

provided feedback after each submission. This project assesses the students' ability to identify and describe the following portions of the article: research question, methods, results, and conclusions. Data were analyzed using a rubric that placed students' ability in each of the areas as "Explains," "Mentions," "Misconceptions," and "Does Not Mention." Of the 18 students enrolled in the course, 14 completed both the pre- and post-test. Of these 14, 12 showed improvement in describing 1 or more categories and 5 of these scored better in 2 categories. No student demonstrated consistent improvement in every category. Possible issues with the current intervention include the comparability of the chosen readings, the timing of the pre- and post-test during the semester, and student motivation based on allotted points.

Survivorship from historical death records and skeletal remains from the Oakwood Cemetery in Austin, Texas (1866-1914)

MICHELLE H. NGUYEN¹, CHRISTOPHER A. WOLFE², MICHELLE D. HAMILTON³ and NICHOLAS P. HERRMANN³

¹Anthropology, Trinity University, ²Anthropology, University of Nevada, Reno, ³Anthropology, Texas State University

Human survivorship as determined from historic records and from the analysis of human skeletal remains often produce conflicting profiles of longevity and community mortality risk. This project examines survivorship as determined from historic cemetery records and a sample of human burials exhumed from the Oakwood Cemetery in Austin, Texas. Individual burials were exhumed as part of ongoing renovations of the historic chapel at the cemetery. Cemetery records identify this section as the "Colored Section" and/or "Stranger Ground" with the inference that these individuals represent people of lower socioeconomic status. Skeletal analysis and historical death records indicate that these individuals come from diverse ancestral backgrounds. Using biological profile data collected from thirteen of thirty-six exhumed individuals and preexisting death records, this project compares mortality parameters of the late 19th and early 20th century Austin community. Using a combination of the documented city-wide historical records and the burials, the results suggest that the skeletal sample highlights the broad demographic trends in historic American populations, such as high infant and childhood mortality. These results also shed light on the demographic profile of early groups from Austin, Texas.

This project was supported by the McNair Scholars Program.

Genomic ontologies provide evidence against environmental adaptation during the Beringian standstill

SARA D. NIEDBALSKI and JEFFREY C. LONG
Anthropology, University of New Mexico

A goal of genetic anthropology is to identify signatures of adaptation made by human populations to novel environments. The Beringian environment first encountered by the founding population of Native Americans in their migration from East Asia into the New World is a prime example. However, this same migration includes a substantial population bottleneck, which provided an opportunity for enhanced genetic drift. The result of which would produce similar genomic patterns to those that natural selection would create. Previous research from our lab has identified a unique genetic architecture private to the Americas that dates to the period of Beringian occupation. Our dataset consists of high frequency SNP alleles ($p > 0.30$) identified from whole genome scans in the Thousand Genomes Project. Here we aim to identify signatures of natural selection embedded within this American architecture.

We generated novel software to annotate 5,434 unique American SNPs with respect to four lines of evidence that are indicators of functional change related to adaptation: (1) genic or non-genic, (2) synonymous or non-synonymous, (3) ontological class, and (4) clinical significance. We compare the distributions for each category between the American SNPs and a set of matched African specific SNPs, which serve as a control that has not migrated, experienced a bottleneck, or occupied an extreme environment. Broadly, the distribution of the four genotypic and phenotypic categories we investigated conform to the same pattern. This suggests that neutral processes – migration and drift – explain the majority of variation that arose during the Beringian standstill.

The Genomic Landscape of the Peruvian Andes

MARIA A. NIEVES-COLON^{1,2}, ERIN RAWLS², ALEXANDRA OBREGON-TITO³, RAUL TITO³, CECIL LEWIS³, KARLA SANDOVAL MENDOZA¹, CARLOS D. BUSTAMANTE^{4,5}, GENEVIEVE L. WOJCIK⁵, CHRIS GIGNOUX⁶, JULIE BAKER⁵, LAURA FEJERMAN⁷, TATIANA VIDAURRE⁸, BEATRIZ LIZÁRRAGA⁹, VERÓNICA RUBIN DE CELIS¹⁰, ANNE C. STONE² and ANDRÉS MORENO-ESTRADA¹

¹Laboratorio de Genómica para la Biodiversidad, Unidad de Genómica Avanzada CINVESTAV, ²School of Human Evolution and Social Change, Arizona State University, ³Laboratories of Molecular Anthropology and Microbiome Research, University of Oklahoma, ⁴Department of Biomedical Data Science, Stanford University, ⁵Department of Genetics, Stanford University, ⁶Colorado Center for Personalized Medicine, University of Colorado, ⁷Department of Medicine, University of California

San Francisco, ⁸Dirección, Instituto Nacional de Enfermedades Neoplásicas, ⁹Emeritus Professor, Facultad de Ciencias Biológicas, Universidad Nacional Mayor de San Marcos, ¹⁰Laboratorio de Genómica y Biología Molecular Evolutiva, Facultad de Biología, Universidad Ricardo Palma

The Peruvian Andes was home to multiple major civilization centers of the pre-contact Americas, and contemporary peoples in this region retain a large reservoir of Native American genomic diversity. Although large genomic studies have been conducted in Peru, most available data is limited to urban areas or comes from a small number of rural populations. Other studies with more comprehensive sampling focus solely on uniparental markers or small subsets of autosomal variants. Here we expand upon these efforts by examining genetic diversity among a large sample of 17 indigenous or traditional lifestyle communities located in each of the three Andean ecozones: the desert Pacific Coast, the Highlands and the jungle Lowlands, and two coastal Afro-Peruvian communities (N=161). Our preliminary findings indicate that most communities have large components of Native American ancestry and varying proportions of European ancestry. African ancestry is present at low frequencies and limited to coastal communities or self-identified Afro descendant groups. We did not find significant differences in global ancestry patterns between individual communities, or between lowland and highland populations. Moving forward, we will deploy local ancestry determination methods and ancestry-specific PCA to characterize further Native American ancestry in these populations. With these data we aim to elucidate local patterns of population structure, critically reassess existing models for the original peopling of the Andes, provide a better understanding of how ancient demographic processes shaped the genetic diversity of present-day Andean peoples, and lessen the underrepresentation of diverse populations in available genomic datasets.

National Science Foundation SBE Postdoctoral Research Fellowship 1711982 and grant BCS-024958, National Cancer Institute R01CA204797, Instituto Nacional de Enfermedades Neoplásicas Peru, International Centre for Genetic Engineering and Biotechnology Italy CRP/ MEX15-04_EC.

A Symposium in Honor of Erik Trinkaus: Talk to the Hand

WESLEY NIEWOEHNER
Anthropology, CSUSB

Erik's career is an amazing combination of teaching, mentoring, stellar publications, and international collaborative research that few can match.

I came to know Erik during the late 1990s because he was my dissertation advisor at the University of New Mexico (UNM). I had come across some

ABSTRACTS

of Erik's research papers as an MA student in biological anthropology at a different university, and I immediately became fascinated by his ability to combine detailed primary anatomical descriptions with comparative analyses, functional anatomy, and behavioral inferences from the archaeological record to produce testable hypotheses. I had no specific research agenda in mind (other than studying some aspect of human evolution) when I applied to UNM's program. I just knew that I wanted him as my advisor

Little did I know that my future research agenda would hinge on a term paper for one of Erik's graduate seminar classes. I struggled for weeks to find a focus for my paper. With the deadline looming, I finally broke down and went to ask Erik for help. Without hesitation, he went into his office, returned with a stack of publications, said that they were all focused on the Neandertal hand, and told me that I should synthesize them for the paper.

That research paper formed the basis for my dissertation on Neandertal and modern human hand functional anatomy. In fact, I could not have found my niche in academia without Erik's unflinching support.

Covariation bone biomechanics and enthesal changes in reindeer long bones – implication of activity?

SIRPA T.J., NIINIMÄKI, HANNA-LEENA A. PUOLAKKA and ANNA-KAISA K. SALMI
Archaeology, University of Oulu

Our aim was to study the relationship between bone formation related enthesal changes (abbreviated EC) in humerus (deltoid, infraspinatus, lateral digital extensor, ulnaris lateral, and superficial and deep digital flexor) and in radioulna (anconeus, flexor profundus, biceps brachii, and flexor profundus digiti) and mid-shaft cross-sectional robusticity indicators (CA and J) of humerus and radioulna in reindeer in order to evaluate their etiology. Oulu Zoological Museum contains samples of free-ranging and corralled reindeer. We focused on humerus and radioulna as feeding behaviour (digging for lichen versus being fed) is known to affect EC scores of these bones. Bone robusticity measures CA and J were divided into three categories of EC for each enthesis, and statistically significant differences between these categories were tested with one-way analysis of variance. We found that CA and J values increased from one EC category to next. Differences were mostly statistically significant regardless whether origins versus insertions, or fibrous versus fibrocartilaginous enthesis were observed. This relationship was not confined within a bone element: EC scores of radioulna were related with humeral bone properties, and vice versa. However, CA and J values correlated with body size, and in case of EC there was an

increase in body size between EC categories. Thus, bone robusticity and EC relationship might be an indicator of body size effects. These results provide relevant new insights in the methodological aspect of physical activity reconstructions as our results indicate ordinal nature of bone formation EC scores, and that EC are related to skeletal robusticity.

This research was funded by European Research Council Starting Grant 756431, Academy of Finland grant number 308322 and University of Oulu.

Intraspecific variation in ebony langurs: the importance of long-term data and broad geographic coverage

VINCENT NIJMAN

Anthropology and Geography, Oxford Brookes University

Ebony langurs *Trachypitecus auratus* are endemic to the islands of Java, Bali and Lombok, Indonesia. They are found in mangroves, lowland rainforest and deciduous forest, and montane forests up to 3,700 masl. While the species does rely on forest with continuous canopies, they persist in human-dominated landscapes. Between 1994 and 2018 I studied ebony langurs throughout their range and recorded larger than expected flexibility in behaviour and ecology, including group sizes, group composition, diet, densities and ranging. Mean group sizes varied from five in Lombok to >25 in coastal forest; groups were smaller where they live sympatrically with grizzled langurs *Presbytis comata*. Small groups have one adult male; larger ones may contain two or three adult males. The diet comprises a large proportion of leaves but this differs greatly between habitats. In deciduous forest it is 46%, in montane forest 64% and in teak forest 86%. The number of food plants likewise differs, from 92 in montane forest, 88 in coastal forest down to just nine in mangroves. Densities in lowland areas are 26-40% higher than in montane areas, and 45-61% higher in areas with a long dry season compared to rainforests. Home ranges in rainforest are between 5-20 hectares, but 40-50 hectares in deciduous forest. I conclude that, based on long-term studies in a wide variety of habitats, the intraspecific variation in this one species is equal or larger than what has been described for the genus as a whole. This emphasizes the importance of long-term data from different sites

Morphometric affinities of a new fossil ulna from Buluk, Kenya

ABIGAIL C. NISHIMURA¹, GABRIELLE A. RUSSO², ISAIAH NENGO³ and ELLEN R. MILLER⁴

¹Interdepartmental Doctoral Program in Anthropological Sciences, Stony Brook University, ²Department of Anthropology, Stony Brook University, ³Turkana Basin Institute, Stony Brook

University, ⁴Department of Anthropology, Wake Forest University

Buluk is an early Miocene site (16 Ma) located on the eastern side of Lake Turkana, Kenya. Here, we explore the morphological affinities of a new primate proximal ulna fossil from Buluk (KNM-WS 65401). We used a 3D geometric morphometric approach to evaluate 23 ulnar landmarks in a broad sample of 37 extant anthropoid species (N = 154 individuals) as well as extinct Miocene primates. The landmark data were transformed using a Generalized Procrustes Analysis and then visualized using a principal components analysis (PCA). Shape differences among clades and positional behavioral categories were tested using principal component scores in Kruskal-Wallis and discriminant analyses. Results indicated that the principal components effectively differentiate among clades and positional behavior groups. The discriminant analysis results also suggested that the Buluk specimen is predicted to have hominoid and suspensory group memberships. The PCA was then used to identify shape trends, and relevant linear metrics were extracted from the coordinate data to test for correlations with principal components. For example, PC1 correlates with the size-adjusted length of the olecranon process and the size-adjusted length of the trochlear notch opening. These results can be used to interpret the positions of taxa in the PCA, with hominoids having shorter olecranon processes than the other anthropoids, and quadrupeds having smaller trochlear notch openings than suspensory, knuckle-walkers, and bipeds. In sum, our findings indicate hominoid and suspensory affinities for this Buluk taxon.

Funding support was provided by The Leakey Foundation and the National Geographic Society.

Sexual Dimorphism in the Proximal Phalanges of the Hand: Verification of Logistic Regression analysis methods

IAN T. NOBLE and DAWN MULHERN

Anthropology, Fort Lewis College

The purpose of this research is to conduct a validation study by applying measurements of the proximal phalanges of the hand in humans to two previously developed multiple regression models for sex determination. These models, calculated by Mahakkanurauh and colleagues (2013), and Scheuer & Elkington (1993), were calculated using contemporary populations from Thailand and the United Kingdom, respectively, and were tested on a contemporary sample of adults from Maxwell Museum in Albuquerque, New Mexico (n=58, mostly of European ancestry) in order to determine whether either model may be applied in forensic contexts in the United States. It was found that the model calculated using a sample from the United Kingdom achieved an accuracy of 91% on the right hand and 73% on the left hand when applied to the full sample collected from

ABSTRACTS

the Maxwell Museum. The discrepancy between the left and right-hand results points to a greater difference between the right hands of males and females than in the left hand. The models calculated using a Thai population were rejected for use on the test sample due to extreme male bias resulting in 100% of individuals being classified as males. These results support populational differences in proportions of proximal phalanges that indicate the Thai equations would be ineffective for use on United States samples. These results provide strong rationale for calculation of regression equations using a sample of contemporary individuals from the United States to supplement current methods of sex determination in forensic contexts.

The Physical and the Digital: a test of the reliability of craniometric data collection from 3D models

LARA NOLDNER

Office of the State Archaeologist, University of Iowa

The University of Iowa, Office of the State Archaeologist's Bioarchaeology Program is actively 3D scanning all diagnostic human skeletal elements in its possession to preserve data while still being proactive in repatriation/reburial of Native American remains. The 3D models acquired can be measured many ways with new methods and technologies. This poster summarizes a preliminary study of the reliability of collecting standard metric data from 3D models of crania. This involved: 1) assessing inter- and intra-observer error for landmark placement on 3D models, and 2) comparing landmark distances calculated with Stratovan's Checkpoint software to standard measurements taken on corresponding physical remains. 3D models of 10 individuals' crania were acquired with a NextEngine 3D scanner. Three observers independently placed 16 standard landmarks on the 3D models and exported the landmarks' x, y, z coordinates. One of the observers conducted the same landmark placement two additional times and recorded 15 landmark distances both digitally and on actual crania. Mean standard deviations calculated for inter-observer error in landmark placement ranged from 10.79 to 0.21, with the majority of landmarks (14 of 16) having values of 2.06-0.20. Mean standard deviations for intra-observer error ranged from 1.92-0.19. With the exception of orbital breadth, orbital height, and interorbital breadth there were no other significant differences between landmark distances derived from 3D models and standard measurements of the crania. These results demonstrate a relatively high reliability for accurate data collection from 3D models of crania. Inconsistencies in inter-observer landmark placement and measures of the orbits are discussed.

Pigmentation variation and in admixed populations and associated genetic loci

HEATHER L. NORTON¹, ABIGAIL BIGHAM² and ESTEBAN J. PARRA³

¹Anthropology, University of Cincinnati,

²Anthropology, University of Michigan,

³Anthropology, University of Toronto, Mississauga

In order to better characterize pigmentation variation and associated genetic loci in admixed populations, we report on quantitative pigmentation phenotype data from three population samples (African Americans, n=259, US Hispanics, n=90, and Mexicans from the city of Palenque, n=101). All three samples are significantly different ($F=215.5$, $df=2$, $p<2\times 10^{-16}$) from each other in skin Melanin Index (M). A Tukey post-hoc test indicates that this is not explained by the higher M of the African American sample alone, as the US Hispanic and Palenque samples are also significantly different ($p<1\times 10^{-10}$). Hair M also differs significantly among the three populations ($F=41.96$, $df=2$, $p<2\times 10^{-16}$), driven by the lower values of the US Hispanic sample, which is significantly lighter than the Palenque and African American samples ($p<0.00001$). We use high-resolution iris images to quantitatively assess iris pigmentation in a subset of the African American (n=147) and US Hispanic (n=48) samples. MANOVA shows that the two groups are significantly different ($F=20.882$, $p<2.2\times 10^{-16}$) from each other in CIE Lab color space. While CIE Lab values are generally lower in the African American sample (indicating darker irises), they are more variable in the US Hispanic sample, consistent with previous reports. These results suggest that considerable variation in skin, hair, and iris pigmentation phenotype exists between populations, and that using social categories (e.g. "Hispanic" or "African American") as a stand-in for phenotypic variation may mask important within-population variation. Finally, we use dense genotype data and admixture mapping methods to test for genotype-phenotype associations, conditioning on variation in individual ancestry.

Data collection was supported by a grant to HLN and EJP by the US Department of Justice (2013-DN-BX-K011).

Rich grave goods, bad health? The preliminary results of the bioarchaeological study of the Middle Bronze Age cremation burials from Jagodnjak, Eastern Croatia

MARIO NOVAK¹, IVOR JANKOVIC¹ and DINKO TRESIC PAVICIC²

¹NA, Institute for Anthropological Research, ²NA, Kadeucje Ltd.

The paper presents preliminary results of the bioarchaeological analysis of the remains recovered from 29 cremation burials from Jagodnjak in Eastern Croatia. The archaeological rescue excavations of the Jagodnjak-Krčevine site (AN 7) in the Osijek-Baranja County in Eastern Croatia

carried out in 2014 and 2015 revealed the presence of the cemetery dated to the final periods of the Early and to the Middle Bronze Age, the so called Transdanubian Encrusted Pottery culture (ca 2000-1500 BCE).

All recovered burials were quite "rich", and alongside human remains, each grave contained numerous pottery vessels accompanied by large quantities of cremated and non-cremated animal remains and some metal (mostly bronze) objects. Approximately one third of all studied burials were double – all of these contained the remains of at least one child, and in some cases, both individuals were children.

At least 37 individuals were present in the sample: 18 subadults, three females, six males, and ten adults whose sex could not be established. Although the human remains were well-cremated, based on the bone coloring and fragmentation, most of them exhibited traces of various pathologies such as multiple cases of cribra orbitalia, porotic hyperostosis, vertebral osteophytosis, ante-mortem tooth loss and abscesses, as well as one case of new periosteal bone formation.

Based on the presented data, we argue that the "richness" of grave goods does not necessarily have to indicate good health and quality of life in a certain population as seen on the example of the Bronze Age burials from Jagodnjak.

This study was funded by the Croatian Science Foundation grant HRZZ IP-2016-06-1450.

Runs of homozygosity and admixture dynamics in the African-derived Brazilian quilombo populations

KELLY NUNES, RENAN B. LEMES, LILIAN KIMURA, JULIANA E.P. CARNAVALLI, REGINA C. MINGRONI-NETTO, PAULO A. OTTO and DIOGO MEYER

Genetica e Biologia Evolutiva, Universidade de Sao Paulo

Related individuals share haplotypes identical by descent (IBD). The offspring of these individuals can inherit these IBD segments, creating long stretches of homozygosity called runs of homozygosity (ROH). The number, size and total length of ROH in a population are the result of inbreeding, genetic drift and recombination, providing information about population's demographic history. Long ROH are produced by recent inbreeding, whereas short ROH reflect the background relatedness created by ancient inbreeding. In admixed populations, the processes shaping ROH distributions are complex, since (1) the demographic history of the parental populations shape short ROH distributions; (2) and the demographic history after admixture can contribute to long ROH. Here, we explore how these processes are shaping the ROH distribution in admixed Brazilian individuals, descendants of African, European, and Native-Americans. We used 600k SNP array data from ~600 individuals to estimate local ancestry,

ABSTRACTS

allowing us to investigate the ROH patterns in relation to ancestries, and to relate these to population demographic history. Our results show that these admixed individuals on average have higher total ROH length than Africans, and lower than Europeans. However, the extent of ROH is lower than the average of the ancestral contributions, indicating that in admixed individuals, the presence of two ancestries can reduce total ROH. We also identified many cases where ROH had distinct ancestries, including large ROH (40Mb) within which there were ancestry switches. These cases document recent inbreeding, creating large ROH of mixed ancestries. These findings show the value of ROH studies in admixed populations.

FAPESP 2012/18010-0, FAPESP-CEPID 13/08028-1 and NIH GM-075091.

Anticipating turns: How many steps are affected?

MIGUEL OCHOA¹, STEVEN G. LAUTZENHEISER^{1,2}, ADAM D. SYLVESTER³ and PATRICIA A. KRAMER^{1,2}

¹Anthropology, University of Washington, ²Department of Orthopaedics and Sports Medicine, University of Washington, ³Center for Functional Anatomy and Evolution, The Johns Hopkins University School of Medicine

The ground reaction forces (GRF) required to change direction when walking differ from those experienced in walking in a straight path. For instance, shear forces (those in the plane of the substrate) are higher during the propulsive phase of a turn. We questioned if the GRFs in the step before a turn occurs also differed from those of walking in a straight path.

Kinematic and kinetic data of 20 individuals were collected using a ten-camera Qualisys system and three Kistler force plates in two conditions: walking unshod in a straight line with and without a 90° turn. Forward (X), side (Y), and vertical (Z) ground reaction forces (GRF) were measured and analyzed to determine if differences exist in the shape of the GRF curves between the conditions in the step before a turn. In a straight line, X forces in late stance propel the body while Y forces stabilize it. In a turn, Y forces change the body's direction while X forces brake the body's motion.

Forward GRFs in the step before a turn are different ($p < 0.001$) from those generated while walking in a straight line, although vertical and side GRFs are not ($p \geq 0.097$). More braking and less propulsive force is generated immediately before commencement of the turn, indicating that a turn is anticipated with changing kinetics in the step before it happens. Consequently, multiple steps require examination to understand the forces generated by turning.

Neanderthal thermoregulation: old ideas and new

CARA OCOBOCK and ALEXANDRA NICLOU
Anthropology, University at Albany

Early work on Neanderthal cold climate adaptations focused on anatomical dimensions such as chest size, limb length, and nose size. More recently, researchers have attempted to elucidate Neanderthal bioenergetics by estimating total energy expenditure (kcal day^{-1}) and some of its components such as basal metabolic rate, locomotor costs, and thermoregulatory costs. Recent work on modern human energetics and thermoregulation has brought to light a number of potential physiological routes for Neanderthal cold adaptation. For example, a new study demonstrating the interaction between thermoregulation and physical activity suggests that the proposed Neanderthal high levels of physical activity and locomotor inefficiency may have provided a thermoregulatory benefit in glacial environments. Furthermore, there have been a number of advances in understanding the thermoregulatory capacity of brown adipose tissue, a type of fat that burns solely to produce heat. This new work has only just started to chip away at this recently re-discovered tissue in adult humans and its adaptive implications. Though imperfect, these analyses have improved our understanding of how cold climate selective pressures may have driven observed morphological and proposed physiological variation among Neanderthals. Here, we describe the journey of Neanderthal thermoregulatory research. We reassess past ideas that laid a strong foundation as well as present data and new hypotheses that may lead to a greater understanding of how Neanderthals survived in and interacted with their harsh environments.

Funding for part of the data discussed in this abstract was provided by the Leakey Foundation.

Adolescent female orangutans benefit from associations with their mother in Gunung Palung National Park, West Kalimantan, Indonesia

CAITLIN A. O'CONNELL¹, WURYANTARI SETIADI² and CHERYL D. KNOTT³

¹Human and Evolutionary Biology, University of Southern California, ²Genome Diversity and Diseases Laboratory, Eijkman Institute of Molecular Biology, ³Department of Anthropology, Boston University

In semi-solitary *Pongo pygmaeus wurmbii*, the adolescent period is characterized by increased sociality, with young, independently ranging nulliparous females being the most likely age-sex class to have a social encounter ($\beta = 0.095$, $F = 3.742$, $p < 0.011$). Because orangutans are female philopatric, we predicted that the most social time and the most affiliative interactions occur between adolescent females and their mothers. To test

this, we performed day-long focal follows from 2013-2014 at Gunung Palung National Park, Borneo, Indonesia, and recorded the duration of all social associations within 50 meters and categorized the nature of all interactions. We found that more adolescent female social time is spent in the company of adult females (85%) than with other classes ($\beta = 0.141$, $F = 4.086$, $p < 0.05$), and in most cases, the adult female was the adolescent's mother (70% of the time). Contrary to our predictions, we found only one interaction between an adolescent and her mother that could be characterized as affiliative. Instead, most associations between adolescent females and their mothers were neutral or slightly agonistic. Despite limited affiliative interaction, adolescent females seek proximity to their mothers (Hinde Index of 0.12), suggesting that they benefit from maternal associations. Submissive behavior was most often performed by two orphaned adolescent females toward adult females. These orphans were also involved in the most affiliative interactions, with unflanged males as their primary partner (36% of all affiliative events). We propose that a lack of maternal social support forces orphaned adolescent females to adopt alternative social strategies that resemble those of immigrating female chimpanzees.

BU GRAF, National Geographic Society (9447-14, EC0690-14, GEFNE68-13), US Fish and Wildlife Service (F12AP00369), Disney Wildlife Conservation Fund, Wenner-Gren Foundation, Nacey-Maggioncalda Foundation, Primate Conservation Inc., BOS-Canada

The infancy-childhood transition in rural Gambian infants

G. KESLER O'CONNOR¹, ZOFIA STANLEY¹, JAMES DYKES², DANIEL J. NAUMENKO^{2,3}, NABEEL AFFARA⁴, DAVID B. DUNGER⁵, KEN K. ONG^{5,6}, ANDREW M. PRENTICE⁷, SOPHIE E. MOORE^{7,8} and ROBIN M. BERNSTEIN^{2,3}

¹Department of Applied Mathematics, University of Colorado Boulder, ²Institute of Behavioral Science, University of Colorado Boulder, ³Department of Anthropology, University of Colorado Boulder, ⁴Department of Pathology, University of Cambridge, ⁵Department of Paediatrics, University of Cambridge School of Clinical Medicine, ⁶MRC Epidemiology Unit, University of Cambridge School of Clinical Medicine, ⁷MRC Unit The Gambia, London School of Hygiene and Tropical Medicine, ⁸Department of Women and Children's Health, King's College, London

A delay in the transition from the infancy to the childhood growth stage has been proposed to contribute to sub-optimal growth outcomes. A recent approach considered centile crossing and the correlation structure of monthly growth measures during the first year of life as a way to identify the infancy-childhood growth transition. The transition is identified by a change in correlations of z-score deviations from month to month, from a large negative correlation to zero correlation, and in UK infants was proposed to

ABSTRACTS

occur at around age 12 months. Here, we use alternate-day growth measurements from rural Gambian infants taken across the first year of life to identify the infancy-childhood transition. We analyzed weight data pooled across both sexes (N=225 (F=105, M=120)). In R, we calculated Pearson correlation coefficients for adjacent monthly z score deviations, as well for adjacent 2-day z score deviations separated by 10 and 30 days. Our results suggest that the infancy-childhood transition occurs between 100 and 150 days of age in HERO-G infants, pointing to an accelerated rather than delayed transition to a childhood pattern of growth. A later transition, as seen in UK infants, allows maximization of the high rates of growth during the infancy stage; an earlier transition as seen in Gambian infants cuts short this period of rapid growth, potentially impacting on growth outcomes in childhood while diverting energy into other processes critical to responses to acute challenges. Delayed adolescence in this population offers an extended window for catch-up growth.

Funded by the Bill and Melinda Gates Foundation (OPP1066932).

Does dental fluctuating asymmetry predict lesion status in systemic stress indicators? Kind of...

ALEXIS O'DONNELL^{1,2}, EMILY MOES¹ and KATELYN RUSK¹

¹Anthropology, University of New Mexico,

²Laboratory of Human Osteology, Maxwell Museum of Anthropology

Fluctuating asymmetry (FA), the deviation from symmetry between bilateral features, is a widely used indicator of developmental instability (DI). We hypothesize that higher FA will predict active or no lesions due to higher frailty. We used a composite measure of FA from bilateral dental metrics to predict status of stress markers in a sample of 200 Ancestral Puebloans (adults: n = 111; juveniles: n = 89) from New Mexico dating to approximately A.D. 1000-1400. We scored porotic hyperostosis (PH), cribra orbitalia (CO), and linear enamel hypoplasia (LEH), as these are traditional non-specific indicators of developmental stress often associated with frailty. PH/CO lesions were coded as active, healed, or absent. LEH was coded as present or absent. We found no significant differences in composite FA calculated from deciduous or permanent teeth ($p = 0.941$), so samples were pooled to create a composite FA score for all available teeth. Logistic regression was used to estimate odds-ratios that were then used to examine FA's relationship to lesion status and LEH. We found no relationship between FA and CO lesion status or FA and LEH presence/absence. However, people with higher FA are more likely to have no PH lesions (OR=3.4, $p=0.05$) and less likely to have healed lesions (OR 0.185, $p=0.009$). FA was not a significant predictor of

active PH lesions (OR=1.5, $p=0.8$). These findings suggest that individuals with higher DI were less likely to survive insults to their health long enough to develop skeletal lesions.

Partial funding provided by the Center for Regional Studies, University of New Mexico.

Comparative two-dimensional relative enamel thickness (RET) of South African hominin premolars

MACKIE C. O'HARA¹, MATTHEW M. SKINNER^{2,3,4} and DEBBIE GUATELLI-STEINBERG^{1,2}

¹Department of Anthropology, Ohio State University,

²School of Anthropology and Conservation, University of Kent, ³Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology, ⁴Evolutionary Studies Institute, University of Witwatersrand

Homo naledi had molarized premolars and thick molar enamel, suggesting that, like *Paranthropus robustus*, it may have been adapted to eating hard and/or abrasive foods. In non-human primates, molarized premolars can correspond with thick premolar enamel. In *H. naledi* and *P. robustus* molars, relative enamel thickness (RET; enamel thickness scaled to crown size) is similar. This study tests the hypothesis that RET in *H. naledi* premolars will also be similar to that of *P. robustus*. We compare two-dimensional RET in unworn *Australopithecus africanus* (n=10), *H. naledi* (n=16), and *P. robustus* (n=19) premolars. RET was calculated from a microCT-derived plane of section passing through the primary buccal and lingual cusps. Kruskal-Wallis tests were used to identify differences among species by tooth class and position. Across all premolars, *P. robustus* had the thickest enamel (RET=25.10), followed by *H. naledi* (23.10), and *A. africanus* (19.50). When upper premolars were combined, *A. africanus* had significantly lower RET than *H. naledi* and *P. robustus*, though the latter do not differ from each other. When lower premolars were combined, the only significant difference was between *A. africanus* and *P. robustus*, with *P. robustus* averaging significantly thicker enamel. When premolars were analyzed by tooth type, *H. naledi*'s lower third premolar RET was significantly lower than that of *P. robustus*, but the two species do not differ significantly otherwise. These findings suggest that, like the molarization of premolars, the premolar enamel thickness of *H. naledi* is comparable to *P. robustus* (with the exception of the lower third premolar).

This research was supported by a workshop grant from the Wenner-Gren Foundation and NSF GRFP DGE-1343012 to Mackie O'Hara, and the Max Planck Society.

Comparative palaeodemography of medieval British archaeological populations, with reference to the Libben Site, Ottawa County, Ohio

JAMES C. OHMAN^{1,2} and CAROLE A.L. DAVENPORT¹

¹School of Natural Sciences & Psychology, Liverpool John Moores University, ²Department of Physical Anthropology, Cleveland Museum of Natural History

Palaeodemography provides information about what life was like in a past human population, as long as the death cohort meets certain criteria and some assumptions are made. Palaeodemographic analyses of British archaeological sites provide a comparison of life in rural versus urban populations in medieval Britain. Survivorship curves were similar for the sites of rural Poulton Chapel (Cheshire, U.K.) and urban St Owens Church (Gloucester, U.K.). Subadult death rates were high in both populations; >29% of St Owens and 39% of Poulton individuals died before 10 years of age. However, mortality profiles demonstrated higher subadult and lower adult death rates in the rural Poulton site. Thus, expectation of life differed across the age categories between the two sites. An additional three rural and seventeen urban medieval British sites showed a similar rural versus urban pattern. Perhaps the landmark palaeodemographic analysis was that of the Late Woodland Libben Site, Ottawa County, Ohio, which is penecontemporaneous with the medieval British sites. Principal Component Analysis of expectation of life across age categories showed a clear difference between the medieval British urban and rural sites along the first principal component (PC1) that reflected the differing mortality rates. The North American Libben site overlapped with the urban sites along PC1. British sites were similar along the second principal component (PC2), but all differed from the Libben site. Libben's separation along PC2 resulted from higher expectation of life for individuals <10 years of age relative to both rural and urban medieval Britain.

Variation in enamel formation front angles and enamel thickness in anterior and posterior cercopithecoid teeth

LEIGH OLDERSHAW, MACKIE O'HARA, DEBBIE GUATELLI-STEINBERG and SCOTT MCGRAW
Anthropology, The Ohio State University

Enamel formation front (EFF) angles represent the leading edge of enamel formation. These angles are affected by rates of enamel extension, rates of enamel secretion, and the angles prisms make with the enamel-dentine junction. Previous studies have shown that across a range of primates, these angles are related to brain and body size, but not to tooth size. The relationship of EFF angles to enamel thickness has not been sufficiently explored, even though

ABSTRACTS

It has been suggested that wider angles in the cervical region of the tooth may be related to thicker enamel. More specifically, wider angles have been hypothesized to reflect a slowing in the rate of enamel extension, which could provide time for thick occlusal enamel to complete maturation. Here, we test the hypothesized association between EFF angles and enamel thickness in nine cercopithecoid taxa, in anterior (N = 18) and posterior (N = 12) teeth. We find that the largest EFF angles and greatest degree of change in EFF angles from cusp to cervix occurs in the thickly enameled molars of *Cercocebus atys* and *Cercocebus torquatus*. However, across taxa, there is no clear relationship between enamel thickness and either the magnitude of EFF angles or their pattern of change from cusp to cervix. These results suggest that large EFF angles and thick enamel may be associated in *Cercocebus* molars, but that other enamel formation variables (e.g., ameloblast lifespans, daily secretion rates, crown formation times, periodicities) are involved in producing enamel thickness variation in cercopithecoids.

Science Engagement with Religious Institutions and Publics

ROBERT C. O'MALLEY and ELIZABETH CROCKER
Dialogue on Science, Ethics, and Religion Program, American Association for the Advancement of Science

In national polls, most Americans self-identify as religious or spiritual, and affirm that religion is "somewhat" or "very" important in their lives. This social context should inform scientists and educators seeking to foster inclusive classroom instruction and public science engagement with diverse publics- including on topics central to biological anthropology such as conservation, human origins and evolution, diversity, and health. Such engagement is a priority for two active programs of the Dialogue on Science, Ethics, and Religion (DoSER) program of the American Association for the Advancement of Science (AAAS).

"Science for Seminaries" (2015-) assists seminary/theological schools in incorporating forefront science content into their core curricula, so that future religious leaders have more familiarity with science concepts, practices and practitioners. Most (4/7) institutions in the 2018 cohort are developing coursework relating theological instruction to archaeology and/or biological anthropology. Anthropologists number among formal seminary advisors and host or participate in research site/lab visits, on-campus forums, and guest lectures.

"Engaging Scientists in the Science and Religion Dialogue" (2016-) supports scientists and others in becoming effective ambassadors for science with diverse (and particularly with

religious) publics. The project offers evidence-based toolkits, strategies, and examples to guide constructive science engagement, particularly on topics that intersect with religious/spiritual perspectives. Outputs and activities include online/print resources, professional workshops, symposia and other programming at academic meetings, and university campus events. Workshop participants ($n_{preworkshop}=143$, $n_{postworkshop}=84$) report greater comfort with and interest in engagement with religious publics, and in responding to questions informed by faith. Long-term impact assessments are ongoing.

Both AAAS-DoSER projects are supported by grants from the John Templeton Foundation and individual donors.

Large mammal community structure and habitat variation in southern African *Paranthropus* and *Australopithecus*

KELSEY D. O'NEILL and AMY L. RECTOR
Anthropology, School of World Studies, Virginia Commonwealth University

Southern African *Paranthropus* and *Australopithecus* overlapped temporally and geographically, but differed in potential niche occupation. Despite multiple hominin sites in South Africa, only the Sterkfontein assemblage samples both genera. Isotope and microwear data suggests that both species relied on variable diets. We combine paleoecological and paleobiological approaches to compare faunal community variation in southern African hominin sites.

To compare the paleoecological contexts of southern African hominins, the associated assemblages of large mammals from 11 South African *Paranthropus* and *Australopithecus* sites were analyzed using a community approach. Multivariate correspondence analyses compared the fossil communities to 191 extant communities in modern African habitats. The modern African sample includes abiotic variables such as mean annual temperature and seasonality, annual range in temperature, annual precipitation, and precipitation seasonality. Using presence/absence data of 243 extant large mammal species, and their locomotor and dietary adaptations, modern communities were described in terms of the abiotic data, and this variability was used to retrodict community affinities that would have served as ecological parameters for Plio-Pleistocene hominins.

Results suggest that large mammal communities associated with *P. robustus* were most ecologically similar to those of modern open seasonal grasslands influenced by seasonality in temperature and rainfall. Unlike the paranthropith paleoecology, the australopith paleoecology is described with more variation in seasonality and habitats. This difference in seasonality would

have affected resource availability for both species, and further speaks to how hominin variation in the Plio-Pleistocene was influenced by habitat and climatic variability.

Muscle myosin heavy chain content and the evolution of hominin walking costs

MATTHEW C. O'NEILL¹ and BRIAN R. UMBERGER²
¹Anatomy, ²Kinesiology, ²University of Michigan

Humans have a predominance of myosin heavy chain (MHC) I fibers (i.e. 'slow-twitch fibers') in their skeletal muscle. This contrasts with chimpanzees and other similarly-sized terrestrial mammals, which exhibit a significantly lower fraction of MHC I overall. It has been proposed that MHC I content increased in hominin skeletal muscle over the past 7-8 million years, enhancing our capacity for repetitive, low-cost contractile behavior. Here, we integrate experimental and modeling-simulation approaches to determine the effect of increasing MHC I content in hominin pelvis and lower limb muscle on the metabolic cost of upright walking.

Marker and force platform data from humans (N=3) walking were integrated with subject-specific three-dimensional pelvis and lower limb musculoskeletal models to calculate individual muscle forces via static optimization. Muscle fiber dynamics were derived from forces and muscle-tendon kinematics using an inverse muscle model. A muscle energetics model was used to calculate the instantaneous metabolic rate of 35 pelvis and lower limb muscle-tendon units based on human-like and chimpanzee-like MHC I content.

Using human-like MHC I content, walking costs for our subjects were similar to expectations based on predicted rate of oxygen consumption for individuals of similar age, mass, height and speed. Reducing MHC I content to chimpanzee-like quantities (and thereby increasing MHC IIa+IIc content) increased the metabolic cost of walking by 15-25%, on average. These results indicate that an evolutionary increase of MHC I content in hominin pelvis and lower limb muscle would have lowered the metabolic cost of upright walking.

NSF BCS-0935321 and BCS-0935327

Metric and Non Metric Comparative Study of Sexual Dimorphism of the Zygomatic

MACIE L. ORRAND and SARA GARDNER
Anthropology, Georgia State University

The zygomatic region includes the maxillary and temporal processes as well as the zygoma, forming an anteriorly convex and inferiorly recessed bony arch. This lateral bony extreme of the face has received attention for its efficacy in establishing identity of unknown individuals.

ABSTRACTS

However, the degree to which sex differences of the zygomatic region can be captured using non-metric and metric traits has yet to be conclusively demonstrated. Five linear distance measurements were created that describe the dimensions of the zygomatic arch and measured on 27 crania housed at Georgia State University and Middle Tennessee State University. The measurements were taken by both authors and an interobserver error study indicates the lack of a significant difference between the two observers for all traits. Mann-Whitney U and t-tests both show a significant difference between males and females for all linear distances with *p* values ranging from 0.032 to <0.001. A discriminant function analysis yields a classification rate of 85.2%. A principal components analysis shows that males are distinct from females from their taller and broader zygoma bones, whereas females differ by their smaller masseter rugosities and shorter zygomatic processes of the temporal bone. Sex differences were identified in the number of zygomaticofacial foramina but not in the number of zygomatico-orbital foramina. These measurements demonstrate the utility in identifying sexual dimorphism in the human zygomatic arch. These patterns may be useful in estimating the sex membership of fragmentary remains arising from forensic cases and bioarchaeological fieldwork.

Enamel thickness in the deciduous dentition of humans and great apes

ALEJANDRA ORTIZ¹, SHARA E. BAILEY^{2,3}, JEAN-JACQUES HUBLIN³, MATTHEW M. SKINNER^{3,4} and GARY T. SCHWARTZ¹

¹Institute of Human Origins, School of Human Evolution and Social Change, Arizona State University, ²Center for the Study of Human Origins, Department of Anthropology, New York University, ³Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology, ⁴School of Anthropology and Conservation, University of Kent

Enamel thickness features prominently in studies of hominoid evolution and has long been thought to provide valuable taxonomic, phylogenetic, and functional information. To date studies of enamel thickness and its distribution patterns in humans, great apes, and their fossil relatives have focused on the permanent molar row, resulting in few, if any, data on these aspects of crown anatomy in deciduous teeth. Here, we analyze enamel thickness in maxillary and mandibular deciduous second molars (dm2) of *Homo sapiens* (n=42 teeth), *Pan troglodytes* (n=27 teeth), *Gorilla* spp. (n=10 teeth), and *Pongo* spp. (n=10 teeth). Using microcomputed tomography, we virtually image dental tissues and create two-dimensional sections through the mesial cusps to quantify both average and relative enamel thickness, as well as the distribution of enamel across the crown. Our results reveal no significant differences in enamel thickness among the great apes.

Unlike in permanent molars, orangutans do not stand out as having relatively thicker-enameled dm2s compared to African apes. Gorilla dm2s, however, tend to have slightly thinner enamel than either chimpanzees and orangutans. Humans, on the other hand, possess significantly thicker deciduous molar enamel in comparison to great apes. Contrary to the patterns observed in permanent teeth, the "functional" side (paracone, protoconid) of dm2 crowns in both humans and great apes does not possess significantly thicker enamel than the "nonfunctional" side. Our study lends empirical support to anecdotal observations that patterns of enamel thickness observed for permanent molars of large-bodied apes do not apply to deciduous molars.

This research was supported by the Wenner-Gren Foundation, the Institute of Human Origins, and the Max Planck Society.

Using commingled and fragmentary remains to reconstruct social interaction and social change

ANNA J. OSTERHOLTZ¹, ANDREA LOPEZ¹, JULIANNE PAIGE¹, DEBRA L. MARTIN² and KATHRYN BAUSTIAN³

¹Anthropology and Middle Eastern Cultures, Mississippi State University, ²Department of Anthropology, University of Nevada Las Vegas, ³Department of Anthropology, Skidmore College

Commingled and collective burials are found worldwide and span human history. Analysis of these materials necessitates a detailed approach focused on individual fragments, features, and elements (instead of individuals), and focuses the questions asked to population-level questions since individuals can rarely be identified within the assemblages. With specialized methodologies, data from commingled remains can be used to examine questions of population health, mobility, violence, and mortuary practices, and so on. This presentation will detail how commingled remains from three different assemblages were used to examine questions of social change and interaction. Tell Abraq, an ossuary from the UAE (ca. 2100 BC) contains the remains of at least 400 individuals; this has been used to understand the variety of Umm-an-Nar mortuary practices as well as understand population health and marriage patterns. Sacred Ridge, a massacre assemblage consisting of at least 33 individuals from Colorado (ca. AD 810) has been examined to understand the social role of violence in the pre-contact Southwest. Finally, the assemblage of Gustav II, a small assemblage consisting of at least 9 individuals from three tombs from the Gusića Gomila II site (ca. 2200-2000 BCE) in Croatia, helps to provide context for the interpretation of mortuary monuments of the Cetina culture. Their analysis marks the formation of baseline data which can be compared with other

sites in the future. Without analyzing these materials to their fullest extent, we risk an incomplete understanding of social interaction and social change.

Arboreality and fruit-feeding in Bwindi mountain gorillas (*Gorilla beringei beringei*)

KELLY R. OSTROFSKY¹ and MARTHA M. ROBBINS²

¹Center for the Advanced Study of Human Paleobiology, The George Washington University, ²Department of Primatology, Max Planck Institute for Evolutionary Anthropology

While apes are generally arboreal and frugivorous, large body size may constrain arboreal behavior. Mountain gorillas have historically been viewed as folivorous and terrestrial, based on studies of Virunga mountain gorillas. However, mountain gorillas in Bwindi Impenetrable National Park, Uganda have more fruit available to them, leading to differences in feeding ecology and behavior.

Here, we investigate age-sex class differences in patterns of frugivory and arboreality of Bwindi mountain gorillas. We used instantaneous scan sampling to measure the proportion of time in different activities (feeding, resting, traveling) and arboreality for two gorilla groups (n=35 individuals), from March 2012 to December 2017. Consistent with previous studies, we find large variation in fruit-eating within and between years (e.g., yearly averages ~7-20%, with highest monthly values per year ranging from 25-70%). While the amount of fruit-feeding does not consistently vary across age-sex classes, degree of arboreality differs across age-sex classes, with infants and juveniles most arboreal. Arboreality and fruit-feeding follow similar patterns for larger-bodied adult females, blackbacks, and silverbacks, as the majority of their time spent arboreal is for feeding. However, infants and juveniles spend relatively more arboreal time in non-feeding activities. Arboreality of mountain gorillas at Bwindi (adult females, ~20%; silverbacks, ~12%) is notably greater than that reported for the Virungas (adult females, 7%; silverbacks, 2%; Doran, 1997), likely due to greater fruit availability in Bwindi. Such variation across ape populations has implications for understanding relationships between ecology, body size, and energetics, as well as arboreal behavior of fossil apes and humans.

This research is supported by the National Science Foundation (BCS 1753963), The Max Planck Society, The Leakey Foundation, and The George Washington University.

Sexual dimorphism in absolute and relative enthesal length in *Colobus gureza* and *Hylobates lar*

ANTONIO R. OTERO

Geography and Anthropology, Louisiana State University

ABSTRACTS

A number of traits are used to ascertain sex from the skeleton. This study considers sexual dimorphism of entheses – where muscles and tendons attach to bone – in *Colobus guereza* and *Hylobates lar*. Previous research shows that *C. guereza* is sexually dimorphic in skeletal size (males larger than females), whereas *H. lar* is sexually monomorphic. Sample sizes are 6 males and 6 females in *C. guereza* and 35 males and 35 females in *H. lar*; all specimens were wild caught. Measurements included maximum length of humerus and femur, and enthesal length of pectoralis major, teres major, deltoid, and gluteus maximus. Relative enthesal length was calculated as enthesal length/bone length. Student's t-test was used in analysis. Results show that males are significantly larger than females in *C. guereza* for six of the 10 variables: length of humerus and femur, enthesal length for pectoralis major, deltoid, and gluteus maximus, and relative enthesal length of pectoralis major. None of the 10 variables is significantly different between the sexes in *H. lar*. Results show that sexual dimorphism in enthesal length is generally consistent with sexual dimorphism in bone length but generally not consistent with relative enthesal length. Two interpretations of results are that (1) enthesal length could be useful in assessment of sex in a sexually dimorphic species when complete long bones are not available (e.g., fossil material) and (2) while sexes may differ in muscle mass, they may not differ in relative enthesal length.

Using whole mitochondrial genomes from 100 ancient Indigenous British Columbian individuals to infer the impacts of European colonization

AMANDA C. OWINGS¹, JESSE W. JOHNSON², JOHN LINDO⁴, YINQIU CUI⁵, SHIZHU GAO⁵, HONGJIE LI², CRIS E. HUGHES², BARBARA PETZELT⁶, JOYCELLYN MITCHELL⁶, CHARLA MARSHALL^{7,8}, JEROME S. CYBULSKI⁹ and RIPAN S. MALHI^{1,2,3}

¹Program in Ecology, Evolution, and Conservation Biology, University of Illinois at Urbana-Champaign, ²Anthropology, University of Illinois at Urbana-Champaign, ³Carl R. Woese Institute for Genomic Biology, University of Illinois at Urbana-Champaign, ⁴Anthropology, Emory University, ⁵College of Life Sciences, Jilin University, ⁶Metlakatla Treaty Office, Prince Rupert, British Columbia, ⁷Armed Forces Medical Examiner System's Armed Forces DNA Identification Laboratory (AFMES-AFDIL), Department of Defense DNA Operations, ⁸ARP Sciences, LLC, Rockville, MD, USA, ⁹Research Division, Canadian Museum of History

Human remains from more than 270 individuals have been unearthed from nine archaeological sites along the British Columbia (BC) coast. Previous studies have demonstrated a genetic link between these ancient Prince Rupert Harbour (PRH) people and the Coast Tsimshian and Laxgalts'ap First Nations residing in BC, supporting that these present-day communities

have lived in this area for the last ~6000 years. A previous study of the ancient and present-day BC Coast Tsimshian and Laxgalts'ap First Nations using the Hypervariable Segment 1 (HVS1) showed multiple instances where an ancient and present-day individual shared a haplotype, further suggesting population continuity. Here we present high-throughput sequencing results of the full mitochondrial genome (mitogenome) of 104 ancient individuals with a population haplogroup composition of 74.2% A, 11.1% D, and 14.8% X. These PRH individuals were compared to 33 present-day BC Coast Tsimshian mitogenomes with 52% A, 4% B, 20% C, 12% D, and 12% X haplogroups. Unlike the HVS1 study, the majority of the ancient mitogenomes are unique and do not share the same haplotype as a present-day individual. However, a few do share the same haplotype or differ by 1-2 mutations. These data indicate population continuity but also that some haplotypes may have been lost over time possibly due to European colonization, and/or new haplotypes have been introduced to the community by migration. These results also demonstrate the importance of using the whole mitogenome when possible to gain a more complete understanding of the maternal population history of a community.

Funding for this project was provided for by the National Science Foundations' Doctoral Dissertation Research Improvement Grants (BA-DDRIG).

Adventures in museomics: The use of next generation sequencing to uncover great ape host and microbial genomes

ANDREW T. OZGA¹ and ANNE C. STONE^{1,2,3}

¹Center for Evolution and Medicine, Arizona State University, ²School of Human Evolution and Social Change, Arizona State University, ³Institute of Human Origins, Arizona State University

An understanding of the great ape microbiome is imperative to assessing the distribution of commensal and pathogenic bacteria across primates. As access to saliva or plaque samples from living wild chimpanzees and gorillas is typically not feasible, an alternative resource is calcified dental plaque removed from skeletons in museum collections. Here, we use dental calculus recovered from great ape collections from four U.S. museums to address questions of host and microbial genetic variation; specifically, how do oral microbiomes differ by host species and how much does the human microbiome differ from that of other primates? Decontamination and extraction protocols were used to process 40 calculus samples in a dedicated ancient DNA facility, followed by shotgun amplification and Illumina next generation sequencing. In a normalized MEGAN analysis, a Bray-Curtis PCoA of great ape oral microbial signatures showed no evidence of clustering based on host species or the museum from which they were initially

collected. We also report significant differences in abundance across members of the red complex including *Porphyromonas gingivalis* (higher in chimpanzees and gorillas) and *Treponema denticola* (higher in orangutans and historic human samples). Despite obtaining primarily microbial sequences from our analyses, we were able to reconstruct full mitogenomes in 5 of the samples and discern subspecies (for those unreported in museum records). We will discuss the implications of these findings on our understanding of the evolution of the human and non-human primate oral ecosystem and assess future directions of research utilizing museum collections.

Funding for this research was provided by the Center for Evolution and Medicine at Arizona State University and the Extreme Science and Engineering Discovery Environment (XSEDE) (NSF ACI-1548562).

Violence and the "other": migration and sacrifice in pre-Hispanic central Mexico

SOFÍA PACHECO-FORÉS

School of Human Evolution and Social Change, Arizona State University

Despite substantial evidence that socio-political upheaval is often accompanied by an increase in identity-based violence, few archaeological studies examine how the perception of social difference can incite violence. Archaeological and ethnohistoric sources indicate that an individual's place of origin was often a salient indicator of social difference in pre-Hispanic Mesoamerica. This project uses a bioarchaeological approach to examine identity-based violence at the Non-Grid 4 shrine site in central Mexico during the central Epiclassic (600-900 CE), a period characterized by large-scale political upheaval and social reorganization. 173 individuals exhibiting evidence of ritual exsanguination and decapitation were interred at the Non-Grid 4 shrine. This study uses biogeochemical analysis to reconstruct the geographic and residential histories of a sample of sacrificed individuals ($n = 72$) to examine if and how the perception of social difference contributed to their selection as sacrificial victims. Radiogenic strontium and stable oxygen isotope analyses of sampled human enamel and bone tissues indicate that 58% of victims were immigrants to the region, while 27% were foreigners, and only 14% of sacrificed individuals were locals. The high proportion of immigrant and foreign individuals among the sacrificial victims suggests that victims were likely targeted for violence based on their divergent residential histories. This work contributes to anthropological knowledge about the social

ABSTRACTS

context of violence by examining the interaction between specific social identities; complex social processes like political fragmentation, migration, and demographic change; and mass violence.

This research was supported by grants from the National Science Foundation (#2013155229, 1744335) and the Center for Bioarchaeological Research at Arizona State University.

The ontogeny of infant aye-aye (*Daubentonia madagascariensis*) vocalizations

LISA M. PACIULLI, DAVID Q. WATTS, ANNA P. PANNICK and ANNA P. MILLER

Biological Sciences, North Carolina State University

Vocalizations are a vital part of communication for many species. In particular, some species' infants rely heavily on vocalizations to survive their first days of life. The aye-aye (*Daubentonia madagascariensis*) is a nocturnal prosimian, and not much is known about their vocalizations. To date, only two studies have been conducted on aye-aye calls, and both were published almost 25 years ago. Stanger and Macedonia (1994) reported that aye-ayes have six vocalizations – scream, plea, whimper, sneeze, snort, and screech, while Winn (1994) found that infants produced four vocalizations – creee, fuff, ron-tsit, and hoo-hoo. Infants made two fewer calls than adults, and all four vocalizations had not been heard in adults. Therefore, in this study, the ontogeny of infant vocalizations was examined in one captive female aye-aye, Agatha, at the Duke Lemur Center. A Sennheiser ME66 condenser microphone was placed in the infant aye-aye's nest box to record any sounds made. Vocalizations were captured and stored in audio-files. Adobe Audition was used to listen to and code the type of call. The results showed that Agatha emitted her first vocalization within two hours of birth, when she eeped. Agatha also drummed and huffed. Therefore, of the four adult aye-aye vocalizations previously reported, Agatha made three of them. The missing / fourth adult vocalization is an ack, which is an estrous call, made during sexual receptivity. These results contradict previous reports that infant aye-ayes make different vocalizations than adults. Future research should include increasing the sample size and data collection period.

Funding generously provided by NCSU's Biological Sciences Support for Undergraduate Research Experiences and the Office of Undergraduate Research.

The mechanical and nutritional properties of African savanna vegetation: potential implications for early hominin feeding behavior

OLIVER C.C. PAINE¹, ABIGALE KOPPA², AMANDA G. HENRY³, JENNIFER N. LEICHLITER¹, EMMA J. DEVEREUX³, CHRISTINA RYDER¹, DARYL

CODRON^{4,5}, JACQUELINE CODRON⁴ and MATT SPONHEIMER¹

¹Anthropology, University of Colorado Boulder, ²Department of Ecology and Evolution, State University of New York, Stony Brook, ³Faculty of Archaeology, Leiden University, ⁴Florisbad Quaternary Research Department, National Museum, South Africa, ⁵Centre for Environmental Management, University of the Free State

Data collected over the past decade have challenged our understanding of early hominin feeding behavior. Notably, dental microwear analysis suggests that *Paranthropus boisei* consumed a diet of soft and/or tough foods, contradicting earlier interpretations arguing that its hyperrobust craniodental morphology was a direct adaptation to a diet focused on hard-object foods. Additionally, stable carbon isotope analysis reveals that early hominins began to consume significant amounts of C₄ grasses and sedges, and/or animals that ate those plants more than 3 Ma, culminating with the ~80% C₄ diet of *P. boisei*. This result was surprising because grasses and sedges are generally regarded as being too tough and nutritionally deficient for hominins lacking the dental and digestive adaptations seen in grazing herbivores. As such, there is renewed interest in understanding the mechanical and nutritional properties of hominin plant foods (C₄ or otherwise) and how they may have influenced early hominin evolution. Here we explore the mechanical and nutritional properties of modern savanna vegetation growing in Amboseli N.P., Kenya, and The Cradle Nature Reserve, South Africa during wet and dry seasons. We find that on average, the vegetation growing in Amboseli is higher in protein, lower in dietary fiber, and mechanically less challenging than the vegetation growing in The Cradle N.R. In particular, we find strong differences between the C₄ grasses growing at each site, which is to be expected considering their inherent climatic and geological differences. This may have important implications for the contrasting dietary signals we find among *Paranthropus* species.

Factors associated with cardiovascular diseases in men and women: epidemiological transition in traditional Brazilian African-derived communities (*quilombos*)

SABRINA G. PAIVA^{1,2}, MATHEUS C. NOBREGA¹, MARIA DE NAZARE KLAUTAU-GUIMARAES¹, LORENA MADRIGAL³, ANNA RIVARA³ and SILVIENE F. OLIVEIRA¹

¹Institute of Biological Science, University of Brasilia, ²Science and Technology of Tocantins, Federal Institute of Education, ³Department of Anthropology, University of South Florida

The origin of Brazilian Afro-derived communities is tied to slaves runaway or abandoned slaves. In Brazil, these communities are known as *quilombos*. Overall, *quilombos* suffer from greater inequality in their health. Here we present the

prevalence of risk factors associated with hypertension, obesity, and diabetes mellitus in rural and urban *quilombos* in Central Brazil. We conducted a cross-sectional study in three communities: Cocalinho (a non-isolated rural village; n = 70), Pé do Morro (an urban community; n = 63), and Kalunga (an isolated rural community; n = 214). Anthropometric traits, blood pressure, and blood samples were collected using standard protocols. Statistical analyses were performed using the SAS statistical software, version 9.4. The prevalence of hypertension (p=0.0209) and obesity (p<0.001) were higher in the non-isolated and urban than the isolated rural community. Despite to same social economic background, women from isolated community showed higher prevalence of hypertension (36.94% vs 21.98%), obesity (10.91% vs 3.26%), and diabetes (3.57% vs 1.04%) than men. Robust regression results showed that behavior factors such physical activity level, smoking and alcohol consumption supported the lifestyle and environmental factors as determinant of prevalence of cardio-metabolic. The isolated population is still not suffering from high levels of cardiovascular diseases, however women are more affected than men by epidemiological transition. Brazilian African-derived communities are currently going through an epidemiological transition, with modification of standards of health and disease. Our work may allow researchers to make recommendations on policies and actions aimed at improving the living conditions of ethnic minority.

FAPDF; UNB; CAPES; MEC; Prefeitura de Cavalcante

Insights into the paleobiology of early Colobinae: new views from the Late Miocene of Central Africa, Chad

LAURENT T.J. PALLAS¹, HASSANE T. MACKAYE², ANDOSSA LIKIUS³, PATRICK VIGNAUD¹, FRANCK GUY¹ and GUILLAUME DAVER¹

¹PALEOVPRIM: Laboratoire Paléontologie, Évolution, Paléoécosystèmes, Paléoprimatologie, Université de Poitiers, ²Département de Paléontologie, Université de N'Djamena

Stemming from an African stock (*i.e.* Victoriapithecidae) adaptively linked to frugivory and terrestrial locomotion, extant colobus monkeys departs from this adaptive zone in exhibiting morphophysiological adaptations associated with folivory and arboreal locomotion. Yet, the onset of the morphological hallmarks of this adaptive radiation remains poorly documented. Similarly, while a large number of early colobine taxa had been documented in the Neogene of East and South Africa, phylogenetic affinities of those early colobines relative to the African colobine (*i.e.* Colobini) crown or stem group are poorly constrained.

Here we report dentognathic and postcranial remains of a new medium-sized colobine monkey (*Cercopithecoides bruneti sp. nov.*) from

ABSTRACTS

the Central African hominin-bearing fossiliferous area of Toros-Menalla, Chad at ca. 7 Ma. Thanks to traditional and original odontometric indices and morphometric protocols, we tackle hypothesis related to the ecomorphology and phylogenetic affinities of early African Colobinae.

In addition to filling a gap in the spatial and temporal record of early cercopithecids evolutionary history, we provide evidence on the onset of a folivorous diet (e.g. increase in dental occlusal relief) and a reacquisition of terrestrial locomotor habitus (e.g. medial epicondyle angulation and humeral medial trochlear keel) among African fossil colobines as early as the Late Miocene. We also clarify the phylogenetic affinities of the genus *Cercopithecoides* among the stem Colobini based on dento-gnathic morphology. Toros-Menalla not only put forth the essential role of Central Africa on human evolution but also bring new paradigm to the early evolutionary history of cercopithecids.

Applying BayesModelS to body mass prediction; comparisons with traditional approaches and recommendations for future paleontological reconstructions

JAMES D. PAMPUSH^{1,2}, GABRIEL S. YAPUNCICH³ and EDWARD J. FUSELIER⁴

¹Exercise Science, High Point University,

²Physician Assistant Studies, High Point University,

³Evolutionary Anthropology, Duke University,

⁴Mathematical Sciences, High Point University

Among the most important aspects for reconstructing an extinct animal's ecology is determining their body mass. Across mammals, body mass is correlated with many other ecological characteristics including: diet, social structure, reproductive strategies, longevity, locomotor patterns, and basal metabolic rate. Thus, paleontologists have spent considerable research effort in developing effective mechanisms and proxy variables for predicting the body mass of extinct taxa. One recently developed tool—BayesModelS—detects “phylogenetic outliers” (such as the diminutive molar size relative to body mass in *Homo*) as a means of highlighting trait-complex rearrangements, which can then be interpreted as evidence of novel selective regimes. Because outliers are identified by the contrast between the observed and expected trait values, prediction of trait values (e.g., body mass) is a more conservative application of BayesModelS. Using seven proxy variables (i.e., upper and lower molar occlusal area, surface area of three tarsal articular facets, humeral and femoral cross-sectional areas) measured in a sample of 49 extant euarchontan species, we show that BayesModelS is consistently more accurate (lower prediction error) than other commonly used prediction methods (i.e., Phylogenetic Independent Contrasts, Ordinary Least Squares Regression, and Phylogenetically Generalized Least Squares Regression) for all

measures. Consistent with other studies, dental measurements are the least reliable proxies for predicting body mass. We recommend researchers looking to reconstruct extinct taxa body masses employ the BayesModelS tool, for which we will be providing an executive script with embedded directions for novice R users in a forthcoming publication.

Scientific Racism: From Dissident Professionals to Citizen Science

AARON PANOFSKY

Institute for Society and Genetics, UCLA

This talk presents preliminary research from a study about white nationalists and their efforts to appropriate genetics research for their own ideological and identity projects. Using historical sources and online data and interpretive methods, I show that ideas from genetics have been prominent in their public pronouncements and in online discussions among white nationalists. For example, they discuss genetic ancestry tests to demonstrate pure European/white ancestry, population genetics to “prove” the biological reality of race, and behavior genetics to claim the intellectual and behavioral superiority of whites. Through the 20th century there was a strong cadre of professional scientists eager to promulgate racist interpretations of genetics research, but facing effective scientific and ethical opposition by other researchers, their ranks and authority greatly attenuated in the 21st. White nationalists have relied on these scientists for scientific racist ideas, but with their decline white nationalists have crafted themselves into a kind of citizen science movement. I show that their activities include gathering and promulgating the claims of academic scientific racists, reinterpreting ostensibly non-racist genetics in racist ways, and even using publicly available statistics and data to generate novel racist analyses. This movement's bid for authority is based on their claim that they represent the true spirit of scientific objectivity and a willingness to pursue data and arguments that have been suppressed by the academy that is overcome by politically correctness.

This project is supported by NIH grant R21 HG010258-01.

Coping strategies of maternal and infant feeding practices after a natural disaster among Zapotec peoples in Oaxaca, Mexico

NERLI PAREDES RUVALCABA

Anthropology, Michigan State University

Natural disasters magnify the vulnerabilities of mothers and infants who may be more susceptible to safe water and food shortage following a natural disaster. This study explored the coping strategies mothers used to feed themselves

and their infants following the earthquake of September 7, 2017 in Oaxaca. **Methods:** Thirteen mothers with young infants were recruited. Semi-structured interviews were conducted on how mothers fed themselves and their infants following the earthquake. **Results:** Mothers shifted the emphasis on securing food quantity over food quality. Mothers with infants in weaning transition relied more on either breast milk or infant formula due to the lack of access to safe complementary foods. A challenge for breastfeeding mothers was the folk belief of *susto*, which happens when mothers experience a strong emotion; this strong emotion may be passed to the infant through breast milk and make the infant sick. To prevent this, some mothers avoided breastfeeding for a short period of time and used formula instead. A challenge for mothers relying more on formula was the limited access to clean water. Mothers with limited access to clean water prioritized it to prepare formula sacrificing their own consumption. Additionally, some mothers reported combining infant formula with *atole*, a maize based drink to fill-up the infant. **Conclusion:** Mothers face complex challenges to feed themselves and their infants after a natural disaster. The coping strategies mothers implement may place mothers and infants at risk for insufficient or unsafe food and water consumption.

National Science Foundation Graduate Research Fellowship Program; Tinker Research Grant for Graduate Research in Latin America

Timing of reproductive onset among female vervet monkeys (*Chlorocebus pygerythrus*) in wild and human-impacted populations

STACY-ANNE R. PARKE¹, ALICIA M. RICH¹, MARYJKA B. BLASZCZYK² and CHRISTOPHER A. SCHMITT¹

¹Anthropology, Boston University, ²Anthropology, University of Texas

The timing of female maturation can be influenced by variation in energetic status, socio-demographic factors, and ecological context. Plasticity in age at first reproduction is, in particular, intimately tied to nutritional context. Here, we explore differences in age at first reproduction among wild female vervet monkeys (*Chlorocebus pygerythrus*) in South Africa living in “wild-feeding” (Soetdoring Nature Reserve) and “food-enhanced” (!Gariep Dam) social groups. We used ordinal logistic regression models to explore the relationship between body fat (measured by skin fold thickness), parity (assessed through nipple length), and dental age in these populations, and used chi-squared tests to assess proportional differences of nulliparous to parous females between populations. Our results suggest that the maturational milestone of age at first birth occurs in accordance with predicted

ABSTRACTS

energetic differences, as it appears delayed among “wild-feeding” females in Soetdoring - which have significantly lower subcutaneous body fat - compared to those in !Gariep Dam. This outcome, however, has only weak statistical support, presumably due to the small sample size of females at pubertal age in !Gariep. We predict that further sampling will strengthen our model and allow for more detailed investigations of the interaction between sexual maturation and human impacts.

Ancestral determination of crania from the ancient Roman necropolis of Sanisera

MADLINE F. PARKER^{1,2}, BERNARDO VILA² and FERNANDO CONTRERAS²

¹Biology, University of Indianapolis, ²Archaeology, Sanisera Archaeology Institute

During the 2018 field season at the Roman necropolis of Sanisera in Menorca, Spain (dated 400-700 AD), three intact crania were recovered from comingled tombs and analyzed to obtain demographic information about the population. These three crania from two tombs as well as the cranial fragments of six individuals from a third tomb were analyzed using standard bioarchaeological methods. Of the intact crania, one displayed strong Asian characteristics, one displayed strong African characteristics, and one displayed strong European characteristics. The cranial fragments, including portions of the facial skeleton, temporal bones, and the mastoid processes, themselves were either strongly African or strongly European. There were a mix of ancestries, ages, and sexes within each tomb showing no clear segregation between individual tombs. Additionally, the range of skeletal ancestral traits indicates that saying the population is “Roman” does not mean that the population is displaying solely European ancestral traits. Menorca is an island in the Mediterranean and was conquered by the Romans due to its strategic geographical location. The necropolis population is reflective of the broad geographical scope of the Roman empire, the assimilation of people of different ancestries into the empire, and the proximity to Roman Carthage.

Selective mortality of tuberculosis after the 1918 influenza pandemic in two Newfoundland regions

TAYLOR PASKOFF

Anthropology, University of Missouri

Newfoundland's mortality during the during the 1918 flu pandemic was one of the highest in the West, but it was also in a decades-long battle against another respiratory illness: tuberculosis (TB). Early 20th century TB mortality peaked in 1906 at 43.5 deaths per 10,000, compared to a total mortality of 19.3 deaths per 10,000 from bronchitis, pneumonia, and influenza combined.

Other studies have suggested that TB mortality declined after 1918, likely due to high pandemic mortality of individuals infected with TB consequential of co-infection with influenza and/or pneumonia. Data on TB deaths in Newfoundland and Labrador death records were used to analyze sex- and age-based post-pandemic mortality for two specific regions: the urban Avalon Peninsula and the rural South. Average mortality in the Avalon region (years 1910-1917) was 29.9 and 26.2 deaths per 10,000 for males and females, respectively. For both sexes there were six years between 1918 and 1930 in which yearly TB mortality was significantly less than this baseline. The South's average mortality (years 1910-1917) was 33.5 and 33.4 deaths per 10,000 for males and females, respectively, but there were no significant decreases in mortality post-pandemic. These results suggest there were differences in TB epidemiology in urban and rural regions. Historical documents such as vital reports, government correspondence, and original manuscripts that describe the history of TB in Newfoundland, the reforms put forth to combat the illness, and the socioeconomic impact of the considerable mortality of the disease are used to explain these epidemiological differences.

Current and proposed qualifications for forensic anthropologists

NICHOLAS V. PASSALACQUA¹ and MARIN A. PILLOUD²

¹Anthropology and Sociology, Western Carolina University, ²Anthropology, University of Nevada, Reno

The qualifications for a discipline are composed of the education and/or training requirements considered necessary to provide individuals with adequate knowledge to perform discipline-related tasks (Passalacqua and Pilloud 2018). There are currently few available guidelines and no standards for the qualifications of a forensic anthropologist and as such, there is great diversity in the individuals currently practicing forensic anthropology.

In order to examine the range of current qualifications of forensic anthropology practitioners, the authors distributed an online survey hosted by Western Carolina University and approved by the Institutional Review Board of this institution as well as the University of Nevada, Reno. Questions were focused on education and training in forensic anthropology as well as quantity and nature of forensic anthropological casework performed by each respondent.

Results demonstrate that there is very little consistency in coursework or training of currently practicing forensic anthropologists. Approximately 85% of respondents were members of an appropriate professional organization, but less than 20% were certified by the

American Board of Forensic Anthropology. Interestingly, there was a great deal of consensus from respondents in terms of proposed qualifications for future forensic anthropologists.

As forensic anthropology grows as a discipline, the standardization of qualifications will become increasingly important, both in terms of setting requirements for education and training, as well as for the certification of its practitioners. This standardization will likely further differentiate forensic anthropology from other biological anthropology sub-disciplines (e.g., bioarchaeology); other sub-disciplines may also consider establishing their own qualification standards following this model.

Differences in fore- vs. hindlimb autopod function in extant hominoids is reflected in pollical vs. hallucal metapodial strength properties

BIREN A. PATEL^{1,2}, TEA JASHASHVILI^{3,4} and CALEY M. ORR^{5,6}

¹Integrative Anatomical Sciences, Keck School of Medicine, University of Southern California, ²Human and Evolutionary Biology Section, Department of Biological Sciences, University of Southern California, ³Molecular Imaging Center, Department of Radiology, Keck School of Medicine, University of Southern California, ⁴Department of Geology and Paleontology, Georgian National Museum, ⁵Department of Cell and Developmental Biology, University of Colorado School of Medicine, ⁶Department of Anthropology, University of Colorado Denver

Functional comparisons of cortical bone strength properties between hominoid hallucal and pollical metapodials (Mt1 and Mc1, respectively) are lacking. Determining which of these two elements is stronger, and by how much, could be informative because the hallux and pollex are used differently both within and among extant hominoids during locomotion and manipulation (i.e., functional differentiation between autopod pairs). Here we compare Mt1 and Mc1 midshaft cortical area, polar section modulus, and polar second moment of area, calculated from micro-CT data in *Homo* (n=21), *Pan* (n=47), *Gorilla* (n=24), *Pongo* (n=20), *Symphalangus* (n=8), and *Hylobates* (n=21). Intra-individual comparisons between bones within species were made using paired t-tests. Log transformed Mt1:Mc1 ratios were created to assess relative strength asymmetry between bones, and interspecific comparisons of these proportions were made using ANOVAs. Absolute strength differences between the Mt1 and Mc1 for all variables were significantly larger in the Mt1 for all species ($p < 0.05$). Significant differences across species in Mt1:Mc1 proportions were also found, thereby demonstrating that strength asymmetry between bones differs among taxa ($p < 0.05$); asymmetry was lowest in *Pongo*, intermediate in *Gorilla*, and greatest in *Homo*, *Pan*, *Hylobates*, and *Symphalangus*. These

ABSTRACTS

findings support the hypothesis that the Mt1 is better adapted structurally than is the Mc1 for bearing mechanical loads during weight support of locomotion in all hominoids, and that pedal hallucal grasping likely engenders higher loads than does manual pollical grasping in non-human hominoids. Thus, functional differentiation in autopod use within and among hominoids is reflected in hallucal and pollical metapodial strength properties.

Funded by the National Science Foundation (BCS-1317047; BCS-1317029; BCS-1539741), Wenner-Gren Foundation, and Leakey Foundation.

Validating foundational assumptions of dental morphology using quantitative genetics

KATHLEEN S. PAUL¹, CHRISTOPHER M. STOJANOWSKI¹, WILLIAM N. DUNCAN² and KENT M. JOHNSON³

¹School of Human Evolution and Social Change, Arizona State University, ²Department of Sociology and Anthropology, East Tennessee State University, ³Department of Sociology/Anthropology, The State University of New York College at Cortland

The Arizona State University Dental Anthropology System (ASUDAS) or Turner-Scott System revolutionized the use of dental morphology for reconstructing evolutionary processes in past populations. By providing globally-recognized data collection standards, the system has elevated the status of dental morphology to an indispensable line of evidence in biodistance research. The efficacy of morphological data rests upon foundational assumptions about underlying tooth crown biology; namely, that the traits are highly heritable and minimally sexually dimorphic. Scott and colleagues have also outlined best practices for the application of dental morphology to biodistance studies, most aimed at curtailing genetic redundancy in multivariate datasets (see Turner et al., 1991). Quantitative genetic approaches have the potential to validate these assumptions. Here, we present the first robust estimates of heritability and genetic correlation for ASUDAS crown characters. Data were collected from a casted sample of South Carolina Gullah individuals (N=469) and analyzed using maximum likelihood variance components analysis. While several postcanine traits yielded heritability estimates of 0.0, mean estimates across statistically significant models were moderate to high (anterior=0.34; postcanine=0.75). Results of covariate screening support the long-held assumption that ASUDAS traits are sexually monomorphic, with the exception of canine marginal/cingular ridge characters and certain molar accessory cusps. Additionally, patterns of heritability and genetic correlation groundtruth most prescribed biodistance practices: dichotomizing trait expression, collapsing bi-antimeric datasets, and prioritizing traits scored on key (sensu Scott et al., 2018)

teeth. Notwithstanding, our results suggest that certain assumptions require reconsideration and underscore the importance of continued validation work in additional populations.

NSF Research Grants: BCS-1063942 and BCS-1750089; IRB: ASU Exemption 45CFR46(4) and The Ohio State University

Engaging students in anthropology through the exploration of ancestry identity

LAUREL N. PEARSON

Anthropology, Pennsylvania State University

Anthropology, Ancestry, and You is a course created to engage undergraduate students in learning biological anthropology at The Pennsylvania State University through the investigation of their own genealogical and genomic ancestries. During the semester students learn about genetics, evolution, human variation, and ethical considerations in personal genomic testing through lectures and discussions of assigned readings. The students synthesize what they have learned by creating personal genealogies, conducting oral history interviews with grandparents, and interpreting the results of their own optional direct-to-consumer genomic ancestry tests. To gauge student learning and engagement, anonymous surveys are administered at the mid-point of the semester and again at the end of the term. In the first half of the initial course offering, students have demonstrated that they better understand how evolution has shaped the variation seen in modern human genomes and traits and the ethical and privacy concerns regarding direct to consumer genomic testing. Only one student, of the 95% who chose to participate in a genomic ancestry test, expressed reduced interest in personal genomics testing at mid-semester. Incorporating personal ancestry exploration into anthropology courses also has the potential to reach students from a diversity of majors and colleges, nearly three-quarters of the students enrolled in the course are non-anthropology majors and half are from colleges outside of The College of the Liberal Arts. Preliminary findings suggest that active engagement of students in the investigation of their own ancestries may improve learning of anthropological concepts and generate better-informed consumers of personal genomics tests.

Prediction of humerus length from the insertions of pectoralis major and the deltoid

OSBJORN M. PEARSON and ETHAN C. HILL

Department of Anthropology, University of New Mexico

In an effort to produce a reliable means of estimating the length of partial humeri lacking both epiphyseal ends, we measured 98 complete

humeri drawn from the Documented collection of the Maxwell Museum of Anthropology and the teaching collection of the Department of Anthropology at the University of New Mexico. The maximum length of each bone was traced on a piece of paper and position of the middle of the insertion for the pectoralis major and the inferior-most extent of the insertion for the deltoid were marked. Distances between these muscle landmarks, drawn as perpendicular lines to the long axis of the diaphysis, were used as data in this analysis. Our rationale was that the projected distance between the two muscular landmarks would encompass a substantial amount of the length of the bone and perhaps lead to an accurate prediction. The resulting regression equation was: maximum length = $194.214 + 1.483(\text{distance from mid-pectoralis major to the bottom of the deltoid}) \pm 17.576 \text{ mm}$ ($R^2 = 0.385$). The position of the middle of the pectoralis major insertion fell at $25.5 \pm 1.8\%$ of maximum length while that of the bottom of the deltoid lay at $52.0 \pm 2.2\%$ of maximum length (both measured from the proximal end). The low R^2 value for the intermuscular length equation means that it provides an undesirably low degree of accuracy; the use of either muscle position alone with a preserved epiphysis would be preferable.

Arthropathic changes in the human skeletal remains from the Eastern Zhou China

KATE PECHENKINA¹ and WENQUAN FAN²

¹Anthropology, Queens College, CUNY, NYCEP,

²Archaeology, Henan Provincial Institute of Cultural Relics and Archaeology

The Zhengnan Ancient city, located in the Central Plains of China, reached its florescence during the Eastern Zhou dynasty (770-221 BC) that preceded the unification of China and the rise of Chinese empire. Several parts of this early city have been excavated, providing a detailed skeletal record of its stratified urban population as well the satellite farming communities during the Bronze Age. Our earlier research demonstrated considerable variation of diet and health among people buried in different parts of the city. The present analysis examines the arthropathic changes in 262 adult remains from Zhengnan and provides a decision tree used for developing the diagnoses. Arthropathic changes were very common in the examined skeletal collections. Ninety two percent of examined skeletons displayed at least mild degenerative changes affecting multiple joints. Skeletons that displayed arthropathic changes unusual for degenerative joint disease, such as ankyloses or destructive changes, were subjected to further analysis to establish the diagnosis. The majority of these severe arthropathies could be explained by an earlier traumatic injury to the joint with a bone reaction to subsequent inflammation. Among the remaining cases two were identified as diffused

ABSTRACTS

idiopathic skeletal hyperostosis (Xinghong M17 and Tiancheng M129) and one as possible ankylosing spondylitis (Shuanlou M13). Redianchang M35 skeleton displayed an ankylosis of the wrist bones and metacarpals as well as focal lytic lesions throughout small joints of hands and feet suggestive of rheumatoid arthritis. We discuss possible relation between the observed arthropathies and living conditions in different parts of the city.

Caves in the Classroom: Explore Hominid Fossils with Virtual Reality in DinalediVR

BECCA PEIXOTTO^{1,2}, ANDREW MONTGOMERY¹, DANIEL GARCIA MARTINEZ³, NOMPUMELELO HLOPHE³, MIGUEL OCHOA⁴, MAROPENG RAMALEPA², MATHABELA TSIKOANE², STEVEN J. TUCKER², JOHN MEAD⁶, MARINA ELLIOTT² and LEE R. BERGER²

¹Center for the Exploration of the Human Journey, Perot Museum of Nature and Science,

²Evolutionary Studies Institute, University of the Witwatersrand, ³Department of Sociology and Anthropology, Georgia Southern University, ⁴Department of Anthropology, University of Washington, ⁵CSIC, Museo Nacional de Ciencias Naturales, ⁶Middle School Science, St Marks School of Texas

The DinalediVR virtual reality package aims to engage students and the public with paleoanthropology through themes of exploration and discovery and by highlighting the diversity of scientists and specializations contributing to the field. DinalediVR contributes to an open access ethos where accessibility includes linguistic representation, reduced economic barriers to engagement with emerging technologies, and informative content tailored to non-specialists. The accompanying website (<http://perotmuseum.org/dinalediVR>) offers learning objectives and student activities to help teachers incorporate the VR app into broader science curricula and identify specific Texas Education Knowledge and Skills (TEKS) standards addressed. Scientist profiles, FAQs, and other materials are also provided. App users are virtually transported 30 meters underground to the Dinaledi Chamber of the Rising Star Cave in South Africa where the fossils of *Homo naledi* were discovered in 2013. Students see the main excavation area and can find a skull, mandible, femur fragment, and an articulated hand and foot. By choosing one of six audio tracks, each recorded by a member of the research team in their native language, students also learn about excavation methods, cave geology, and the adventure of getting to the chamber itself. DinalediVR is available as a free download, is Google Cardboard compatible and includes a monoscopic mode for group explorations. Among the available teacher resources are instructions for students to build their own VR headset with recycled materials (cardboard and

a soda bottle). DinalediVR complements other outreach efforts such as teacher workshops and as a corollary activity for virtual classroom visits from the field.

We gratefully acknowledge support of the Perot Museum, the Lyda Hill Foundation, National Geographic Society, and the University of the Witwatersrand.

The evolution of body size in Strepsirrhine primates

ANNA PENNA and LUCA POZZI

Anthropology, University of Texas San Antonio

Body size is a critical life history trait. It affects locomotion, metabolism, social structure, and behavior in primates, therefore playing a central role in primate origins and diversification theory. Nocturnal Strepsirrhine (lemurs, lorises, and galagos) species are often used as a proxy to the ancestral primate due to their small bodies and other "primitive" traits. On the other hand, it has been suggested that nocturnal lemurs and galagos experienced independent events of body size reduction, perhaps as a further adaptation for life in unpredictable environments. The average body mass among living Strepsirrhines ranges from ~30g (mouse lemurs) to ~7g (indri), while recently extinct lemurs weighted up to ~160kg (sloth lemurs), substantially increasing the variation in the clade. Nevertheless, investigations of body size never accounted for the giant subfossil lemurs, neither the middle-sized loriform (Galagidae and Lorisidae) fossil record. Here we integrate data from 17 fossil and 105 living species in a comprehensive phylogenetic context to investigate the trends of body size evolution on a macroevolutionary scale. We performed body mass ancestral state reconstruction in two contrasting scenarios, one including and the other excluding extinct species. We argue that the exclusion of fossils hampers the interpretation of body size evolution, particularly in more internal nodes and within clades with more extinct representatives. Our results recovered smaller estimates for the root of Strepsirrhines, and supported the hypothesis of convergent dwarfism between members of Cheirogaleidae and Galagidae families, which have experienced at least four major events of drastic reduction of body size (~50%).

Penna, A. is supported by UTSA Presidential Distinguished Research Fellowship

Raising the Roof: Assessing Global Frequencies of Palatine Torus

ROSE L. PERASH, STEPHANIE J. COLE and G. RICHARD SCOTT

Anthropology, University of Nevada, Reno

Palatine torus is an exostosis expressed on the palate and palatal processes on both sides of the intermaxillary suture. While previous research

has studied regional variation of palatine torus expression and global frequencies of mandibular torus, there has been no comprehensive examination of palatine torus on a macro-scale. This study assessed palatine torus presence and absence using a global sample (k=180) of 9,467 individuals from the Christy G. Turner II database. All observations in this dataset were made by CGT, thus obviating interobserver error across this large sample. Palatine torus exhibits a slight sexual dimorphism with total male and female frequencies of 47.7% and 51.8%, respectively. The geographic distribution of palatine torus shows correspondence to variation in mandibular torus among world populations. Palatine torus was most frequent in Arctic populations (79.2%) and least frequent in equatorial samples (28.8%). While data suggest a correlation between northern latitudes and palatine torus, intermediate trait frequencies among Slavic and Uralic populations (50.8%) complicates this generalization. There is, however, a cline in the New World where frequencies decrease from the Arctic to the Pacific Northwest (63.6%), California (57.1%), Mesoamerica (43.8%), and South America (31.0%). Increasing European and African palatine torus data could reveal a similar Old World latitudinal cline. Future studies will combine palatine and mandibular torus frequencies to further evaluate global trends and better explain the hereditary and environmental components of variance underlying oral tori expression.

Impact of gait selection on potential limb interference in primates and cats

BERNADETTE A. PERCHALSKI and ANGEL ZEININGER

Evolutionary Anthropology, Duke University

Primates bring their hindlimbs relatively far forward during a stride compared to non-primates. However, doing so increases risk of limb interference during diagonal sequence (DS) gaits because foot touchdown occurs while the ipsilateral hand is still in contact with the substrate. We test two hypotheses: 1) the primate foot is displaced farther than the hand, resulting in short foot-to-hand distances at hindlimb touchdown in DS gaits, and 2) lateral sequence (LS) gaits release constraints of limb interference. Walking strides were analyzed from video of strepsirrhines, monkeys, apes, and cats. Animals traveled, unrestrained, on terrestrial or arboreal supports. Displacement of the hand and foot between touchdowns and distance between the foot and ipsilateral hand at hindlimb touchdown were standardized to trunk length.

In DS diagonal couplets (DC) gaits, primates displaced the foot an equal or greater distance than the hand, and foot-to-hand distances were short. In primate LS gaits, *Propithecus* displaced its foot significantly farther resulting in no change to foot-to-hand distance; other

ABSTRACTS

primates increased foot-to-hand distance by reducing foot displacement. In the chimpanzee and gorilla walking trot, the foot was displaced a greater distance than the hand and limb interference was avoided by overstriding. In the LSDC gait of cats, foot displacement was greater than hand displacement and foot-to-hand distances were short, similar to primate DSDC gaits, but interference was avoided by the timing of forelimb takeoff. Results suggest that LS gaits reduce risk of interference but do so at the cost of distance traveled by the hindlimb in primates.

This research was supported by the Duke Lemur Center, NSF BCS-1751686, and NSF BCS-1517561.

Anthropology-parasitology-microbiome perspectives on human evolutionary medicine

GEORGE PERRY^{1,2,3} and DIEGO HERNANDEZ¹

¹Anthropology, Penn State University, ²Biology, Penn State University, ³DFG Center for Advanced Studies, University of Tübingen

By studying how our parasites have adapted to human biology and behavior we can learn about our own evolutionary history. Furthermore, many parasites host their own diverse communities of microorganisms. How are the microbiomes of our parasites affected by the human environment, or by how our parasites have biologically adapted to us? Given that parasites can be vectors for dangerous pathogens, these are critical questions. In this talk I will discuss what is known concerning relationships among humans, our parasites, and their microbiomes. Given the topic of this symposium I will focus in particular on cases in which the human niche environment or parasite adaptation to this habitat may be related to pathogen vector competency status. For example, human head and body lice diverged relatively recently at some point (or potentially multiple points) following the innovation of clothing, on which body lice are dependent. Thankfully, head lice are not known competent vectors for any human pathogens. However, body lice are vectors for three pathogenic bacteria, including epidemic typhus, representing a public health problem for homeless populations, for individuals living in refugee camps or prisons, and (based on ancient DNA data) for past human populations as well. To close I will illustrate one approach for integrative anthropology-parasitology-microbiome research via the preliminary stages of head and body lice experiments that we are conducting. Ultimately we aim to differentiate between environmental and genetic components of the head-body louse pathogen vector competency difference and to reconstruct the evolutionary history of any genetic components identified.

Biological distance at the center of the Viking world

EMILY M. PESCHEL¹, BENEDIKT HALLGRIMSSON² and M. ANNE KATZENBERG¹

¹Anthropology and Archaeology, University of Calgary, ²Cell Biology and Anatomy, University of Calgary

This study explores movement and genetic relationships of Viking Age populations through analyses of nonmetric traits of the cranium and dentition. The aim of this study is to better discern the complex relationships between groups during the Viking Age. Specifically, I investigate whether nonmetric morphological variations of two populations, Fröjel and Kopparsvik, from Gotland, Sweden are indicative of gene flow with populations from mainland Sweden, Denmark, and Norway. Although current theories on the political alliances or identity of the people of Gotland during the Viking Age are tenuous, archaeological research so far suggests Gotland was in some way associated with Swedish polities.

Biodistance analyses, using the mean measure of divergence statistic, of both the cranium and dentition indicated that individuals from Fröjel were morphologically distinct from other Viking Age populations, including Kopparsvik. These data complement a previous strontium isotope analysis, which indicated a primarily local population at Fröjel. Kopparsvik, on the other hand, was closely related to populations from southern mainland Sweden and two populations from Denmark. These results suggest that although some successful settlements were isolated from gene flow from the rest of Scandinavia, the island of Gotland as a whole was not separate from the influences of the Swedish mainland. In particular, the Kopparsvik population showed a greater degree of phenetic similarity to populations from southern Scandinavia, including the Mälaren and Skåne regions of modern Sweden, and Denmark. The small biodistances between these areas furthers the notion of dynamic and changing political boundaries during the Viking Age.

The reproductive ecology of the Kinda baboon: female synchrony and male reproductive skew

MEGAN PETERSDORF^{1,2}, JAMES P. HIGHAM^{1,2} and ANNA H. WEYHER³

¹Anthropology, New York University, ²NYCEP, New York Consortium in Evolutionary Primatology, ³Anthropology, University of Massachusetts Amherst

Variation in mating systems is linked to variation in the potential for males to monopolize reproductive access to females, which is influenced by the spatio-temporal distribution of fertile females. In polygynandrous primate species where males can monopolize female reproduction due to low synchrony, males undergo

contest competition over dominance rank and exhibit strong reproductive skew. When males cannot monopolize reproduction due to high synchrony, males undergo stronger indirect competition, may queue for dominance, and exhibit lower reproductive skew. Polygynandrous baboons (yellow, olive, chacma) generally exhibit the former pattern, whereas Kinda baboon (*Papio kindae*) morphology is more reflective of stronger indirect, and weaker male-male contest, competition. We assessed short- and long-term patterns of reproduction in a wild population of Kinda baboons in Zambia. Seven years of birth data show relatively strong seasonality, with 84% of births occurring in a 6-month period. Data from 13 months of daily monitoring also show congruence in the timing of cycling, lactation, and pregnancy as confirmed from fecal hormone analysis. Further, observational data from 45 reproductive cycles (N=13 females) show higher levels of synchrony in mating behavior compared to other polygynandrous baboon species. Finally, we tested the degree of male reproductive skew based on mating success (short-term, 13 months of copulations) and reproductive success (long-term, 7 years of paternity) in this population. Our data are consistent with the hypothesis that Kinda males are under reduced direct and increased indirect male-male competition relative to other polygynandrous baboons.

This research was supported by NSF (DDRIG 1732321, DGE 0966166 to NYCEP IGERT), Leakey Foundation, Fulbright US Student Program, Sigma Xi, SICB, Explorer's Club, ASM, DAAD, AAUW, & NYU MacCracken.

Sacral vertebral count and locomotor behavior of extant primates: An evaluation of selective constraint that locomotion exerts on sacral vertebral formula

AMY L. PETERSON

Institute of Human Origins, Arizona State University

It has been theorized that there is a relationship between locomotor behavior and variance in the vertebral formula of the spine. Previous studies of this have been focused on the thoracolumbar spine as it most directly relates to locomotor posture via flexibility of the lower back. Since the spine is modular, selection on one region of the spine is likely to influence the other regions, whether by homeotic or meristic changes to the spine. Therefore, evidence of selection in the thoracolumbar spine may also be present in the sacrum. Further, because the suspensory primates display lumbar entrapment via anteriorly projected ilia, it can be hypothesized that a greater area of sacroiliac contact is also favored by suspensory taxa, leading to greater number and reduced variability of sacral vertebrae. This study examines the relationship between sacral vertebral count and locomotion in primates, and the degree to which sacral vertebral formula is constrained by locomotor posture. Primates were

ABSTRACTS

assigned broad locomotor categories to capture postural and locomotor data, and the sacral mean and mode were calculated for each locomotor category. Then, to assess the degree of selective constraint on variation in sacral vertebrae, both the standard deviation and the coefficient of variance for both mean and mode were calculated. There is a strong correlation between locomotor category and sacral vertebral mean and mode ($p=0.0077$ and $p=0.00039$, respectively). However, there does not appear to be a difference in selective pressure on the maintenance of sacral vertebral count in any locomotor pattern.

Individual Variation in Long-Tailed Macaque (*Macaca fascicularis*) 'Robbing and Bartering' Practices at Uluwatu Temple, Bali

JEFFREY V. PETERSON and AGUSTIN FUENTES
Anthropology, University of Notre Dame

The long-tailed macaques of Uluwatu take objects from tourists, then exchange them for food through a behavioral sequence termed "robbing and bartering". This cultural behavior consists of three phases: 1) a macaque steals an item (e.g., sunglasses or a hat) from a tourist; 2) it holds onto, and manipulates, the item until 3) a human (e.g., temple staff) gives the macaque food in exchange for the stolen object's return. This study identifies individual variation in patterns of robbing and bartering activities in relation to social network position. Data were collected from two groups at the Uluwatu temple site from May 2017 to March 2018. Here we present data totaling 197 observation hours on 13 sub-adult male macaques. A total of 90 robbing and bartering events were recorded, with 46 from the Celagi group and 44 from the Riting group. All seven sub-adult males in Riting engaged in robbing and bartering at least once, while only four of the six Celagi sub-adult males did so. A one-way chi-squared test revealed significant differences in total robbing and bartering events between individuals at Riting ($X^2=44.773$, $df=6$, $p<0.001$) and Celagi ($X^2=16.783$, $df=3$, $p=0.001$). Furthermore, there were strong positive correlations between individual robbing and bartering frequencies and social network centrality in Riting ($r_s=0.78$) and Celagi ($r_s=0.75$), suggesting that engaging in this cultural behavior may be influenced by social position. This is the first study to investigate the relationship between individual behavioral profiles and robbing and bartering propensity.

This research is funded by a National Geographic Society Waite Grant (WW-082R-17).

Covariance among zygomatic bone shape, eye orbit shape, and the zygomaticotemporal space

ALESHA PETTIT and BRIAN VILMOARE

Anthropology, University of Nevada Las Vegas

The unique position of the zygomatic bone in both hominins and non-hominin primates has remained a focus of research for decades. Because of the unique position of the zygomatic bone, as connected to both the face and cranium, especially the eye orbit, evolutionary changes to this bone might be indicative of other adaptive responses other than those involved in mastication. The zygomatic bone makes up a significant portion of the eye orbit, with implications for vision, but also makes up a significant portion of the zygomaticotemporal space, with implications for mastication. Since both of these functions require a specific shape and structure of the zygomatic bone, we hypothesize that there might be constraints due to functional relationships. In order to examine these relationships, to determine if the different anatomical uses of the zygomatic bone are constrained and/or independent of each other, 28 different facial landmarks were collected from humans, fossil hominins, chimpanzees, and gorillas using CT scans and the data collection software Checkpoint. For this study, specific hypotheses include 1. that the shape of the zygomaticotemporal space covaries with orbit shape, 2. that zygomaticotemporal space covaries with zygomatic thickness, and 3. that the eye orbit covaries with zygomatic thickness. Results indicate that there is a relationship between the zygomaticotemporal space, the eye orbit, and the thickness of the zygomatic bone, suggesting that the zygomatic reflects functional constraints associated with surrounding anatomy.

Science and Anthropology in Underrepresented Spaces: Discovery Program and Full STEAM Ahead

SAMANTHA M. PHILBEN¹, KELSEY D. O'NEILL¹, MARIE VERGAMINI², CLAIRE M. CARTOZZO², JACOB JONES¹ and AMY L. RECTOR¹

¹Anthropology, School of World Studies, Virginia Commonwealth University, ²Integrative Life Sciences, Virginia Commonwealth University

Education beyond required Virginia Standards of Learning (SOL) is integral for the development of deeper levels of student inquiry and engagement with disciplines, like Anthropology, that are not covered in SOL curricula. Anthropology faculty and students at Virginia Commonwealth University participated in two summer programs in Richmond, Virginia, designed to teach students Science, Technology, Engineering, Mathematics, Health Science, and Arts. The Mary and Frances Youth Center Discovery Program focuses on

rising 8th-9th graders, and Full STEAM Ahead is for female middle schoolers. In our programs, students were predominantly from underrepresented populations.

Several modules were taught at both programs to give students a foundation in Biological Anthropology: Becoming Human, Monkeying Around, and Dig Into The Past. Archaeology, Linguistics, and Cultural Anthropology were also introduced, along with Human Evolution, Primate Diversity, and Forensic Anthropology. Students were given a brief lecture from VCU faculty and graduate students on their fields, and then multiple hands-on activities were completed to foster collaboration and approach real-world situations. All activities give students a chance to learn about what makes us uniquely human and understand the important processes of evolution.

The Discovery and Full STEAM Ahead Programs are great outreach tools for Anthropologists to educate students about human and primate diversity in a fun, collaborative environment where students are able to ask questions and shape their understanding of us as a species. For underrepresented students, these programs are especially important in providing early and engaging access to disciplines, like Anthropology, that lack inclusivity in the profession and academy

Nonspecific Stress and Age-at-Death in Colonial Period North Coast Peru

MEGANN PHILLIPS, HAAGEN D. KLAUS and DANIEL H. TEMPLE

Department of Sociology and Anthropology, George Mason University

The relationship between age at death and biological stress experience is vital to consider, especially in the bioarchaeology of Colonial Latin America, where drastic changes in indigenous health and population size followed European contact. The ways in which early-life and adult stress indicators appear in relation to age-at-death can reveal differences in the ways that individuals experienced stress episodes and their long-term impacts.

Here, we test the hypothesis that stress indicator presence is related to decreased survivorship. This study associates stress experience with transition analysis-derived age estimations in Mórrope and Eten (1535-1750), contemporaneous Colonial communities in the Lambayeque region of northern coastal Peru separated by 50 kilometers as well as marked differences in ecogeographic diversity and Spanish influence. Individual biological experiences at these sites are explored via Kaplan-Meier survival curves to assess differences in survivorship related to the presence or absence of nonspecific early-life and adult stress indicators (enamel hypoplasia, porotic hyperostosis, periostosis).

ABSTRACTS

The hypothesis is partially supported. Results show greater mortality risk among males with enamel hypoplasia relative to those without at Eten ($\chi^2 = 8.335$; $p = 0.004$). However, significant differences in survivorship of individuals with and without periostosis at Mórrope ($\chi^2 = 5.116$; $p = 0.024$) show that individuals with periostosis lived longer ($\chi^2 = 47.27$ years) than those without ($\chi^2 = 33.62$ years). These findings illustrate complex biocultural outcomes in Colonial Peru, including possible heightened immune/inflammatory response as a result of infectious disease exposure and increased vulnerability of indigenous males to stress consequences.

Trade-offs between Reproduction and Immunity in Wild Female Chimpanzees (*Pan troglodytes schweinfurthii*) of Kibale National Park, Uganda

SARAH PHILLIPS-GARCIA¹, TONY L. GOLDBERG², MARTIN N. MULLER¹, ZARIN P. MACHANDA³, SAGAN FRIANT⁴, EMILY OTALI⁵, JESSICA CARAG², KEVIN E. LANGERGRABER⁶, JOHN C. MITANI⁷, RICHARD W. WRANGHAM⁸ and MELISSA EMERY THOMPSON¹

¹Anthropology, University of New Mexico, ²Veterinary Medicine & Pathobiological Sciences, University of Wisconsin - Madison, ³Anthropology, Tufts University, ⁴Anthropology, Pennsylvania State University, ⁵Kibale Chimpanzee Project, Uganda, ⁶Human Evolution and Social Change, Arizona State University, ⁷Anthropology, University of Michigan - Ann Arbor, ⁸Human Evolutionary Biology, Harvard University

The female life course differs considerably from males, particularly where investment in reproduction is concerned. Ape mothers spend a lengthy portion of their adult life in energy-demanding phases of gestation and lactation. Heavy investment in reproduction is predicted to leave deficits in other necessary functions like immunity. We characterized gastro-intestinal parasite infection in female chimpanzees, and examined reproductive parameters in concert with infection to determine consequences for health. We predicted females with high parity, regardless of age, or in high-cost reproductive stages of pregnancy and lactation would have higher parasite loads and species richness of infection. Fecal samples were collected from 70 chimpanzees (N=313) from Kibale National Park, Uganda. Samples were processed for parasites utilizing formalin/ethyl-acetate sedimentation and light microscopy. Species richness of infection and intensity of *Oesophagostomum* infection were evaluated with parity, reproductive effort, age, community, and season, in mixed-effects regression models. Parity predicted lower species richness of infection ($F(1/86) = 4.42$, $p = 0.038$), particularly for helminths ($F(1/82) = 5.99$, $p = 0.016$), and was not associated with *Oesophagostomum* infection. High reproductive effort was marginal in predicting higher species richness of infection

($F(1/170) = 2.94$, $p = 0.087$), but revealed no relationship with *Oesophagostomum* infection. Results do not support maternal depletion in wild chimpanzees, despite heavy investment in reproduction. Impacts to health appear limited to bouts of high reproductive effort, without long-term effects. Slow life-history patterns in chimpanzees and other apes may allow recovery of energetic reserves between births, mitigating impacts to health over the female life course.

NSF (1613185), NIH (R01AG049395), the Leakey Foundation, University of New Mexico, University of Wisconsin - Madison, Harvard University, Tufts University, and University of Michigan - Ann Arbor

Social structure, postmarital residence, and mortuary practice at Hualcayán, Peru

CHRISTINE M. PINK¹, EMILY A. SHARP² and REBECCA E. BRIA³

¹Sociology and Anthropology, Metropolitan State University of Denver, ²Center for Bioarchaeological Research, Arizona State University, School of Human Evolution and Social Change, ³Anthropology, University of Minnesota-Twin Cities

The dead, quite often, are situated both physically and figuratively by the living to reify sociocultural constructs. This study focuses on biological relationships in comparison to mortuary practices at Hualcayán dating to AD 1-1450. Hualcayán was occupied by a community of agro-pastoralists, and is situated on the eastern side of the Callejón de Huaylas in the north-central Peruvian Andes. Hualcayán exemplifies a tradition where the dead were considered active participants in the community, and ancestors remained accessible in above-ground, collective tombs. Mourners placed their dead in *machays* on the mountainside, as well as in *chullpas* within the habitation sector of the site. This study addresses the hypothesis that placement of the dead was patterned by kinship, which underpinned community organization.

Cranial nonmetric traits (n=22) were recorded in samples from six tombs at Hualcayán (n=49) and Aukispukio (n=33), a contemporaneously occupied site just to the north. Biological distances, based on trait frequencies, were then calculated between contexts. The relative heterogeneity of trait expression in males and females is also compared to assess postmarital residence pattern.

Results indicate a pattern of biological affinity that relates to spatial organization. Contexts that are geographically proximate exhibit smaller biological distances, with samples from tombs that are upslope versus downslope more closely related to each other, respectively. Aukispukio samples are also distinct from Hualcayán. The data suggest postmarital residence at Hualcayán was matrilocal; however, the pattern is not statistically significant. These preliminary results indicate a dual, or moiety, organization consistent with many other ancient Andean communities.

Estimating Body Mass for Subadults: A Radiographic Study of the Femur

ERIN F. E. PINKSTON^{1,2}, SHEENA GLASGOW¹, ARIEL GRUENTHAL-RANKIN^{1,3}, MARISSA RAMSIER¹ and SHERWIN CHAN⁴

¹Department of Anthropology, Humboldt State University, ²Buffalo Human Evolutionary Morphology Laboratory, Department of Anthropology, University at Buffalo, ³Department of Anthropology, Binghamton University, ⁴Department of Radiology, Children's Mercy Hospital

For decades, anthropologists have attempted to identify unknown decedents via standard aspects of biological profiles, i.e., estimation of sex, age, ancestry, stature, and body mass. However, subadults are still undergoing development of many of the features used to create biological profiles, thus sometimes making profiles more complicated to complete. The femur, which is often relied upon for body mass and stature estimations, does not fully fuse until early adulthood. This study builds upon previous research that focused on the estimation of body mass for subadult remains. Three dimensions of the femur were examined in relation to body mass to determine which might most closely estimate the body mass of a subadult during life. Measurements of the mediolateral neck breadth (n=545), mediolateral head breadth (n=536), and superoinferior head breadth (n=536) were collected from existing hospital radiographs of living subadults ranging in age from 1 year old to 17 years old, along with the weight reported at the time of imaging (+/- 14 days). Reported body weights were collected from the subadult's medical record in PowerChart Pro, and measurements were performed on radiographs using IntelViewer. Data were stored in Research Electronic Data Capture (REDCap). In all cases, there was a highly statistically significant relationship between body mass and the dimensions of the femur ($P < 0.001$, R-square = 0.75-0.87), with the strongest relationship demonstrated by mediolateral neck breadth. This study contributes a diverse dataset to the discussion surrounding the complicated issue of identifying unknown subadults.

Strategic risk portfolios in humans: Are preferences for new between-community social relationships a function of a chronic lack of resources and existing between-community relationships?

ANNE C. PISOR

Department of Anthropology, Washington State University

As has been well-documented in the social sciences, human intergroup behavior is highly plastic. Patterns of resource availability in humans not only incentivize or disincentivize intergroup aggression, but can also incentivize intergroup tolerance and relationship building to

ABSTRACTS

gain resource access. If resource access is a key player, we should expect it to differentially affect interest in relationships that span distance – that is, community boundaries – relative to other kinds of group boundaries (e.g., ethnolinguistic, religious). Further, if an individual's intergroup behavior is a response to her or his needs, we might expect that both an individual's (1a) experience of a lack of resource access, (1b) especially if recurrent, and (2) existing between-community relationships should modulate her interest in forming relationships with extra-community individuals, more than it does her interest in individuals from other ethnolinguistic or religious groups. For two populations of market-integrating horticulturalists living in the Bolivian Amazon, I find that participants who were hard hit by a recent community-wide shortfall or who lack non-local resource access are more likely to prefer a new friendship with an extra-community individual over a same-community individual, especially if they have experienced a lack of resource access in the past. This pattern is more pronounced if participants do not have existing extra-community partners who can provide resource access. I conclude by identifying ways forward for studying plasticity in between-community relationships in humans.

Funding for this study provided by the Max Planck Institute for Evolutionary Anthropology.

An ethological investigation of the evolutionary causes and consequences of fasting in humans

CAITLYN D. PLACEK

Anthropology, Ball State University

Fasting, the abstention of food or drink for a prolonged period, is a widespread practice existing in cultures that vary in religious beliefs and social complexity. Despite the widespread occurrence of fasting and other forms of calorie restriction, the evolutionary causes and consequences of fasting have not been fully elucidated. This systematic review applied Tinbergen's ethological framework to fasting by investigating the proximate causes, ontogeny, fitness value, and evolutionary history of fasting in humans. The following databases were searched to gather information on fasting: Web of Science, Google Scholar, PubMed, and eHRAF. Inclusion criteria consisted of original peer-reviewed research studies, review articles, and cultural/ethnographic accounts. In addition, journal article references were scanned for additional studies that did not emerge in database searches. Relevant information regarding proximate causes, ontogeny, fitness value, and evolutionary history were coded, entered into an Excel file, and qualitatively analyzed to generate themes. Findings reveal that fasting is caused by varied biological, environmental, and cultural factors, however the onset of fasting varies according to religious beliefs and

ritual practices. Individuals who engage in fasting demonstrate increased survivability; however, reproductive outcomes are less clear, despite emic accounts that promote fasting during reproductive years. Overall, given the widespread occurrence of fasting, along with the positive health consequences and cultural evidence for the psychological and social benefits, this study concludes that fasting is an adaptation that enhances survivability via physiological and psychosocial pathways. Future research, however, should focus on the reproductive fitness value for the different forms of fasting.

How much does size dimorphism in *Australopithecus afarensis* reflect changes in male or female body size?

J. MICHAEL PLAVCAN

Anthropology, University of Arkansas, Fayetteville

It is widely accepted that among primates sexual selection acting on male size produces sexual size dimorphism. However, there is also evidence that selection impacting female size can contribute to variation in sexual dimorphism, and several models propose that sexual size dimorphism in *Australopithecus afarensis* may reflect selection for small female size, as opposed to selection for large male size. This raises the question of how much dimorphism can be attributed to changes in female or male size alone. Addressing this issue is important, because dimorphism in extinct species is usually interpreted as evidence for behaviors producing selection on male size. Teasing apart independent male and female contributions to size dimorphism is difficult, though, because a size change in either sex can produce the same degree of dimorphism. Here, a combination of regression and phylogenetic analyses are used to identify where and to what degree dimorphism reflects changes in one or both sexes. Data for skull size and body mass were gathered for 90 species of primates. Changes in female and male size both can impact dimorphism, however, there is little evidence that changes in female size alone produce substantial dimorphism. This accords with a model that changes in male size are partly contingent on changes in female size, assuming that female size reflects an ecological optimum. The results suggest that simple models attributing changes in hominin size and size dimorphism to a single sex do not reflect a more complex interaction between size and selection in both sexes.

Funded by NSF SBR 9616671

Kenyan biology teachers' experiences teaching evolution

BRIANA POBINER^{1,2}, HABIBA CHIRCHIR^{1,3,4}, JOANNE MUNGA², MCKENZIE GRANATA³ and HOLLY FARKOSH³

¹Anthropology, Smithsonian Institution, ²Center for the Advanced Study of Human Paleobiology, George Washington University, ³Biological Sciences, Marshall University, ⁴Anthropology, New York University

In July 2018, we conducted a one day workshop focused on teaching evolution in Mogotio, Kenya. Here, we report pre- and post-workshop survey data collected from the 22 participating current high school biology teachers, who ranged from 2-22 years of teaching experience. All teach evolution in their classes (some from a religious perspective) and most teach human evolution; overall, they were more comfortable teaching evolution of plants and animals vs. humans. Many teachers described teaching evolution as "challenging" (but also "interesting"), and most reported facing concerns from students about learning evolution. Although all teachers described themselves as Christian (and all answered a question about their views on the origin of life with a response involving a deity), they were more concerned about ways to reconcile students' uncertainty about the relationship between science and religion than their own uncertainty. About half already directly address the relationship between science and religion in their classrooms; some actively try to help students reconcile these two ways of knowing the world, while others outline the differences between them. Like published data on teachers in other countries, they overwhelmingly acknowledged a desire for stronger background knowledge about the science of evolution and more engaging teaching materials. Their average pre-workshop MATE (Measure of the Acceptance of the Theory of Evolution) score of 65.71 was lower than studies of science teachers from the US and Korea, but higher than science teachers from Turkey. All teachers reported that the workshop increased their knowledge and comfort with teaching evolution.

This project is supported by the European Society for Evolutionary Biology and Marshall University.

Navigational demand and how it's linked to olfaction and spatial memory in primates

STEPHANIE A. POINDEXTER, REBECCA M. DECAMP and EVA C. GARRETT

Sensory Morphology and Genomic Anthropology Lab, Anthropology Department, Boston University

In the context of primate behavioral ecology and sociobiology, navigational demand is the need to move towards a specific goal over a long distance. The internal motivators leading to long-distance movement in wild environments and the methods individuals use to reach these

ABSTRACTS

locations are diverse. Primate olfaction can aid short distance food selection and in communication with predators and conspecifics, while spatial memory aids primate navigation. Here we focus on the relationships among olfaction, spatial memory and three internal motivators for long distance movement; reaching sleep sites, securing food resources, and monitoring offspring. We ran a series of phylogenetic least-square regressions to identify any links among dependent variables: olfactory receptor gene count (intact and relative), vomeronasal receptor (V1R) gene count (intact and relative), relative olfactory bulb size, and relative hippocampus size, against independent variables: mobile and immobile diet composition, sleep site fidelity, and infant care system. We found that infant care system had a moderate relationship with the number of intact V1R genes ($R^2=0.45$). Relative hippocampus size had a moderate association with mobile and immobile diet types ($R^2=0.59 / R^2=0.50$) and sleep site fidelity ($R^2=0.47$). These results highlight the role that olfaction and long-term memory play in meeting the varying navigational demands wild primates face. Improving our understanding of wild movement and behavior will further illuminate the evolutionary mechanisms contributing to the genetic, morphological, and behavioral relationships seen across primates.

How did the Neanderthal juxtamastoid eminence come into being although it does not exist?

MARCIA S. PONCE DE LEÓN and CHRISTOPH P. E. ZOLLIKOFER

Dept. of Anthropology, University of Zurich

The juxtamastoid eminence is widely recognized as a Neanderthal autapomorphy. Despite its prominent status in Neanderthal taxonomy, however, this structure has been named and defined in various and often contradicting ways. For example, Santa Luca (1978) – often cited in this context – provides a detailed description of the Neanderthal occipitomastoid crest, not the juxtamastoid eminence. Here we study morphological variation in the juxtamastoid region to resolve these inconsistencies. In modern humans, the region between the mastoid process and the foramen magnum displays a sequence of antero-posteriorly oriented elevations and depressions with highly variable expression. From lateral to medial these are the mastoid process, the digastric groove, the juxtamastoid crest, a groove that lodges the occipital artery, the occipitomastoid suture often featuring a crest along its course, and a crest on the anterior part of the inferior nuchal line. In many crania, the region between the mastoid process and the occipitomastoid crest is mediolaterally compressed, such that the occipital artery groove is missing, and the juxtamastoid crest is absent

altogether or coincides with the lateral side of the occipitomastoid crest. This morphological variant is frequent in mid-Pleistocene fossils and modern humans, and the norm in Neanderthals. What is characteristic for the Neanderthals is the small size of the mastoid process, the absence of a juxtamastoid crest, and the inferior position of the occipitomastoid suture and its crest, which is adequately termed "occipitomastoid crest".

The future of craniometrics in archaeology?: A focus on diversity

SARAH A. PONIROS

Archaeology, University of Sheffield

Recent critiques regarding the reliability of craniometric ancestry software, namely CRANID (Wright 2012) and FORDISC (Ousley and Jantz 2005), have contributed to their underuse in anthropological research, especially of archaeological material. This paper responds to these criticisms by presenting a different approach to analyzing craniometric variation, illustrated through a case study of 45 individuals from the late-Roman cemetery at Lankhills, Winchester. Rather than classifying crania, this approach uses Multidimensional Scaling (MDS) and k-means clustering based on Euclidean distance to explore and quantify the diversity within and between groups of crania. MDS and k-means analysis revealed that the individuals were optimally split into three groups representing 40%, 55.6%, and 4.4%, respectively. These methods also identified one significant outlier ($X^2=14.909$, $p=0.0001$). In contrast, CRANID6 classified 52.5% of individuals into a variety of different ancient and medieval European reference groups, 27.1% of individuals into many modern, ancient, and prehistoric Asian, African, and South American reference groups, and could not classify 18.6% of individuals. MDS and k-means analysis were able to quantify intrinsic patterns in phenotypic variation throughout the cemetery independent of, and therefore unbiased by, assumptions based on extant samples whereas the relevance of the classifications offered by CRANID6 is limited. This paper argues that MDS and k-means analysis methods are better suited to answer questions about diversity in the past, and offer more effective complementary data than CRANID6 for multidisciplinary studies which integrate ancient DNA, stable oxygen and strontium isotopes, and evidence of foreign identities through material culture.

Funded by the University of Sheffield Doctoral Academy

Inter- and intra-group variation in infant transport in wild Weddell's saddleback tamarins (*Leontoebus weddelli*) in north-western Bolivia

LEILA M. PORTER¹ and WENDY M. ERB²

¹Department of Anthropology, Northern Illinois University, ²Department of Anthropology, Rutgers University

Tamarins are cooperative breeding primates in which all adult group members participate in infant care. The costs and benefits of allo-maternal care are likely to vary among group members depending on their sex, breeding status, group tenure, and group size. In this study, we aimed to identify the effects of these variables on infant carrying, and to evaluate the costs of this behavior. We studied four groups of *Leontoebus weddelli* comprising 2-3 adult males (both long-term residents and recent immigrants) and a single breeding female who gave birth to twin infants. One group contained a non-breeding adult female. We used group scans and focal animal sampling at 5-min intervals to record data on activity and infant transport ($n=2,537$ focals, $n=3,074$ group scans) on 175 days between August 2013 and September 2014. All adult group members carried infants, but adult males transported infants significantly more than breeding females [$F(2,116)=3.2$, $p<0.05$] and non-breeding females [$F(1,108)=6.2$, $p<0.05$], and resident males transported infants more than immigrant males [$F(1,64)=5.8$, $p<0.05$]. Surprisingly, infants in larger groups were carried less than infants in smaller groups [$F(1, 29)=9.5$, $p<0.01$]. Individuals fed less [$F(1,130)=54$, $p<0.001$], were less social [$F(1,130)=4$, $p<0.05$], and were more inactive [$F(1,130)=54$, $p<0.001$] while carrying infants. As male residents transported infants most, they likely benefit most from this costly behavior, but the uneven distribution of carrying efforts across males suggests differential costs and/or benefits. Additional research is needed to evaluate the benefits different group members receive in return for allomaternal care.

This research was supported by the Leakey Foundation, a Goldberg Research Grant from the Nacey Maggioncalda Foundation, and the Primate Action Fund of Conservation International.

Hohlenstein-Stadel mitochondrial DNA and the "Middle Pleistocene Out of Africa Model"

COSIMO POSTH^{1,2} and JOHANNES KRAUSE^{1,2}

¹Department of Archaeogenetics, Max Planck Institute for the Science of Human History, Jena, Germany, ²Institute for Archaeological Sciences, University of Tübingen, Tübingen, Germany

Ancient DNA has revealed the inconsistency between nuclear and mitochondrial DNA (mtDNA) phylogenies of archaic and modern humans. It has been proposed that the closer similarity of Neanderthal and modern human

ABSTRACTS

mtDNAs compared to Denisovans is the result of a Middle Pleistocene gene flow from Africa into Neandertals. However, the timing of this out of Africa dispersal into Eurasia is largely unknown. We report the complete mtDNA of a hominin femur (HST) displaying archaic features from the Hohlenstein-Stadel cave in southwestern Germany. HST represents a novel deeply divergent mtDNA lineage on the Neandertal branch showing substantial branch shortening. Using a Bayesian statistic framework we date the age of HST to ~124,000 years before present (BP) and its split time from all other Neandertal mtDNAs to ~270,000 years BP. Our analysis of the highly divergent HST indicates a larger Neandertal mtDNA diversity during the Middle Pleistocene, followed by a decline in the Neandertal effective population size. The HST mtDNA further allow us to constrain the boundaries for the time of the putative introgression event from Africa into Neandertals between 410,000 and 270,000 years BP. We show that over a large time interval a complete mtDNA replacement is plausible even if the introgressing lineage represented a minimal proportion of the initial gene pool.

Revisiting Heterozygous Advantage for Phenylketonuria Carriers

AMIEE B. POTTER^{1,2} and MARIANNE J. COOPER²

¹Knight Diagnostics Laboratory, Oregon Health and Science University, ²Anthropology Department, Portland State University

Phenylketonuria (PKU) is an autosomal recessive disorder caused by pathogenic variants in the *PAH* gene that disrupt production of phenylalanine hydroxylase. The result is accumulation of serum phenylalanine leading to clinical symptoms such as intellectual disability and motor disorders in affected individuals. PKU carriers have elevated phenylalanine levels without clinically significant features. PKU prevalence varies by population and region (1 in 2,000 to absent) with carrier rates varying correspondingly. Such high carrier frequency in some populations is unexpected given the morbidity and mortality associated with PKU. The non-random distribution and persistence of high carrier rates suggests positive selection on PKU heterozygotes. Others have proposed that this distribution pattern is the result of heterozygous advantage with chronic exposure to the cereal-borne mycotoxin ochratoxin A (OCA) the selective pressure (Wolff, 1986). This systematic review is a pilot test of the hypothesis that PKU carriers have increased reproductive success in an environment with chronic OCA exposure. Extensive literature review was conducted, integrating existing genetic, medical, and anthropological data to test this hypothesis. Experimental animal models demonstrate chronic exposure to OCA results in reduced fertility, fecundity, and significant fetal loss and that excess serum phenylalanine

completely attenuates OCA's deleterious effects. These data support the hypothesis that PKU carriers experience a heterozygous advantage under chronic OCA exposure. This exploratory systematic review has led to formulation of additional population specific lines of research which may contribute to greater understanding of the adaptive significance of and evolutionary forces creating the extant pattern of PKU carrier frequency distributions.

The making of a paleoanthropologist: The influences of Erik Trinkaus

RICHARD POTTS

Human Origins Program, Smithsonian Institution

Renowned for his meticulous studies of Neanderthals and late Pleistocene evolution, Erik Trinkaus has also influenced students and colleagues by the breadth of his understanding of paleoanthropology. Beginning with his earliest seminars and lectures at Harvard in 1975, Trinkaus urged that a synthesis of human and non-human paleontology, Paleolithic archeology, paleoenvironmental studies, genetics, among other fields, was central to understanding the origin of hominin behavioral adaptations. The relevance of modeling evolutionary processes and integrating African, Asian, and European fossil evidence were also major points in his academic teaching. This breadth encouraged and dared his students to diligently pursue research in the many fields that bear on hominin evolution. Trinkaus's first and perhaps most wayward student thus embarked on a research career that has included the taphonomy, behavior, and paleoecology of East African hominins; modeling and testing of how environmental variability affects the origin of adaptations; integration of East Asian and African evidence on the biogeography of early *Homo*; as well as the discovery, description, and analysis of hominin fossils from Kenya and China. Research findings in each of these domains, exemplified in this presentation, illustrate the inspiration of Trinkaus's synthetic perspective on human evolution. Among many influential aspects of his career, foremost is the power of sustained research and teaching – which has proved a distinct motivation behind the long-term development of international field projects and public learning about human evolution for millions of people based at the U.S. National Museum.

Activity, labor demands, and sex shape sleep patterns among Himba pastoralists

SEAN P. PRALL¹, GANDHI YETISH², BROOKE A. SCELZA¹ and JEROME M. SIEGEL²

¹Department of Anthropology, UCLA, ²Department of Psychiatry and Biobehavioral Science, UCLA

To date, no research on sleep physiology has been completed in a pastoralist population, despite the prominence of this subsistence strategy and the

insight that the variation in the ecology, activity, and behaviors of pastoralists can yield toward better understanding variance in human sleep. To remedy this deficiency, we report actigraphy-based sleep measurements from Himba agropastoralists in northern Namibia. Using 721 days of actigraphy data from 75 participants, we find that this group has among the lowest sleep duration and quality of any population studied, with an average sleep time of 5.5 hours. Exploration of the predictors of onset and offset time, along with activity and recall data, reveal that sex and age specific patterns drive inter-individual variation and reflect differences in the division of labor and decisions related to mating and parenting. In particular, men have shorter, lower quality sleep associated with higher activity levels after sunset and before sunrise. Nighttime mate seeking behavior impacts sleep in men, who suffer frequent sleep loss as a result of late night and early morning travel to visit the households of informal partners. Contrary to predictions, livestock disturbance was not reported as a frequent cause of sleep disruption. Among women, number of child co-sleepers was not shown to impact sleep, but women who share their hut with other adults show benefits to sleep duration and quality. The predictors of variation in sleep quality in this group highlight the need to further study the ecology and behavior in sleep health from diverse populations.

This material is based upon work supported by the National Science Foundation under Grant No. (BCS-1534682)

Morphometric affinities of the Burtele hallux with implications for inferring hominin pedal grasping capabilities

THOMAS C. PRANG

Center for the Study of Human Origins (CSHO), Department of Anthropology, New York University, New York Consortium in Evolutionary Primatology (NYCEP)

The discovery of the BRT-VP-2/73 partial foot from Woranso-Mille, Ethiopia suggests that a Pliocene hominin taxon practiced a different form of bipedalism compared to *Australopithecus afarensis*. Part of this interpretation is focused on the purportedly more primitive, *Ardipithecus*-like grasping hallux of the Burtele foot. However, the hallux grasping capability of the Burtele hominin has not yet been evaluated. This study uses a combination of landmark-based shape analysis and geometric mean-standardized linear distances to characterize the morphometric affinities of the Burtele first metatarsal (MT1) and first proximal phalanx (PP1) in a comparative context of anthropoid primates and early hominins. Multivariate analyses demonstrate that the Burtele hallux is most similar to early hominins, whereas the analysis of the linear data set shows the *Ardipithecus ramidus* MT1 to be most similar

ABSTRACTS

to eastern gorillas. The Burtele MT1 lacks axial torsion and is instead characterized by a mediolaterally narrow plantar half of the proximal articular surface, a head that is moderately domed and mediolaterally wide dorsally, in addition to a dorsally canted PP1 base. The morphology of the Burtele hallux is consistent with hallucal toe-off as observed in most other hominin taxa and its hallucal grasping capabilities may have exceeded those of modern humans, but surprisingly, not those of other taxa such as *Au. afarensis* and *P. robustus*. At the same time, other elements of the Burtele foot preserve characteristics hypothetically primitive for hominins, which is consistent with prior suggestions of taxonomic and functional distinctness from *Au. afarensis*.

This research was supported by a Wenner-Gren Foundation Dissertation Fieldwork Grant.

Assessing craniofacial variation and sexual dimorphism in a skeletal sample from medieval Prussia

CARRISA S. PRITCHARD¹, ARIEL ARIEL GRUENTHAL-RANKIN^{1,2}, ARKADIUSZ KOPERKIEWICZ³, MAREK POLCYN⁴ and MARISSA RAMSIER¹

¹Department of Anthropology, Humboldt State University, ²Department of Anthropology, Binghamton University (SUNY), ³Institute of Archaeology, University of Gdansk, ⁴Department of Anthropology, Lakehead University

The objective of this study is to assess the degree of sexual dimorphism and craniofacial variation exhibited by a skeletal sample from Beżławki, a medieval (14th-15th century) Prussian cemetery site located in what is modern northeastern Poland. During this time period, the Teutonic Knights from Western Europe were actively colonizing the region, therefore the cemetery is likely to include both indigenous Prussians and settlers. This study utilized three-dimensional geometric morphometrics to assess the degree of cranial morphological variation exhibited by a sample of 32 adult (14 probable female, 15 probable male, 3 indeterminate) crania from Beżławki. Cranial landmark data were collected using a MicroScribe; in addition, traditional cranial metrics and nonmetric trait inventories were completed. The data were analyzed using General Procrustes Analysis (GPA) and Principal Component Analysis (PCA) within EVAN, and linear regression and ANOVA within R. The results were evaluated with respect to the isolation by geographic distance hypothesis (IBD), historical records of regional activity during the time period, and comparative bioarchaeological studies of sexual dimorphism and craniofacial variation. Some patterns in the craniofacial data indicated sexual dimorphism and evidence of individual outliers. Prior to this study, there are no published findings focusing on craniofacial variation or sexual dimorphism in this region or population. Thus, the results contribute

to the robusticity of craniometric studies in north-eastern Europe during the late medieval period, generate population-specific data on human morphological variation, and potentially inform historical patterns of migration into the region.

None.

The effects of diet on chewing muscle ontogeny in lemurs

KRISTEN A. PRUFROCK and JONATHAN M.G. PERRY

Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine

The time at which an animal obtains feeding independence is critical to its reproductive fitness. In primates, diet influences the pacing of dental development with folivores having more advanced dental development both in general and at weaning than like-sized frugivores. These differences might be a result of selection for efficient food breakdown. However, it is unknown if other components of the chewing system that are critical to feeding performance follow these dietary trends. Here, growth of the masticatory muscles is examined in lemuriforms to assess the influence of diet on chewing muscle development.

We examined fiber length, mass, and physiological cross-sectional area in the chewing muscles of infant, juvenile, and adult lemurs from four different species (*Varecia rubra*, *Lemur catta*, *Eulemur macaco*, and *Propithecus coquereli*) across the frugivore-folivore continuum. Muscle properties were plotted in growth curves and were regressed against cranial length.

The results show that the majority of chewing muscle growth occurs before lemurs are weaned, although fascial divisions within muscle groups are not fully established until adulthood. There is no clear dietary nor phylogenetic pattern—instead, masticatory muscle growth occurs similarly across the lemur species examined. The same is true when muscle dimensions are considered relative to skull length. These findings suggest that the selective pressures have influenced dental development and masticatory muscle development in different ways. They also suggest that, although pre-weaned lemurs might have the muscularity to feed on solid foods, they might lack the muscle divisions to permit adult-level coordination and efficiency.

This work is supported by the Duke Lemur Center Director's Fund Award to KAP.

Transmigration of impacted mandibular canines in ancient Nubia

ALEXANDRA J. PTACEK¹, BRENDA J. BAKER¹ and KATELYN L. BOLHOFNER²

¹Center for Bioarchaeological Research, School of Human Evolution and Social Change, Arizona State

University, ²Department of Sociology, Anthropology, and Social Work, Texas Tech University

Permanent mandibular canine impaction is uncommon in modern clinical literature (< 1.3%; rates typically between 0.07 and 0.44%), and transmigration occurs very infrequently. The etiology of impaction and transmigration is unclear, and little is known about their occurrence in past populations. Examination of 120 individuals with observable permanent dentition from the Bioarchaeology of Nubia Expedition project area of northern Sudan yielded two instances of transmigrated impacted permanent mandibular canines, producing an unusually high frequency of 1.67%. One example is a female, age 18-20 years, from a Late Kerma cemetery (ASU 15-11, Burial 1; 1500-1200 B.C.). The other is a female, age 60+, from an early Christian period cluster of graves dating to ca. A.D. 600-800 at the nearby Qinifab School site (UCSB 03-01, Burial 69). Both individuals show fully formed permanent right canines embedded in the left side of the mandible. In the younger female, a postmortem break revealed the impacted canine with the crown under the left lateral incisor root. The older adult female exhibits an enlarged right mental foramen and avulsion of the deciduous right canine that potentially affected normal development of the permanent canine, which is visible through a small broken area inferior to the central incisors. Radiographs demonstrate no open pathway for transmigration of the tooth in either individual. These examples are discussed in relation to clinical literature, mandible growth, and permanent canine development to provide insight into canine impaction in this sample and draw attention to this condition in archaeological samples.

Phylogenetic Analysis of Miocene Apes and Early Hominins Using Qualitative and Quantitative Morphological Characters

KELSEY D. PUGH

Anthropology, The Graduate Center, CUNY, New York Consortium in Evolutionary Primatology, (NYCEP)

Phylogenetic relationships among Mid-Late Miocene fossil apes, as well as between fossil and living apes, are poorly resolved. Moreover, the phylogeny of the earliest purported hominins, in particular *Ardipithecus ramidus*, *Ar. kadabba*, *Orrorin tugenensis*, and *Sahelanthropus tchadensis*, have yet to be assessed within the broader context of hominoid evolution. This study examines phylogenetic relationships among fossil and extant hominoids, particularly those that have been hypothesized to be stem or crown hominids and including these early potential hominin taxa. 228 characters (90 qualitative and 138 quantitative) from the skull, dentition, and postcranium were scored separately for males and females of 31 extant and fossil hominoid species. Platyrrhines,

ABSTRACTS

Dendropithecus, and *Ekembo* were constrained as sequential outgroups. Hylobatids were left unconstrained in order to assess the position of taxa relative to the crown hominoid node. Maximum parsimony methods were used to infer phylogeny in the program TNT. Preliminary analyses find *Morotopithecus*, *Afropithecus*, *Equatorius*, and *Nacholapithecus* to be stem hominoids. *Kenyapithecus* and most Eurasian fossil species are found to be stem hominids, while *Ouranopithecus* and *Sivapithecus* group with crown hominids. Support is found for the hominin status of *Ardipithecus*, *Orrorin*, and *Sahelanthropus*. A resolved phylogenetic tree is essential for inferring polarity of key features, hominid ancestral morphotypes including the *Pan-Homo* last common ancestor, and Miocene ape biogeography, which future work will address using the relationships inferred here.

Funding for this project was provided by the NSF (BA-DDRIG-1613434), Wenner-Gren Foundation (9297), The Leakey Foundation, Sigma Xi, and CUNY Doctoral Student Research Grant.

Critical ages of development: Impacts of post-natal early-life stress at the Greek colony Himera (Sicily)

MUSTAFA QUADIR^{1,2}, CAREY J. GARLAND³, LAURIE J. REITSEMA³, STEFANO VASALLO⁴ and BRITNEY KYLE⁵

¹Department of Anthropology, Beloit College,

²Program in Biochemistry, Beloit College,

³Department of Anthropology, University of Georgia,

⁴Archaeological Heritage Section, Superintendency of Palermo, ⁵Department of Anthropology, University of Northern Colorado

The Developmental Origins of Health and Disease approach posits that experiencing early-life stress impacts later-life health outcomes. This research examines how the timing and frequency of enamel micro-defects impacts mortality-risk in 60 skeletons (6th-5thc.BCE) at the Greek colony Himera (648-409 BCE).

Stress during dental development disrupts enamel production, creating micro-defects known as Wilson bands (WB). Enamel is layered systematically and does not remodel; therefore, stress leaves a permanent record on the dentition. This allows for a life-history approach to understanding the effects of early-life stress on mortality. In Greek culture the following childhood life-phases were defined based on cognitive development: Babyhood (approximately 0–1.99 years), Early-Preschool (2–3.99 years), and Real-Preschool (4–6 years). To examine stress during these life-phases, 60 thin-sectioned permanent canines were microscopically analyzed for evidence of WB, and stress chronologies were developed for 15 of these individuals.

At Himera, mean number of WB is 6.3 in adults (90% prevalent; n=39) and 8.2 in individuals who died as subadults (95% prevalent; n=21)

[W=332.5, p=0.3]. Individuals with more defects died younger [$\beta^2=2.9$, p=0.23] and a significant negative correlation exists between age-at-first-defect and age-at-death [p=0.03, r=-0.57]. All individuals experienced most WBs in Babyhood or Early-Preschool; no significant differences existed in mean age-at-death between individuals who experienced more stress in either of these life-phases [W=31, p=0.68]. Stress most frequently occurred between 2-3 years, likely associated with weaning. This study underscores the role bioarchaeology can play in identifying critical-periods during early-life growth and development when stress has the greatest impact on mortality.

This research was funded by National Science Foundation Research Experience for Undergraduates award numbers 1560227 and 1560158, the University of Georgia, and the University of Northern Colorado.

Using a Mouse Model to Study the Evolution of a Bipedal Trait: Characterizing the Regulatory Landscape of Muscles with Divergent MHC I Expression

SAMANTHA R. QUEENO¹, MARIEL YOUNG², DANIEL RICHARD², MATTHEW C. O'NEILL³, TERENCE D. CAPELLINI^{2,4} and KIRSTIN N. STERNER¹

¹Anthropology, University of Oregon, ²Human Evolutionary Biology, Harvard University, ³Anatomy, Midwestern University, ⁴Broad Institute, MIT and Harvard

Recent research suggests that selection for more efficient bipedal locomotion has decreased relative fiber length and increased the expression of MHC I (i.e., slow twitch fibers) in human skeletal muscle over the past 7-8 million years. These traits differentiate humans from many other primates, including African apes. Across mammals the gastrocnemius and soleus muscles of the lower leg, although originating from the same somitic myotome, express divergent levels of MHC I. The soleus predominantly expresses MHC I, whereas the gastrocnemius predominantly expresses MHC II (i.e., fast twitch fibers). Here, we begin by characterizing the regulatory landscape of mouse skeletal muscle tissue to define genomic regions that shape MHC I expression. We dissected gastrocnemius and soleus tissue from three *wt* mice and isolated active genomic regions of open chromatin using ATAC-seq. We used peak calling algorithms to identify thousands of regulatory regions (i.e., open chromatin) that are conserved across 3 biological replicates for each muscle. We identified a subset of regulatory sequences unique to gastrocnemius (n= 259) or soleus function (n= 2571), and 1476 that are active in both muscles. We annotated these sequences using Genomic Regions Enrichment of Annotations Tool and found a significant association with skeletal muscle phenotypes (e.g., actin filament bundle) and disease (i.e., rhabdomyosarcoma). These loci display evidence of differential regulatory activity in soleus and gastrocnemius muscle.

Open chromatin regions specific to the soleus constitute loci of potential importance to the evolution of MHC I expression in human skeletal muscle.

Selection at adenylyl cyclase genes associated with tanning response in populations of the Americas

ELLEN E. QUILLEN¹, NINA G. JABLONSKI² and MARK D. SHRIVER²

¹Internal Medicine - Molecular Medicine, Wake Forest School of Medicine, ²Department of Anthropology, Pennsylvania State University

Facultative, rather than constitutive, pigmentation is the primary means through which human skin interacts with the environment. A robust and persistent tan in response to intense summer ultraviolet radiation would offer protection in a seasonally variable environment and could act as a convergent adaptation to high levels of UVR in equatorial regions of the Americas.

We have recently identified several genes associated with increased tanning response and persistence among 91 Mexican Americans with indigenous American and European ancestry. Association with 2950 candidate SNPs within and upstream of KEGG-defined melanogenesis pathway genes was assessed in PLINK while controlling for basal pigmentation and biogeographic ancestry calculated in FRAPPE. All tests were treated as independent, yielding a Bonferroni-corrected α of 5.6x10⁶. SNPs in eight genes were associated with persistence, including two members of the ubiquitous adenylyl cyclase family found on the surface of melanocytes (*ADCY8* and *ADCY9*). Associated SNP rs378200 (C > T) is an eQTL for *ADCY9* in unexposed skin based on data from the Genotype-Tissue Expression (GTEx) Consortium (p = 0.0022) with the derived allele associated with a reduction in gene expression. *ADCY9* regulates the *MC1R*-cAMP signaling pathway which plays a critical role in the regulation of melanocyte development and survival.

Our previously work indicates that selection at *ADCY9* occurred after the split between East Asian and American populations. Functional studies of adenylyl cyclases suggest that decreased expression may be associated with an increased ability to tan via similar pathways as *MC1R* variant-associated suppression of tanning response.

This work was support by a Post-PhD Research Grant to E. Quillen from The Wenner-Gren Foundation for Anthropological Research.

ABSTRACTS

The Milky Ways: Studying hormones, growth factors and immune function as normal human biological variation in human milk

E. A. QUINN

Anthropology, Washington University in St. Louis

Human biological variation in the phenotype is the cornerstone of modern human biology, evolutionary anthropology, and related studies of human evolution. Few anthropologists however, consider human milk to be part of this phenotypic variation, as we often fail to think about milk as a phenotype or underestimate the measure of biological variation common in human milk. Biological variation is often underappreciated thanks to mental models oriented around commercial infant formula and homogenized cow's milk, both of which present milk composition as static. A general lack of research outside WEIRD populations has contributed to this underestimation of biological variation. However research in the last decade by biological anthropologists and others has greatly increased our understanding of milk phenotypes and the ways in which environmental factors may select for different milk phenotypes. This review examines the different analytical techniques available for the study of human milk composition and how these provide insights into human biological variation. Metabolic hormones, such as leptin and adiponectin, are among the most studied of the milk hormones. Immune factors in milk, such as secretory Immunoglobulin-A have been studied extensively within and outside of anthropology and new assays have greatly expanded the pool of immune factors that can be studied to include lactoferrin, many of the interleukins, TGF- β , sCD14+ and others. This review will provide an extensive literature review and database of the global studies conducted on key milk bioactives and how they illustrate the incredible biological variation inherent in human milk composition.

Quinn's research is supported by NSF BCS #1518013

Isotopic Estimation of Diet and Water Sources at the Archaeological Site of Tumulaca la Chimba, Peru

BREIDY IVAN, QUISPE VILCAHUAMAN¹, BETHANY TURNER-LIVERMORE², NICOLA SHARRATT² and CESAR CHINO³

¹Anthropology, University of California, Riverside, ²Anthropology, Georgia State University, ³Morgue Central de Lima, Ministerio Publico, Peru

This study presents new carbon, nitrogen, and oxygen isotope data to reconstruct diet and water consumption in a diachronic sample of individuals (N=27) from the Moquegua Valley of southern Peru. The collapse of the Tiwanaku State began circa AD. 1000 involving political fragmentation and violence. In the upper Moquegua valley, the late manifestation of Tiwanaku-affiliated culture

and practice is known as Tumulaca, associated with the Terminal Middle Horizon (A.D. 950-1250). However, after A.D. 1250, radical changes occurred in residential space, material culture and mortuary practices, suggesting significant changes in lifeways during the Estuquiña phase of the Late Intermediate Period (A.D. 1250-1470). This research estimates diet and water sources using bone collagen ($\delta^{13}\text{C}_{\text{collagen}}$, $\delta^{15}\text{N}_{\text{collagen}}$) and bone carbonate ($\delta^{13}\text{C}_{\text{carbonate}}$, $\delta^{18}\text{O}_{\text{carbonate}}$) isotope values between Tumulaca and Estuquiña groups at the site of Tumulaca la Chimba in the upper Moquegua valley. It is hypothesized that there is more dietary diversity in Estuquiña groups than maize consumption associated with Tumulaca people. In both populations, $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ results indicate more consumption of terrestrial C_3 plants (tubercles, quinoa, and legumes) rather than C_4 plants (maize). $\delta^{15}\text{N}$ isotopic values also indicate higher trophic levels in Estuquiña people suggesting more access to animal protein such as llama and vizcacha. In addition, $\delta^{18}\text{O}$ values do not vary between the two groups, indicating no change in the source of consumed water or its treatment. Hence, this new isotopic data represents the first attempt in reconstructing diet and water sources among Tumulaca and Estuquiña groups in the upper Moquegua valley.

Diverse and distinct histories of admixture in East African Nilotic speakers

RYAN L. RAAUM^{1,2}, DAN ISABIRYE³ and EDSON I. MUNANURA⁴

¹Anthropology, Lehman College, ²The New York Consortium in Evolutionary Primatology, ³Biochemistry and Sports Science, Makerere University, ⁴Pharmacy, Makerere University

The origin of the Nilotic ethno-linguistic collective is thought to lie in or around what is now South Sudan, where contemporary Nilotic speaking populations show little to no evidence of admixture. These South Sudanese populations are likely to be closely related to the source population(s) of the Nilotic speakers that migrated south into East Africa over the last few thousand years. Nilotic speaking groups in Kenya – in marked contrast to South Sudan – show evidence of extensive admixture. In order to better understand the history of admixture in East African Nilotic speakers, new genome-wide SNP data were generated for two Nilotic ethno-linguistic groups in eastern Uganda: Benet/Sabiny and Teso. These new data were merged with new data from other Ugandan groups and published data to create a working dataset with 1,587 individuals representing 50 populations, with the majority in sub-Saharan Africa and including 8 other Nilotic speaking groups. Population structure was assessed using PCA and ADMIXTURE; formal tests of admixture were conducted using three and four population tests; times of admixture were estimated from linkage disequilibrium

decay distributions; segments of African and non-African ancestry were identified by local ancestry inference; and shared history/drift among populations was estimated using three and four population methods. The results of these analyses reveal distinct histories of admixture in East African Nilotic speakers where linguistic relationships do not correlate with admixture histories, but reflect instead significant gene flow with geographically neighboring populations.

Funding provided by The Leakey Foundation and PSC-CUNY.

Can muscle activity be predicted from surface and internal enthesal morphology?

KARYNE N. RABEY¹, KEVIN G. HATALA^{2,3} and ERIN MARIE WILLIAMS-HATALA^{2,3}

¹Surgery (Division of Anatomy), University of Alberta, ²Biology, Chatham University, ³Center for the Advanced Study of Human Paleobiology, The George Washington University

Many studies use the sizes and shapes of muscle-tendon attachment site (enthesis) surfaces to infer habitual activities. Unfortunately, we do not understand the dynamic co-development of bone and muscle at these sites, and the ways in which age, activity, and other factors affect enthesal growth and morphology. The goal of this collection of studies was to observe the relationships between muscles and their entheses in different taxa (mice, n =50; humans, n =23; non-human primates, n =9), to determine whether consistent patterns are observed in enthesal and corresponding muscle morphology.

Muscle architectural data (e.g., mass, length, PCSA) and histological data (e.g., fibre type) were measured from the forelimb. Surface measurements of entheses (size and shape) and microstructural data of the bone beneath the entheses (e.g., trabecular and cortical density) were also collected. Ages and sexes of all samples were recorded. Activities, activity level, and gait patterns were monitored in mice. Age (in humans) and behavior and age (in mice) were determined to have significant correlations with muscle data (muscle atrophy, changes in fibre type distribution with different activity and increased age). Some trends were found with respect to cortical bone (greater cortical area with increased muscle force) but not trabecular bone. All models failed to show clear relationships between muscle function with the external and internal morphologies of entheses. This research continues to demonstrate that despite the functional plasticity of muscle tissue, those enthesal variables commonly used by biological anthropologists are not informative of muscle anatomy.

This research was supported by the University of Alberta and Chatham University.

ABSTRACTS

Socio-communicative behaviors of West African chimpanzees (*Pan troglodytes verus*) in a savanna habitat at Fongoli, Senegal

ANDREA RABINOWITZ¹, JILL D. PRUETZ² and ANNE BRONIKOWSKI¹

¹Ecology, Evolution, and Organismal Biology, Iowa State University, ²Anthropology, Texas State University

This project researches how the multimodal communicative signals of the Fongoli community of West African chimpanzees (*Pan troglodytes verus*) vary with social relationships. As the sole habituated group of savanna chimpanzees, they exhibit several behaviors of interest to this study, including greater cohesion and lower rates of lethal aggression, potentially related to harsh environmental pressures. Studying the communication of chimpanzees inhabiting an environment similar to that in which hominins evolved provides insight to the evolutionary functions of sociality and communication strategies in our last common ancestor. We proposed that chimpanzees observed to be more communicative would exhibit more or stronger social bonds or be of higher rank, as the ability to successfully communicate with conspecifics would likely increase an individual's fitness. Additionally, the use of visual and auditory signals should vary with social context and strength of bonds between individuals. Observational data was collected on adult males' interactions and communicative signals, and relationships were determined through social network analysis, comparing networks constructed from recordings of gestures and vocalizations with those from social spacing and grooming partners. Evidence of individual variation in signal repertoires was found in relation to males' status in the dominance hierarchy. Observations suggest that higher status was correlated with the production of more signals, most notably for individuals who had recently advanced their position in the hierarchy, as they produced vocal dominance displays at a higher frequency than other males. There also exists preferred partners in joint pant-hoot vocalizations, revealing social affiliations maintained through communicative behaviors.

This project was funded by the National Geographic Society Early Career Grant EC-410R-18.

Allomaternal Care by Conspecifics Influences Activity Budgets of *Colobus guereza* Mothers

DOMINIQUE L. RABOIN¹, ANDREA L. BADEN^{2,3} and JESSICA M. ROTHMAN^{2,3}

¹Anthropology, Rutgers University, ²Anthropology, Hunter College, City University of New York, ³Anthropology, New York Consortium in Evolutionary Primatology

Primate infant care is an energetically taxing time for mothers. Some primate mothers may use allomaternal care (AMC), the care of offspring by conspecifics, to alleviate the burden of infant care by allowing mothers to feed and rest without their clinging infant. The objective of this study was to determine the potential feeding benefits for lactating *Colobus guereza* mothers during AMC. In Kibale National Park, Uganda, seven mother-infant dyads in three groups of guerezas were observed. The average AMC bout-length was 49 seconds (range=638, SD=0.01). Juveniles and subadults handled infants more often than adults (Mann-Whitney U, $p < 0.01$), and females handled infants more often than males (Mann-Whitney U, $p < 0.01$). An infant's distance to mother and the infant's nearest neighbor's age/sex category best predicted the occurrence of AMC (GLMM, $p < 0.001$). Infant-age was the best predictor of the duration of AMC bouts (GLMM, $p < 0.05$), but did not impact the performance of the model ($p = 0.06$). Activity budgets significantly differed when lactating mothers were with and without their infants (Kruskal Wallis, $p < 0.01$). Lactating mothers fed more than other activities when their infants were handled by conspecifics ($Z = 3.49$, $df = 1$, $p < 0.01$). Lactating mothers fed and rested for longer durations during AMC bouts vs. non-AMC bouts (Wilcoxon, $p < 0.001$). No differences were found between feeding rate and metabolizable energy consumed during feeding bouts that took place during AMC vs. non-AMC (Wilcoxon $p > 0.05$, Wilcoxon $p > 0.05$). These results demonstrate the burden of infant care and provide evidence that AMC in *Colobus guereza* gives lactating mothers the opportunity to replenish their energy.

ABC Grant for Thesis Research, Psychology Department, Hunter College; National Science Foundation, (1521528, J. Rothman)

Reconsidering human origins in light of striatal neurochemistry

MARY ANN RAGHANTI and C. OWEN LOVEJOY
Anthropology and School of Biomedical Sciences, Kent State University

An assumption about human evolution is that our unique success is a simple consequence of our extraordinary intelligence. Yet, this fails to reconcile the fact that our lineage embarked on this novel path long before significant brain expansion. In short, we have succeeded where all of our immediate relatives have failed, despite our adoption of an awkward locomotor pattern and its deleterious effect on our ability to engage the arboreal canopy. What could have fueled our clade's success prior to the emergence of *Homo*? It is perhaps ironic that our success may lie in changes within our ancient vertebrate brain and not our expanded neocortex. The neurochemistry of our basal ganglia stands in marked contrast to its homologues in other nonhuman

primates. Our striatum's neurotransmitter profile promotes pro-social qualities including altruism and empathy, as well as the need to conform and cooperate, and these shifts in behavior are consilient with known aspects of the hominid fossil record, especially a precipitous reduction in canine dimorphism. The striatum is intimately associated with the other neurochemical foci including the mesolimbic dopaminergic reward system and current human neurochemistry is consistent with monogamous pair-bonding. Early selection for elements that contributed to such a neuro/locomotor/social complex in our clade would have readily encouraged the adoption of male provisioning of particular females, which would have favored increased reproductive success by encouraging females to manage overlapping offspring. As such, it now appears likely that our "lizard brain" may be more responsible for our success than our mammalian one.

This research was supported by National Science Foundation grants BCS-0921079 and BCS-1316829.

Locomotor ontogeny and trabecular architecture within the hands and feet of great apes

ANNA J. RAGNI

Division of Vertebrate Paleontology, Richard Gilder Graduate School, American Museum of Natural History

Modern primates differ in their ontogenetic strategies as they relate to locomotion. *Pan troglodytes*, for example, becomes more terrestrial through ontogeny, experiencing a corresponding decrease in arboreality. *Gorilla gorilla* slightly reduces arboreal behavior into adulthood, but maintains high terrestriality through ontogeny, while *Homo sapiens* and *Pongo pygmaeus* maintain the same locomotor strategies past infancy. Given this spectrum of locomotor change, this study tests the hypothesis that *Pan*, with substantial locomotor shifts through ontogeny involving changes in substrate use, will show different trabecular bone patterning through ontogeny in the hand versus the foot. This is in contrast to *Homo* and *Pongo*, which are expected to exhibit no differences in trabecular patterning between the hand and foot. *Gorilla* may or may not show differences between the hand and foot. The sample consisted of the capitate, third metacarpal, lateral cuneiform, and third metatarsal of dentally-defined age groups representing juveniles, adolescents, and adults for each taxon ($n = 84$ total individuals). Bones were microCT scanned at approximately 30 micron resolution with scaled volumes of interest placed in each bone. Degree of anisotropy (DA), a unitless quantification of trabecular alignment, was used to assess bony changes related to functional adaptation. The results did not support the hypothesis for *Pan*. No taxa exhibited differences between ontogenetic trends of DA in both bones of the

ABSTRACTS

hand versus the foot. DA only showed significant trends through ontogeny in the lateral cuneiform of *Gorilla* and the third metacarpal of *Homo*. In *Homo*, this may be related to tool use.

Ancient Genetic Analysis of the Northwest Alaskan Birnirk to Thule Archaeological Transition

SARAH L. RAGSDALE, LAUREN E.Y. NORMAN, JUSTIN C. TACKNEY and DENNIS H. O'ROURKE
Anthropology, University of Kansas

As the hypothesized ancestors of the Thule people, the archaeologically defined Birnirk culture lasted approximately 650-1250BP on the margins of the Chukchi Sea. Both ancient and contemporary Inuit and Iñupiat exhibit mitochondrial lineages collectively referred to as "Beringian-specific" haplogroups: A2a, A2b, and D4b1a2a1a. Thus far, only five Birnirk individuals have been sequenced, from the Siberian site of Paipelghak, and they all carry mitochondrial haplotype A2a.

The first hypervariable segment of the mitochondrial D-Loop was sequenced from approximately 20 individuals representing four Birnirk-associated archeological sites from the North Slope of Alaska, Nunavak, Piñiq, Kugok, and Kugusugaruk. These individuals exhibit the expected mitochondrial lineages previously identified in individuals within the Inuit tradition: lineages A2a, A2b, and D4b1a2a1a.

Our results reveal greater genetic diversity in these Birnirk-associated individuals than previously observed from the Siberian site of Paipelghak. Overall, the genetic characterizations imitate the haplotype frequencies seen in the nearby Nuvuk Thule Inuit cemetery, and in the contemporary Inuit and Iñupiat populations. In particular, the presence of haplotypes A2b and D4b1a2a1a expand the known maternal diversity present in Birnirk-associated individuals.

This research was supported by NSF grant #1523160 and the University of Kansas Ancient DNA Research Facility.

When did families in Kodinhi (Kerala State, India) start having unprecedented numbers of twins? Preliminary results

RAVELLA RAKER¹, SARAH RIFAIE¹, AADHYAA SHENOY¹, SAVANNAH EWING¹, EMMA BARAGAR¹, GREGORY SAVARIMUTHU², JANCY FRANCIS², RAYMOND BLAIR¹ and LORENA MADRIGAL¹

¹Anthropology, University of South Florida,

²Anthropology, Kannur University

The people of Kodinhi have become a media attraction due to the high number of twins born in this municipality of 20,000 people. By 2016 the number of twin pairs was 500. The local government welcomed another scientific team (consisting of members of Kerala University of

Fisheries and Ocean Studies and the Institute of Tropical Medicine of the Tuebingan University, Germany) and ours (consisting of anthropologists from Kannur University, and of anthropologists at USF) to do research on causes of this phenomenon. We obtained extensive pedigrees from families located in the different wards within the municipality. We present results on when families started having increased numbers of twins, and whether the increase took place in all areas of the region. Our current sample size is n=873 individuals from 30 pedigrees. The increase in twin births has been precipitous. The frequency of twins vs. singletons in 20-year generations across all families was: 1. 1920-1939: 86%-14%. 2. 1940-1959: 97%-3%, 3. 1960-1979: 86%-14%, 4. 1980-1999: 61%-39%, 5. 2000-2016: 39%-61%. This increase in twinning is highly significant (Fisher's exact test $p < .0001$). We did not detect any location effect on twinning frequency ($X^2 = 0.50$). We are committed to serve the people of Kodinhi in a non-intrusive manner and to collaborate with the other research team. We are also researching the higher mortality for the twins. Our bio-cultural and ethnographic approach will allow us to work with the people of Kodinhi to understand what they describe as a gift from God.

Funded by the NSF EAGER grant #1720091 and by the USF CAS Faculty Travel Grant.

Spatial autocorrelation of bone material stiffness and its implications for skeletal toughness

ANDREW J. RAPOFF¹, W SCOTT. MCGRAW² and DAVID J. DAEGLING³

¹Mechanical Engineering, Union College,

²Anthropology, Ohio State University, ³Anthropology, University of Florida

Variations in bone tissue stiffness over regional and highly localized scales in skeletal elements is common. For example, in the *Macaca* mandible (AJPA 135:100-109), we documented regional variation between the anterior corpus and ramus and variations over millimeter scales within each region. Whether such localized variations have mechanical benefits is not well understood, but localized compliance (e.g., within alveolar bone) may function to reduce peak stress so as to increase the resistance to fracture (toughness), which can be quantified as stored strain energy. In this work, we explore the hypothesis that specific localized variations in stiffness function to increase toughness by increasing stored strain energy. We do this through the implementation of a planar truss model, a two dimensional assemblage of axially loaded struts. The model consisted of a square array of nodes connected by struts to each neighboring node. We generated separate models by populating the elastic modulus of each strut to achieve various degrees of autocorrelation so that the average modulus across all struts was the same for each model.

We loaded each model and determined spatial distributions of stored strain energy as well as the global stored strain energy. We found models with positively autocorrelated ("clustered") distributions of stiffness store more elastic energy than either negatively autocorrelated (e.g., "checkerboarded") or random distributions. Given empirical data that the distribution of elastic modulus tends toward positive spatial autocorrelation, we conclude that spatial variation of elastic modulus represents a material strategy for enhancing toughness in skeletal elements.

Problem-solving with regard to age in Barbary macaques

EVA-MARIA RATHKE and JULIA FISCHER

Cognitive Ethology Laboratory, German Primate Center

Problem-solving and exploration behaviour improve an individual's ability to adapt to a changing environment. The underlying cognitive functions of these traits decline during the normal processes of aging in both humans and nonhuman primates. The main goal of our study was to investigate how age influences different aspects of problem-solving: inhibition control, behavioral flexibility and persistence. Therefore, we conducted cognitive tests with Barbary macaques (*Macaca sylvanus*) at La Forêt des Singes in Rocamadour, France. We used three transparent plastic boxes baited with a peanut (without the possibility to obtain it in the persistence task). We investigated if (i) adolescent and older monkeys needed more time to succeed in the inhibition control task than monkeys during adulthood, if with increasing age, (ii) monkeys needed more time to change their strategy and (iii) became less persistent in exploring. We used generalized additive models to test the impact of age on the time monkeys manipulated the boxes until they succeeded or in case of the persistence task until they quit. Results showed that adolescent and older monkeys did not differ from adults ($p > 0.05$). There was no indication that older monkeys needed more time to change their strategy compared to younger ones ($p > 0.05$). Yet, with increasing age monkeys were less persistent in exploring the box ($p < 0.05$). Contrary to our expectations, age did not seem to have a strong impact on problem-solving behaviour. How other factors like sociality and rank might affect age-related cognitive performance remains to be investigated.

The study was funded by the Deutsche Forschungsgemeinschaft (DFG, German Research Foundation, project number 360742713)

ABSTRACTS

Population history of southern Italy during Greek colonization inferred from dental remains

HANNES RATHMANN^{1,2}, BRITNEY KYLE³, KATERINA HARVATI^{1,2}, RICHARD POSAMENTIR⁴ and GIULIA SALTINI SEMERARI⁴

¹Paleoanthropology, University of Tübingen, ²DFG Center for Advanced Studies 'Words, Bones, Genes, Tools', University of Tübingen, ³Anthropology, University of Northern Colorado, ⁴Classical Archaeology, University of Tübingen

The ancient Greek colonization of southern Italy was a pivotal encounter in antiquity and has greatly impacted the cultural heritage of the region. However, researchers have argued for decades about the colonist's genetic contribution. Especially debated is the scale of the migration from Greece and the degree of admixture between Greek colonists and indigenous populations. To address this debate, we collected an osteological dataset comprising 481 human skeletons from six archaeological sites located along the Gulf of Taranto, southern Italy, dating to precolonial (900-700 y BC) and postcolonial periods (700-200 y BC). For both time periods, we inferred population structure by performing individual-level biodistance analyses based on a comprehensive trait battery of mixed metric and non-metric dental phenotypes. Permutational multivariate analysis of variance (PERMANOVA) and isolation-by-distance (IBD) models were used to reconstruct regional mobility. Naïve Bayesian classification was used to identify individual ancestries. Results show that southern Italy during Greek colonization became a place of high mobility and was hosting ~ 10 % Greek newcomers and their descendants. Individuals of Greek ancestry were equally distributed across Greek colonies and indigenous Italic settlements. Our results have important implications for future research on the Greek colonization as they support a gradual colonization model with substantial involvement of local populations and contradict the theory that Greek colonies were homogenous enclaves within conquered territories. Our study provides a conceptual template for future bioarchaeological research on the Greek colonization of southern Italy and promotes interdisciplinary synergy between the academic fields of classical archaeology and bioarchaeology.

This research was funded by the Gerda Henkel Foundation, by the State Ministry for Science, Research and Arts of Baden-Württemberg, Germany, and by the German Research Foundation (DFG FOR 2237).

A test of Wescott's second cervical vertebra sex estimation method on a middle-aged to senescent sample

KIMBERLY M. RAYMOND, DANIELLE K. JULIEN, LINDSAY C. COOPER, KALI A. WEST and ELIZABETH A. DIGANGI

Anthropology, Binghamton University, State University of New York

Forensic anthropologists and bioarchaeologists are often faced with fragmentary remains or incomplete skeletons. Such cases require the creation of sex assessment methods on a variety of bones. The Wescott (2000) method involves eight measurements of the second cervical vertebra, used to discriminate between sexes. Wescott created 5 discriminant function equations to classify a sample of 153 modern individuals by sex; correct classification occurred 76.9% of the time. In a validation study by Bethard and Seet (2013), Wescott's discriminant functions were found to correctly discriminate sex over 80% of the time. Here, we attempt to further validate this method on a sample of primarily older adults (n=45; 24 females, 21 males; age-at-death 54-90). These individuals were donated to an anatomical supply company and used by our laboratory primarily for a separate project. Preliminary data analysis demonstrated that Wescott's equations 1, 2, 4, and 5 were able to correctly assess the sex of approximately 60% of the sample. Overall, function 3 classified individuals correctly 68% of the time. When examining females, functions 1 and 2 correctly classify 50% of the sample, while function 4 correctly assessed 84% of the sample. Discriminant function 4 correctly classifies males 30% of the time while functions 1, 2, 3, and 5 classify correctly 89% of the time. Based on analysis, we recommend that practitioners use function 3 for highest accuracy due to its performance when sex is unknown. Functions 1, 2, 4, and 5 have a lower success rate and should be further tested.

An award from the National Institute of Justice (2016-DN-BX-0155) supported a larger project involving the procurement of the samples used here.

A Retrospective Analysis of Qualitative Postmortem Interval Estimation in Louisiana

SOPHIA I. RECK

Department of Geography and Anthropology, Louisiana State University

Forensic anthropologists are often called upon to assess the postmortem interval (PMI; i.e. time since death) of remains in varying states of decomposition and skeletonization. These assessments rely on familiarity with general taphonomic sequences and processes, in addition to familiarity with how these processes present in local environments and conditions. For some regions, data on local processes are available from studies conducted at outdoor

decomposition research facilities. The goal of this study was to examine the application of previously collected taphonomic data on individuals in Louisiana through a retrospective analysis of forensic casework. It was hypothesized that unique patterns of taphonomic sequences and processes would be observed, even though Louisiana shares a climatic zone with multiple existing decomposition research facilities. The study sample was selected from the case files of the Louisiana State University Forensic Anthropology and Computer Enhancement Services Laboratory and spanned an 11 year period. Only individuals with both known PMI and PMI estimates were considered (n=79). Results show that actual PMI fell within the range of the estimated PMI for 69/79 cases (87%). Of the 10 that did not, nine cases underestimated PMI and one case overestimated. Deposition environment and other variables were further examined to assess relationships between the state of decomposition, actual PMI, and estimated PMI. The diversity in decomposition stages upon discovery under varying conditions support the need for further research regarding the characterization of decomposition in Louisiana; this could be achieved with the development of an outdoor decomposition research facility in this state.

Biogeography and paleoenvironments of *Paranthropus* and early *Homo*

AMY L. RECTOR

Anthropology, School of World Studies, Virginia Commonwealth University

Paranthropus and early *Homo* overlapped in time and space, and potentially both first appeared in the fossil record concomitantly with increased climatic seasonality. *Paranthropus* in eastern and southern Africa likely further differed in diet, niche space, and ecological context. Here, paleocommunity analyses of *Paranthropus* and early *Homo* faunal assemblages are combined with biogeographic analyses to investigate the paleoecological contexts of these genera, and how broad-scale African biogeographic patterns likely influenced their diverging habitats.

To compare paleoecological contexts, associated assemblages of large mammals from 20+ South and East African *Paranthropus* and *Homo* sites were analyzed using a community approach. Multivariate correspondence analyses compared fossil communities to 191 extant communities in modern African habitats with known climatic variables. Using presence/absence data of 243 extant large mammal species and their locomotor and dietary adaptations, modern communities were described in terms of abiotic data, and this variability was used to retrodict ecological parameters for *Paranthropus* and

ABSTRACTS

Homo. Biogeographic analyses included genus-level calculations of Dice and Simpson's faunal resemblance indices of >75 eastern and southern African fossil assemblages spanning the last 7+ million years.

Multivariate analyses suggest that eastern and southern African *Paranthropus* sites were characterized by different levels of temperature and rainfall seasonality, and that the pattern for early *Homo* is also unique. Further, pan-African biogeographic patterns indicate that habitats, seasonality, and lineages began diverging between eastern and southern Africa ~3 million years ago. *Paranthropus* and *Homo* existed in significantly different ecological and biogeographic contexts.

The development of male chimpanzee reproductive strategies

RACHNA B. REDDY¹, KEVIN E. LANGERGRABER², AARON A. SANDEL³ and JOHN C. MITANI¹

¹Department of Anthropology, University of Michigan, ²School of Human Evolution and Social Change, University of Arizona, ³Department of Anthropology, University of Texas at Austin

Male animals compete for mates, with high-ranking males typically reproducing. Nevertheless, low-ranking males of many species still reproduce by employing alternative mating tactics. For male chimpanzees, high rank contributes to paternity success, but social interactions with females also play a role: males are more likely to sire infants of cycling females to whom they are more aggressive, and infants of non-cycling females with whom they more frequently associate. These female-directed alternative strategies may be especially important for young males who are subordinate to prime adults. We conducted a 17-month study on a cohort of 20 adolescent (9 - 15 years) and 10 young adult males (16 - 20 years) and used long-term paternity data to determine how social interactions with females and female parity influenced young male reproduction. Adolescent and young adult males used a combination of affiliation and sexual coercion to mate with specific females. These strategies changed during development. The impact of aggression on mating success increased with age, while the impact of affiliation and the frequency with which males mated nulliparous females decreased with age. Long-term paternity data showed the youngest fathers often sired offspring of nulliparous females and that rank influenced paternity success only for offspring of parous females. Together, these results suggest young male chimpanzees use a combination of affiliation and aggression to achieve paternity success with females who are

less attractive to older, higher-ranking males. They add to a growing body of evidence on how male reproductive effort may change across the lifespan.

This research was supported by the National Geographic Society, the National Science Foundation (BCS-1540259; DGE-1256260), the Nacey-Maggioncalda Foundation, the Louis. B. Leakey Foundation, and the University of Michigan.

Childhood morbidity and mortality in the rising urban environments of the Industrial Era

SARAH REEDY

Anthropology, University of Massachusetts, Amherst, Sociology, Criminal Justice, and Anthropology, Quinnipiac University

The Industrial Era of Europe (18th - 20th centuries) was a time of rapid urbanization, political instability, and increased inequalities. Societies were not prepared for the rising sanitation, dietary, and medical needs of the populations leading to increased diseases, malnutrition, and increased mortality. Children, some of the most vulnerable members of society, would have been particularly at risk of these environmental stressors.

This study examines morbidity and mortality risks of children (0-18 years) from varied SES backgrounds. The presence of stress markers and Kaplan-Meier analysis were used to test three hypotheses: 1) children from low SES backgrounds will display more evidence of stress and greater risk of death; 2) boys will display greater incidences of stress with increased mortality risk; 3) those with stress markers will exhibit a greater risk of mortality, particularly those with accumulated stress.

Chi-square analysis indicates lower SES children exhibit higher frequencies of stress markers, but similar risk of death to those in the middle and high SES. Overall, boys exhibit higher frequencies of pathologies and higher mortality risk than girls reflecting biological female buffering. However, adolescent girls and young children (0-5 years) display more CO and PH, reflecting maternal stress and cultural buffering of older boys. Those with CO and PH had the greatest risk of death, yet those with LEHs survived best suggesting those who survive acute moments of stress have better survival than those who suffered accumulated metabolic stressors.

This research was funded through the Cultural Heritage in European Societies and Spaces (CHESS) Program, University of Massachusetts, Department of Anthropology, NSF grant IIA-1261172.

The impact of locomotor function and phylogeny on biomechanical neck length of the femur

THOMAS R. REIN

Anthropology Department, Central Connecticut State University

Biomechanical neck length of the femur and its potential association with abductor capability of the gluteal muscles has been widely examined in studies of hominin locomotion. Additional research is needed on non-hominin primates, however, due to the limited number of species directly compared and the conflicting conclusions drawn from previous studies of extant hominoids. The main objective of this study was to compare primate species characterized by a diverse range of locomotor repertoires to evaluate the potential functional and phylogenetic signals present in biomechanical neck length. Measurements were collected on the proximal femora of 30 extant species, and each taxon was assigned to a locomotor and phylogenetic category based on published data. Body mass was estimated using published predictive models that are based on measurement of the superior-inferior height of the femoral head. Mann-Whitney pairwise comparisons with Bonferroni correction were performed using both sets of categories to test the influence of phylogeny and locomotor function on relative biomechanical neck length. Most phylogenetic groups were found to be comparable in terms of relative length of the femoral neck. Species adapted to either bipedalism or leaping had the relatively longest femoral biomechanical neck lengths, whereas taxa that perform locomotion requiring the greatest degree of hip mobility were characterized by the relatively shortest biomechanical neck lengths. The results of this study demonstrate a strong correspondence between biomechanical neck length and locomotor adaptation regardless of phylogenetic position and have important implications for assessing locomotor adaptation based on the primate fossil record.

This study was funded by the Volkswagen Foundation (86 049) and a CSU-AAUP Faculty Research Grant.

Telomere length analysis from minimally invasively collected samples: promises and pitfalls

PETER H. REJ¹ and DAN T.A. EISENBERG^{1,2}

¹Anthropology, University of Washington, ²Center for Studies in Demography and Ecology, University of Washington

Telomere length (TL) is a dynamic genetic biomarker of aging that is of increasing interest. Venous whole blood is the most common and well-validated source of DNA in studies measuring

ABSTRACTS

TL. In order to reduce donor burden, costs, storage requirements, and increase "field-friendliness," more researchers are analyzing TL from minimally invasively collected samples (MICS).

Since TL measurement is difficult and results are often noisy, we conducted a systematic literature review to examine studies using MICS to measure TL. Particular attention was paid to measures of external and internal validity. We found nine studies that used DNA extracted from dried blood spots (DBS), 32 saliva, and 15 from buccal swabs. To assess external validity we examined published correlation values between MICS TL, blood TL, and age. Though getting sufficient DNA yields from DBS was a consistent problem, DBS and venous blood TL correlated strongly (two studies: $r=0.84-0.86$). Saliva TL-blood TL correlation values were slightly weaker (three studies: $r=0.48-0.72$), while correlations with buccal TL were heterogeneous (two studies: $r=NS-0.74$). Age consistently predicted shorter DBS TL, but inconsistently predicted saliva and buccal TL.

Overall, these studies show that MICS can be carefully employed for TL studies. However, caution is warranted because TL dynamics vary by cell type and even when perfectly measured, TL may have different biological meaning in MICS versus venous samples. Further, TL measurement is difficult and we advise against assaying TL without validation in new laboratories, especially from diverse sample types.

Supported by NSF BCS-1519110.

Predation at Denisova cave during the Middle Paleolithic: a story of human and beasts

WILLIAM RENDU^{1,2}, SERGEY VASILYEV³, MAXIM KOZLIKIN³, MALVINA BAUMANN¹ and MIKHAIL SHUNKOV³

¹PACEA, cnrs, ²Department of Anthropology, NYU, ³IAET, Siberian Branch of the Russian Academy of Sciences

The Altai region has become a major laboratory for studying the subsistence strategies developed by different human species for the exploitation of the same environment. Denisova cave occupies a specific place in this topic with its stratigraphy yielding occupations attributed to Neanderthal and Denisovian species.

Previous paleontological analyses underlined the existence of numerous large carnivores accumulating (*Ursus arctos*, *Crocuta Spealaea*, *Canis Lupus* etc..) in the faunal spectrum raising questions about the origin of the faunal stocks for the different stratigraphic units of the Eastern Chambers. This paper proposes the first zooarchaeological and taphonomic analyses of the macro-mammals remains, with two main objectives: firstly to discuss the respective contribution

of human and carnivore to the different layers and, secondly, to approach the ecology of the different human species and their seasonality of occupation.

Our results underlined major evolution in the respective contribution of human and carnivore through the stratigraphy. Preys hunted by carnivores are the same during the whole sequence, Human changed their selections strategies through time. The carnivore Human relationship appears to have been more complex than previously evaluated: numerous exploitation marks on every carnivore species different confirm their exploitation for furs and that they were integrated in the animal raw materials used by the different human groups.

Our papers brings new insights on the strong interactions between past human populations and their faunal environment. It helps to better characterize the human ecology at the sunset of the Middle Paleolithic in the Siberian Altai region.

Part of this research was funded by CemeNTAA program from the Agence Nationale de la Recherche (French National Research Agency) - ANR-14-CE31-0011 [Rendu] and by the LIA Artemir

Tracking early human migrations through the Americas

SAMUEL R. RENNIE¹, SILVIA GONZALEZ² and JOHN JOHNSON³

¹Department of Archaeology, Anthropology & Forensic Science, Bournemouth University, ²School of Natural Sciences and Psychology, Liverpool John Moores University, ³Department of Anthropology, Santa Barbara Museum of Natural History

Palaeomigration into and within the Americas is one of the most debated and thought-provoking areas of human history. However, well preserved human osteological research material is scarce, especially along the pacific coast and inland Mexico.

This preliminary study revolves around the comparison of a Coastal Californian sample, Chumash, with data from South America, Central America and other North American samples.

Craniometric data for the Chumash were collected using the definitions made by Howells to help with comparisons with other data. The remaining samples were sourced from peer-reviewed published articles and books. Comparative samples include: Coahuila, Central Mexico, Archaic and Paleo Colombian, Lagoa Santa, Arikara, Santa Cruz, and Peru. To utilize the full data set ($n=448$), missing data were replaced by running a k Nearest-Neighbor (kNN) analysis.

The results from the PCA and other analyses show a clear separation between groups. For the PCA separation between the samples is being driven by several cranial measurements: GOL, NOL, BBH, XCB and XFB.

It is possible that PC2 shows how the cranium changed through time as the Californian Coast, Mexican, and South American samples are ≥ 1 kya whilst the samples from Peru, Santa Cruz, and South Dakota are < 1 kya.

What is interesting to see is the separation between the Chumash from 4-5kya and those from Santa Cruz < 1 kya. This tells us that the older sample from the Channel Islands belonged to the Paleoamerican stock then subsequently disappeared being replaced by the more modern Amerindian morphology.

Evolutionary and developmental perspectives on human toe reduction

PHILIP L. RENO

Bio-Medical Sciences, Philadelphia College of Osteopathic Medicine

Digit lengths are highly variable among primates, and humans are distinguished by short fingers and particularly short toes. The dramatic reduction in toe length has been hypothesized to limit the excursion and mechanical work of digital flexors during toe-off. Finger reduction has been alternatively proposed to be a correlated response for selection on toe length due to shared gene expression during development or the direct effect of selection for tool use and manipulative behaviors. If the former hypothesis is correct, then human fingers and toes should show similar patterns of digit reduction. Lengths of the proximal (PP) and intermediate (IP) phalanges of the fingers and toes was collected for a large sample of extant and extinct anthropoids. Proximal articular widths and metrics from the carpals and tarsals were used for size normalization. Despite great variation in PP and IP lengths of both the hands and feet, the IP/PP proportion within each digit is remarkably consistent across anthropoids. Human toes are an exception. The IP becomes progressively and disproportionately shorter from digit 2 to digit 5. In fact, lateral IPs are frequently fused to the terminal phalanges or missing altogether. IPs are also short in Neandertals and *Homo naledi*, but typical anthropoid proportions are retained in *Ardipithecus ramidus* and *Australopithecus afarensis*. In light of recent work that demonstrates the remarkable specificity of gene regulatory elements to independently target fore- and hind limb development, it is likely that human fingers and toes evolved independently in response to distinct selection pressures.

Support provided by NSF BCS-1638812 & IOS-1656315.

ABSTRACTS

A new mouse model predicts the evolutionary effects of an ancient deletion polymorphism in the human growth hormone receptor gene

SKYLER D. RESENDEZ, MARIE SAITOU, KIRSTEN DEAN, CHRISTINE E. SCHANER TOOLEY, XIUQIAN MU and OMER GOKCUMEN

Biology, The University at Buffalo

The growth hormone receptor (*GHR*) gene codes for the central receptor protein for the growth hormone pathway. As such, this gene is highly conserved among mammals. Despite this, the third exon of the *GHR* gene is deleted in approximately 50% of the human genomes. The deleted variant (*GHRd3*) has been associated with human height, longevity, and metabolic markers. Our lab has previously reported that this deletion is also found in the sequenced Neanderthal and Denisovan genomes. This suggests that *GHRd3* has been maintained for at least 400,000 years in the human lineage. Based on population genetic analyses, we found evidence of non-neutral evolution acting on variation in this locus in humans. To investigate the phenotypic impact of *GHRd3*, we constructed a CRISPR-Cas9 based mouse model carrying the orthologous exon 3 deletion. We showed that there is a differential rate of growth between *GHRd3* and wildtype in male mice. Moreover, RNA-sequencing analyses showed that *GHRd3* affects the expression of genes which are significantly enriched for metabolic processes. Based on these data, we hypothesize that *GHRd3* has been maintained in a frequency-dependent manner in the human lineage as a response to feast-famine cycles.

Examination of nutritional, endocrinal, and metabolic effects on skeletal development and maturation

KATHRYN REUSCH and JASLEEN GUERRERO

Department of Sociology & Anthropology, Metropolitan State University of Denver

A great deal of attention is paid to metabolic conditions within palaeopathology, but not as much attention is paid to the endocrine system, its effects on the skeleton, and its interactions with the metabolic system. These two systems are closely interlinked, and changes to one frequently cause reciprocal effects in the other, leading to destructive changes to the skeleton which can persist into old age. This paper examines the hormones critical to growth, development, and sexual differentiation and how they are affected by over-, under-, and sufficient nutrition. It then investigates how hormones and nutrition interact to affect skeletal growth, development, and maintenance, as changes to hormones or interrupted growth periods are likely to affect osteometric measurements, body proportion ratios, and skeletal biomechanics. Modern clinical data related to anorexia and obesity have been used as substitutes for under- and over-nutrition, respectively,

on the assumption that basic metabolic and endocrinal processes have remained consistent over the last several millennia. The clinical data are compiled into a list of traits which can be scored during examination of skeletal remains to determine the likely nutritional status of individuals, similar to the scoring of age and sex-related traits in Buikstra and Ubelaker's Standards. This list of traits is then used to evaluate the palaeopathological data published on the post-medieval Spitalfields Crypt known skeletal population to test its accuracy and usefulness. This will provide a useful new method to interrogate the metabolic and endocrine status of past populations.

The world-wide distribution of the C677T allele of the MTHFR gene

LUCIO REYES¹, FRANCISCO GONZALEZ-HERNANDEZ², DAVID GODFREY¹, MARIE JEAN¹, MANVIE BIDAL¹ and LORENA MADRIGAL¹

¹Anthropology, University of South Florida,

²Engineering, University of South Florida

Previous researchers have attempted to describe and explain the Eurasian clines of the T mutation in the MTHFR gene, involved in the metabolism of folate and homocysteine. That this mutation is frequent despite its association in the homozygote state with numerous cardiovascular, fertility and health problems has prompted authors to propose that the polymorphism may be a yet-unrecognized balanced polymorphism (Wang et al. 2012). Loudly missing in previous work are Native American populations. In this paper, we present results of a World-Wide overview of C677T allele frequencies in indigenous populations. Our sample consists of n=176 populations with a total of 33,824 individuals. The region with the highest mean frequency of the T allele (=0.6) is Mesoamerica, where in several populations there is a significant excess of TT homozygotes. In Eurasia there are two areas with relatively high frequencies of the T allele: the Mediterranean (=0.35) and East Asia (= 0.31), in neither of which is the excess of TT homozygotes significant. Our results indicate that if natural selection is responsible for the distribution of this allele, then it is acting in a different manner in Eurasia and in Mesoamerica. The Mesoamerican results have public health implications, as these indigenous populations may have been able to maintain this polymorphism with their traditional diet. However, as they enter the cash economy and adopt a Western diet, the TT homozygotes may be at the medical jeopardy documented in the medical literature for TT homozygotes in Eurasian patients.

Bony labyrinth morphology of the Broken Hill, Eyasi I, and Kabua I hominin fossils

HUGO REYES-CENTENO¹, CHRIS STRINGER² and KATERINA HARVATI^{1,3}

¹DFG Center for Advanced Studies "Words, Bones, Genes, Tools", University of Tübingen, ²Centre for Human Evolution Research, Department of Earth Sciences, Natural History Museum, London, ³Paleoanthropology, Senckenberg Centre for Human Evolution and Palaeoenvironment, University of Tübingen

Despite consensus for the central role that Pleistocene Africa had in the diversification of our species and the emergence of modern human anatomy, the continent's sparse human fossil record is a limitation for reconstructing the mode and timing of these processes. Here we present a comparative analysis of the inner ear morphology of Broken Hill (Zambia), Eyasi I (Tanzania), and Kabua I (Kenya)—hominin fossils often hypothesized to be part of, or ancestral to, the *Homo sapiens* lineage. We conduct morphometric analyses on micro-CT scans of these fossils and compare their bony labyrinth shape to Pleistocene hominins from Africa and Eurasia (N=64), as well as to a recent Holocene population from Eastern Africa (N=16). In addition, we quantify their morphological affinities in a series of univariate and multivariate analyses, including principal component and discriminant function analyses. Our results highlight the diversity of inner ear shape in African Middle and Late Pleistocene hominins. Eyasi I exhibits affinities to Late Pleistocene and Holocene modern humans (posterior classification probability up to 94%), associated with larger anterior and posterior bony labyrinth canals relative to the lateral canal. Broken Hill and Kabua show more variable affinities, exhibiting a combination of features more commonly found in the inner ears of Middle Pleistocene hominins from Eurasia. We discuss these results in light of recent evolutionary models emphasizing the complexity of population isolation and expansion within Africa and Eurasia and between the continents.

This study was supported by the German Research Foundation (DFG grants FOR-2237 and INST 37/706-1), the Cavella Foundation, and the Human Origins Research Fund.

Mitochondrial DNA Demonstrates the Significance of a Western Gateway in Uganda for Eastern Chimpanzee (*Pan troglodytes schweinfurthii*) Gene Flow

ALICIA M. RICH¹, CHRISTOPHER A. SCHMITT¹, MICHAEL D. WASSERMAN², KEVIN D. HUNT² and FREDERIKA A. KAESTLE²

¹Anthropology, Boston University, ²Anthropology, Indiana University

Toro-Semliki Wildlife Reserve, Semliki National Park, and Rwenzori Mountains National Park form a Western Gateway in Uganda: a potential

ABSTRACTS

location of transboundary gene flow between the eastern chimpanzee (*Pan troglodytes schweinfurthii*) stronghold of DRC, the rest of Uganda, and into Rwanda, Burundi, and Tanzania. We used mitochondrial haplotype diversity to examine gene flow between protected areas (PAs), with special attention paid to four "gateway" PAs. We sequenced a 299-bp segment spanning HV1 of the mitochondrial genome for 80 individuals sampled in Toro-Semliki and compared them to published chimpanzee sequences from both closed-forest and savanna habitats in East Africa. Of the 56 haplotypes across sites, one novel haplotype was unique to Toro-Semliki. A Mantel regression of genetic distance against geographic distance showed a significant positive correlation, suggesting relatively consistent gene flow throughout East Africa. Toro-Semliki and Itwara demonstrated close genetic similarity ($\Phi_{ST}=0.09$). An AMOVA showed that genetic variation within and between four PAs in the heart of the Western Gateway was best accounted for when Toro-Semliki and Itwara (but no other PAs) were counted as a single population, suggesting that chimpanzees range between the two reserves. The apparent high levels of gene flow between forested reserves and a savanna-mosaic habitat like Toro-Semliki raise a number of questions and concerns, both calling into question the purportedly deep distinction between "savanna" and "closed-forest" chimpanzees. These results emphasize the pivotal geographic position of protected areas along the westernmost edge of Uganda for maintaining the genetic diversity of chimpanzees throughout East Africa.

Supported by Pittsburgh Zoo, American Society of Primatologists, Animal Behavior Society. At Indiana University: Center for the Integrative Study of Animal Behavior, College of Arts and Sciences, Anthropology Skomp Fund.

Comparative morphology of the Herto 16/5 juvenile cranium (Middle Awash, Ethiopia)

GARY D. RICHARDS

Biomedical Sciences, AA Dugoni School of Dentistry, University of the Pacific

In 1997 the remains of two adults and a juvenile were recovered from the Herto-Bouri locality. Radioisotopic assessments suggest an age of 160-154,000 years for this material. Initial assessments in 2003 showed clear affinities with *Homo sapiens*, making them the earliest anatomically modern humans. An in-depth comparative assessment of these fossils was completed in 2015. Here I present an overview of the morphology of the 16/5 juvenile cranium based on this assessment.

Comparative samples comprise fossil individuals ($n=69$) from a wide region of Europe and Western Asia and a recent human sample ($n=43$). Developmental ages range from 2-17 years for

the fossil and 6-8 years for the recent sample. A total of 154 craniometric dimensions were taken, with ≈ 65 used for metric comparisons. Detailed assessments of relevant morphological features were made between the fossil and comparative samples. Some observations rely on a new virtual reconstruction and endocast.

Herto 16/5 is typical of Late Pleistocene *H. sapiens* juveniles: it has a wide upper face, weakly developed zygomatics, and a supraorbital region lacking torus/sulcus development. The midface possesses a canine fossa, and the zygomaxillary orientation is as in *H. sapiens*. It lacks the distinctive maxillary, nasal, and orbital morphology of contemporaneous Neanderthals. The cranial vault is most similar to recent human juveniles, with vertical parietal walls, developed eminences, and near equal postorbital and maximum cranial vault dimensions. Temporal morphology is mainly consistent with recent humans. In comparison to mid-Pleistocene to recent juveniles, Herto 16/5 is morphologically most similar to the latter.

The role of the precuneus in accurate long-range projectile throwing: a transcranial magnetic stimulation study

JAMES K. RILLING^{1,2,3,4}, LYNNET RICHEY¹, DANIEL GRAF⁵, MINWOO LEE¹ and CHARLES EPSTEIN⁵

¹Anthropology, Emory University, ²Psychiatry and Behavioral Sciences, Emory University, ³Center for Behavioral Neuroscience, Emory University, ⁴Center for Translational Social Neuroscience, Emory University, ⁵Department of Neurology, Emory University

Over the last 300,000 years, the hominin skull evolved a more globular shape involving parietal bulging. Parietal bulging may reflect expansion of the underlying medial parietal lobe within a brain region called the precuneus. The precuneus is relatively larger in humans than chimpanzees. During the last 100,000 years, evidence for projectile weaponry becomes more prominent in the archeological record. The precuneus is involved in visuospatial integration skills that we hypothesize are involved in accurate long range projectile throwing. We used transcranial magnetic stimulation (TMS) to temporarily inhibit the precuneus of human subjects and evaluated its impact on throwing accuracy. In a randomized, double-blind, within-subject design, 23 adult male subjects with high school or greater baseball experience threw 20 baseballs at a target both before and after either TMS or Sham treatment to the precuneus, and throws were scored for accuracy. For each subject, we compared the pre to post treatment scores across TMS and Sham conditions to generate the contrast [TMS (pre-post) - Sham (pre-post)]. The average value of this contrast across all subjects was compared with zero using a one sample t-test. Initial results show a trend for TMS to impair throwing accuracy more than Sham ($p=0.15$). Subsequent analyses will utilize

a mixed effects regression model to account for potential confounding and moderating variables such as throwing experience, TMS stimulation intensity and treatment order. Significant effects of TMS treatment would support the possibility that precuneus expansion in recent human evolution evolved to support accurate long range projectile throwing.

Supported by a grant from the Emory University Research Committee.

How conflicting messages during pregnancy affect U.S. women's self-reported and biological stress levels

GENEVIEVE T. RITCHIE-EWING and BARBARA A. PIPERATA

Anthropology, The Ohio State University

Although stress during pregnancy increases pregnancy/birth complications, few studies have investigated cultural reasons for increased stress levels. Specifically, no studies have explored how conflicting messages pregnant women receive about "appropriate" behaviors affect self-reported and biological stress levels. To address this gap, we collected hair samples and survey responses from 23 women in early (7-13 weeks) and mid-pregnancy (21-27 weeks) and an additional 24 women in mid-pregnancy only. All participants were married, "white," of middle to upper socioeconomic status and lacked prior pregnancy-related complications to control for other potential stressors. Based on participant responses about emotional reactions to messaging, we divided our sample into two groups: participants who reported anxiety due to messaging ($n=25$) and participants who did not report anxiety due to messaging ($n=22$). To measure self-reported stress, participants completed the Perceived Stress Scale (PSS) for general stress and the Pregnancy-specific Anxiety Scale (PSA) for stress associated with pregnancy-specific concerns such as fetal health. Hair samples were analyzed for total cortisol. The group who reported messaging anxiety had significantly more general stress in mid-pregnancy ($t=2.407$; $p=0.02$). The same group also had significantly more pregnancy-specific stress than women in the other group, but only in early pregnancy ($t=2.733$; $p=0.012$). Hair cortisol levels did not differ between groups. Our results suggest conflicting messages affect women's self-reported stress, but not their cortisol levels. Our continued work explores sources of conflicting messages including how competing messages from the biomedical and natural childbirth communities affect pregnant women's self-reported and biological stress levels.

Funding for this research provided by National Science Foundation (BCS Award No. 1528292), Larsen Award (OSU Department of Anthropology), National Center for Advancing Translational Sciences (Grant UL1TR001070)

ABSTRACTS

Diachronic change in the Holocene Baltic head: the effects of farmed and aquatic foods on skull and tooth morphology

MICHAEL B. C. RIVERA¹, GUNITA ZARIŅA² and JAY T. STOCK^{1,3}

¹Department of Archaeology, University of Cambridge, ²Institute of Latvian History, University of Latvia, ³Department of Anthropology, University of Western Ontario

In bioarchaeology, trends of reduced craniofacial, masticatory and dental robusticity following the agricultural transition have been reported in numerous global contexts. An investigation of Estonian and Latvian skull and tooth morphology was conducted to uncover whether human skeletal samples ($n = 100$) derived from the Baltic Holocene (9,000 BCE–1,200 CE) also follow such trajectories of decreasing robusticity.

Our case study demonstrated how significant changes occurred much later than in other Holocene European farming populations. There were novel methods of food preparation, a greater reliance on softer grains and limited reliance on paramasticatory behaviors only once the Baltic Bronze Age began (after 1,800 BCE). These changes in subsistence strategies likely contributed to reducing the hardness, resistance and toughness of Bronze and Iron Age food. As a result of decreased masticatory strain and increased carbohydrate consumption: a) cranial vaults reconfigured to become more globular, b) the mandible became less robust, and c) tooth sizes shrunk, particularly in the posterior and mandibular teeth. However, facial robusticity did not decrease and the palate grew in size. This last finding, though unanticipated, may be explained by climatic stability or important demographic events. Delayed, slower and/or unexpected biological responses to agriculture have been observed in other recent research on coastal populations. Together with these studies, we show how changes in skull evolution can vary significantly under specific environmental, dietary and demographic circumstances.

We thank the University of Cambridge and Sigma Xi Research Society for grants awarded to carry out this research.

New insight on the Neandertal pelvis: Virtual reconstruction of the pelvis of Regourdou 1 specimen

REBEKA RMOUŤILOVA^{1,2}, JAROSLAV BRUZEK², RONAN LEDEVIN¹, ASIER GÓMEZ-OLIVENCIA^{3,4}, CHRISTINE COUTURE-VESCHAMBRE¹, TRENTON HOLLIDAY⁵, STÉPHANE MADELAINE⁶, JANA VELEMÍNSKÁ² and BRUNO MAUREILLE¹

¹UMR 5199 PACEA, University of Bordeaux, ²Department of Anthropology and Human Genetics, Charles University, Prague, ³Departamento Estratigrafía y Paleontología, Euskal Herriko Unibertsitatea, ⁴Centro UCM-ISCIII de Investigación sobre Evolución y Comportamiento Humanos,

⁵Department of Anthropology, Tulane University, New Orleans, ⁶Musée national de Préhistoire, Les Eyzies

The pelvis is a key structure for locomotion, birth mechanism, body form, and thermoregulation. These aspects are highly discussed in Neandertals, but Neandertal pelvic remains are very rare and fragmentary preventing a clear answer to many scientific questions. We present a complex process leading to the virtual reconstruction of the Regourdou 1 Neandertal pelvis. Unlike the previous unpublished reconstruction, all known pelvic fragments of Regourdou 1 are used and a semilandmark-based approach captures more of the preserved morphology. Unlike other specimens, Regourdou 1 has intact, undistorted sacroiliac joints; both ilia can be aligned to the sacrum by their matching surfaces. Exceptional preservation of the trabecular bone enabled us to find matching areas between the right ilium and ischium previously considered as not directly connected. The newly available acetabular diameter falls within the previously estimated interval based on the ischial portion of the lunate surface. Left ischial fragments, lacking direct connection, were aligned using the mirrored right counterpart, and unique parts were transferred from one coxal bone to the other using semilandmark-based warping. Left posterior ilium with a partial iliac crest (recently discovered in the Musée national de Préhistoire) enabled us to reliably estimate a missing portion of the superior ilium. A fragment of the superior pubic ramus was aligned based on a sample of sufficiently preserved Neandertal specimens in order to better estimate the anterior pelvis. This new reconstruction gives new insight on Neandertal pelvic morphology and will provide more information in future studies.

Supported by Grant Agency of Charles University (10882), Irene Levi Sala Archaeological Foundation; the LabEx ANR-10-LABX-52, project „NéMo” and the project “NATCH” convention 2016-1R40240-00007349-00007350 (Région Nouvelle Aquitaine).

Understanding Heterogeneity in Urban Mortuary Behavior: Between Action and Symbolic Meaning in the Indus Age

GWEN ROBBINS SCHUG
Anthropology, Appalachian State University

Anthropologists have long-standing interests in mortuary and other ritual behavior as a window into socio-cultural and symbolic lives of past people. The interpretation of mortuary behavior provides a particularly good window into collective and individual identity, memory, tradition, ritual performance, and ideas about the afterlife. This window into the social relations of the past provides a vision of structure refracted through agency—mortuary tradition is enacted to transform; we interact with the dead to remember but also to renegotiate; and eventually to attain some separation. In this process, power relations

are reified and renegotiated and the material symbolism of the burial and the body provides a rich field for anthropological ventures. This paper describes variation in the mortuary practices of four Indus communities across a period of rapid urbanization. An analysis of mortuary behavior at Harappa, Rakhigarhi, Mohenjodaro, and Kalibangan demonstrates that single primary inhumations of supine, extended skeletons should not be considered the normative practice in the Indus Age; rather there was always a high degree of heterogeneity in synchronous cemeteries, for which a combined nomothetic and social archaeology approach can elucidate some of the structural and symbolic aspects of death in Indus society.

This research was funded by USIEF Fulbright-Nehru Research Fellowship

Treponemal disease in Europe: A critical review of the skeletal evidence

CHARLOTTE A. ROBERTS
Archaeology, Durham University

Exploring and interpreting the Old World evidence for treponemal disease is crucial to understanding its origin, evolution and history, a history that has become contentious in bioarchaeology this century. This paper critically considers the published and unpublished evidence for treponemal disease in (primarily) skeletal remains from Europe. A desk-based review was conducted using searches of the published literature and via personal contact with researchers across Europe. The data show the concentrated evidence in Europe is absent in other parts of the Old World. Virtually all modern-day European countries have evidence, some having questionable evidence, or evidence that needs verification. Surprising was the lack of data from France, Germany, and the Netherlands, with long histories of bioarchaeology. The majority of the evidence was diagnosed macroscopically. Most data were from late (12th–16th centuries A.D.) to post-Medieval (1550–1850) sites. Tertiary bone changes were more common later in time. The extant data show regional knowledge gaps and where skeletal re-evaluations may be needed. The Scandinavian countries, parts of eastern Europe, Greece and the six countries of the former Yugoslavia have not generated much evidence. Additional challenges include incomplete description and illustration of skeletal lesions, a lack of differential diagnoses, or contextual data, most data coming from urban contexts, and a huge grey literature in different languages that has been barely interrogated. Recommendations for future research are proposed to enable scholars to move forward in understanding the origin, evolution and history of the treponemal diseases in Europe and its relevance to the New World.

ABSTRACTS

Ecological context of the South African Middle Stone Age from Sibudu, KwaZulu-Natal

JOSHUA R. ROBINSON

Anthropology, University of South Carolina

Environmental and climatic models contextualizing human behavioral and cognitive evolution during the African Middle Stone Age are primarily contingent on data which are temporally, spatially, and/or stratigraphically separated from key sites. This is particularly true of the South African Middle Stone Age record with its enigmatic and relatively short lived Still Bay and Howieson's Poort industries. To develop a high-resolution 'on the ground' environmental dataset of the South African Middle Stone Age, stable carbon and oxygen isotope data were collected from 113 faunal tooth enamel samples spanning the entire well-dated and extensive sequence of the Sibudu site. Isotope data indicate two periods of habitat change at Sibudu. The pre-Still Bay (> 73,000 years ago) is characterized by more closed, likely heavily forested, and mesic conditions than the rest of the sequence. Late and final Middle Stone Age industries (~ 48,000 – 38,000 years ago) at Sibudu are associated with more open and likely drier conditions than earlier. Drier and more open conditions could have accompanied the appearance of the Later Stone Age in the region, as has been shown at sites in eastern and central Africa, but this remains speculative as no Later Stone Age deposits have been found at Sibudu. No major environmental or habitat changes, however, are identified in the Sibudu record concordant with the Still Bay, Howieson's Poort, or post-Howieson's Poort techno-complexes. These results suggest that social and demographic changes were presumably as significant as environmental conditions, if not more so, in behavioral transitions at Sibudu.

Air travel and analyses for this project were supported by a Rust Family Foundation Grant (RFF-2017-31) to JRR.

The embodiment of social experience: How social support and workplace incivility vary with health indicators in female scientists of color

MICHELLE A. RODRIGUES^{1,2}, RACHEL NEUBAUER¹, DENISE HERRERA¹, RUBY MENDENHALL^{3,4}, ELIZABETH A.L. STINE-MORROW^{2,5} and KATHRYN B.H. CLANCY^{1,2}

¹Department of Anthropology, University of Illinois, Urbana-Champaign, ²Beckman Institute for Science and Technology, University of Illinois, Urbana-Champaign, ³Department of Sociology and African-American Studies, University of Illinois, Urbana-Champaign, ⁴College of Medicine, University of Illinois, Urbana-Champaign, ⁵Department of Educational Psychology, University of Illinois, Urbana-Champaign

Social support is embodied and has powerful effects on health indicators; negative interpersonal interactions, particularly those related to discrimination, can have negative effects. Here we present preliminary analysis of the impact of daily social support and workplace incivilities on female scientists of color, who may be marginalized in their workplace environments. Ten participants completed daily surveys of sleep indicators, mood, supportive social interactions, workplace incivilities, and somatic symptoms of depression for approximately one month (mean=32.5 days). We performed general linear mixed models (GLMMs) to examine the daily effect of talking to friends, family, partners, spiritual engagement, social media use, and workplace incivility, on 1) sleep-onset latency and 2) somatic symptoms of depression while controlling for individual variation. Sleep-onset latency was negatively correlated with frequency of talking with partners ($r=-0.207$, $p=0.001$), friends ($r=-0.133$, $p=0.027$), and family ($r=-0.178$, $p=0.003$). Somatic symptoms were positively correlated with social media use ($r=0.246$, $p<0.001$). In the first GLMM, talking to partners was significantly negatively associated with sleep-onset latency ($F_{1, 268}=5.803$, $p=0.017$). In the second GLMM, talking with partners was significantly negatively associated with somatic symptoms ($F_{1, 268}=4.007$, $p=0.046$). Our findings highlight the positive health benefits of social support, though more analysis is necessary to understand why partner support emerged as a stronger influence than support from friends or family. Our next step is to assay biological samples for cortisol concentrations and inflammatory biomarkers to examine if these variables correspond to markers of physiological stress.

Research was funded by a Beckman Institute Postdoctoral Fellowship, and an American Association of Physical Anthropologists Professional Development Award.

Effects of particle concentration and size on tooth wear

FERNANDO RODRIGUEZ-ROJAS¹, OSCAR BORRERO-LOPEZ¹, PAUL J. CONSTANTINO², FERNANDO GUIBERTEAU¹ and BRIAN R. LAWN³

¹Materials Science and Engineering, Universidad de Extremadura, Spain, ²Department of Biology, Saint Michael's College, VT, ³Materials Measurement Laboratory, National Institute of Standards and Technology, MD

Dental microwear is commonly employed for dietary reconstruction. Micrometer sized particles play a fundamental role. This poster presents recent results on the effects of particle concentration and size on tooth wear, obtained from *in-vitro* tribological tests on human teeth. It is found that, below a given threshold, the wear rate is not affected by particle concentration, and it increases with increasing particle size. Beyond that threshold, tooth wear is decreased with increasing particle concentration and size.

Results are analysed within the framework of a contact mechanics model that pays special attention to transitions in damage modes ('mild' plasticity vs. 'severe' fracture), as a function of contact force and particle geometry and mechanical properties. Implications in paleodontology are discussed.

This study was supported by Junta de Extremadura, Spain, and FEDER/ERDF funds (grant IB16139)

Superarchaic admixture confirms a deep separation of Neanderthals and Denisovans

ALAN R. ROGERS, ALAN ACHENBACH, KIELA GWIN and NATHAN HARRIS

Anthropology, University of Utah

We argued in 2017 for an early separation of Neanderthals and Denisovans and a bottleneck among their ancestors. Mafessoni and Pruefer obtained different results by including singleton site patterns. However, the with-singleton analysis also implied an implausible 4 kya date for the Denisovan fossil. We show now that this anomaly disappears if one allows for admixture into Denisovans from a "superarchaic" hominin, which separated from other hominins early in the Pleistocene. This superarchaic hypothesis is not new. We show that superarchaics separated nearly 2 mya and contributed about 3% of the DNA in Denisovans. This new analysis also confirms our earlier results that Neanderthals and Denisovans separated early in the Middle Pleistocene and that their ancestors survived a narrow bottleneck of population size.

This work was supported by grant BCS-638840 from the National Science Foundation.

The relationship between stress, gene methylation, and reproductive function

MARY P. ROGERS¹, KATHARINE MN. LEE², ANDRZEJ GALBARCZYK⁴, GRAZYNA JASIENSKA⁴, RIPAN S. MALHI^{1,2} and KATHRYN BH. CLANCY^{2,3}

¹Carl R. Woese Institute for Genomic Biology, University of Illinois, Urbana-Champaign, ²Department of Anthropology, University of Illinois, Urbana-Champaign, ³Beckman Institute, University of Illinois, Urbana-Champaign, ⁴Institute of Public Health, Jagiellonian University Medical College, Krakow, Poland

Stress affects reproductive function, but research is lacking on potential connecting mechanisms. Epigenetic traits like gene methylation are responsive to stress and can modify gene expression. We hypothesized that stress affects reproductive function via gene methylation, investigating promoter methylation of the gene *CYP19A1* as a potential mediator between cortisol and an estradiol metabolite, estrone-3-glucuronide (E1G). The glucocorticoid cortisol is used as a marker for stress and is associated with fecundity. *In vitro* studies demonstrate that cortisol

ABSTRACTS

affects *CYP19A1* methylation and expression, and thus could link stress and reproductive function. We conducted this study in a sample of 53 rural Polish women. We used multiplex enzyme linked immunosorbent assays (ELISAs) to measure urinary cortisol and E1G concentrations across the menstrual cycle and used pyrosequencing to assess *CYP19A1* promoter methylation. We first found that average follicular phase cortisol concentrations were significantly positively associated with *CYP19A1* promoter methylation ($p=0.01$) and luteal phase E1G concentrations ($p=0.02$). We then used structural equation modeling to explore a pathway by which cortisol may affect luteal phase E1G concentrations via gene methylation. *CYP19A1* promoter methylation mediated the relationship between cortisol and E1G, where cortisol was positively associated with *CYP19A1* promoter methylation ($\beta=0.30$, $p=0.05$), and *CYP19A1* promoter methylation was negatively associated with luteal phase E1G concentrations ($\beta=-0.28$, $p=0.04$). While many have hypothesized that epigenetic mechanisms can link environmental exposures and reproductive outcomes, this study is the first to demonstrate that *CYP19A1* promoter methylation may serve as a link between stress and adult female reproductive hormone concentrations.

Research support provided by: NSF GRFP #DGE-1144245, NSF Clancy#1317140, NSF DDRIG Rogers#1650839 and Lee#1732117, Lewis and Clark Fund for Exploration and Field Research, and Wenner-Gren Foundation Dissertation Fieldwork Grants.

***Homo heidelbergensis*: what do we need to set the question of the validity of this taxon to rest**

MIRJANA ROKSANDIC¹ and CHRISTOPHER BAE²
¹Department of Anthropology, University of Winnipeg, ²Department of Anthropology, University of Hawai'i

The question what does *Homo heidelbergensis* as a taxon represent has long been debated in the palaeoanthropological literature with no definite conclusion in sight. Does it represent the last common ancestor to Neanderthals, Denisovans, and Modern Humans, is it ancestral to just one of these groups, or is it even a valid taxon? To further complicate these questions, the holotype of this taxon is a single mandible, a skeletal element that notoriously displays a great deal of morphological variation, from the earlier part of the Middle Pleistocene, and from western Europe, a region long considered peripheral to the origin and development of both the genus *Homo* and of *H. sapiens*. Here, we examine well dated Middle Pleistocene hominin fossil material from Europe, Near East, Africa and eastern Asia. Given the variable preservation we only score traits as plesiomorphic, synapomorphic and autapomorphic, without regard to the anatomical region represented. We propose that the source

population for Neanderthals Denisovans and Modern Humans would exhibit a combination of primitive and shared derived traits as a result of an absence of directional selection and that this source population was likely located at the point of contact between all three continents (Africa, Asia, Europe). We suggest that redefined, *H. heidelbergensis* could be a valid taxon, but perhaps under a different name.

The work was supported by Natural Sciences and Engineering Research Council of Canada [grant no DDG-2017-00012]

Examining fluctuating asymmetry in *Macaca fascicularis*

ASHLY N. ROMERO¹, CLAIRE A. KIRCHHOFF², SIOBHAN B. COOKE^{3,4} and CLAIRE E. TERHUNE¹

¹Department of Anthropology, University of Arkansas, ²Department of Biomedical Sciences, Marquette University, ³Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine, ⁴New York Consortium in Evolutionary Primatology, Morphometrics Group

While craniofacial asymmetry has been extensively researched in humans, skeletal craniofacial fluctuating asymmetry (FA) and its implications for developmental stability and physiological stress response remains largely unexplored in non-human primates. Taxa may exhibit differences in craniofacial fluctuating asymmetry that characterize important differences in stress response, and these trends could relate to ontogenetic differences between groups. To better characterize fluctuating asymmetry in primate taxa, three-dimensional models of 39 *Macaca fascicularis fascicularis* crania were generated with an HDI 120 blue light scanner and geometric morphometric techniques employed to examine craniofacial fluctuating asymmetry. These data were then compared with 44 gorilla (*Gorilla gorilla gorilla*) and 37 chimpanzee (*Pan troglodytes troglodytes*) crania to examine differences in FA between taxa. Due to their closer phylogenetic relationship, gorillas and chimpanzees were expected to show similar FA levels when compared with the macaque outgroup. Results showed that *G. gorilla gorilla* and *M. fascicularis* exhibit similar levels of FA, while *P. troglodytes troglodytes* exhibits significantly less FA than either group ($p<0.01$). Because FA is a nonspecific indicator of stress, these results could result from multiple scenarios. Chimpanzees may exhibit greater developmental stability than other primate groups, slower growth rates in chimpanzees compared to gorillas and macaques may contribute to a longer asymmetry compensation period, or differential environmental stress factors could be overwhelming the ability to

develop symmetrically in macaques and gorillas. Further investigation into specific stressors can further clarify the unexpected differences observed in these taxa.

Funding provided by NSF BCS-1551722.

Variation in Long Bone Diaphyseal Morphology in Coastal and Inland Hunter-Gatherers from Prehistoric Alaska

EMILY R. ROSA and DANIEL H. TEMPLE

Department of Sociology and Anthropology, George Mason University

This study compares long bone diaphyseal robusticity between coastal and inland hunter-gatherers from Alaska to understand how differences in geographic terrain and lifestyle may have influenced these properties. Ct-scans of humeri ($\sigma_{\text{coastal}} = 23$, $\sigma_{\text{inland}} = 23$; $\rho_{\text{coastal}} = 18$, $\rho_{\text{inland}} = 33$) and femora ($\sigma_{\text{coastal}} = 20$, $\sigma_{\text{inland}} = 28$; $\rho_{\text{coastal}} = 13$, $\rho_{\text{inland}} = 35$) were collected from samples originating from five sites along the Alaskan coastline and interior regions. Moments, second moments, and polar second moments of area were measured using Image J and MomentMacro. All diaphyseal properties were compared using MANOVA and Mann-Whitney U tests. For femora: Male and female TA ($\sigma_p < 0.001$, $\rho_p < 0.001$), MA ($\sigma_p < 0.001$, $\rho_p < 0.001$), and J ($\sigma_p < 0.006$, $\rho_p < 0.001$) were significantly larger among the coastal group. For humeri: Male CA ($p < 0.005$) and MA ($p < 0.011$) were significantly larger in the inland samples, while female CA ($p < 0.014$) was larger in the inland samples. These results suggest greater femoral robusticity in the coastal compared to inland samples, with little difference in humeral robusticity between the two groups. Femoral robusticity likely differed in association with greater mobility among coastal communities, either migration between communities or seasonal tracking of prey. Differences in humeral robusticity may have been muted by riverine and embayment rowing among inland samples. These results support functional interpretations of long bone diaphyseal morphology, but suggest caution in generalized assumptions relating to coastal and inland distinctions in activity patterns.

Lifespan changes in macaque social and economic decision making

ALEXANDRA G. ROSATI

Depts. of Psychology and Anthropology, University of Michigan

Humans exhibit a suite of changes in social cognition and decision-making during aging that impact social functioning and behavior. However, little is known about whether other primates show similar shifts, even though comparative patterns are crucial to understand the biological basis and evolutionary significance of

ABSTRACTS

cognition and behavior. This study experimentally assessed large samples of semi-free-ranging rhesus macaques (*Macaca mulatta*) and Barbary macaques (*Macaca sylvanus*) ranging from juvenility to old age (80-480 individuals across tasks). Monkeys were assessed on cognitive measures that show key changes in human aging. In particular, older humans show declining sensitivity to social gaze cues; an increasing 'positivity bias' with greater attention to positive emotional information; and exhibit deficits in the ability to track reward values. We found that, as in humans, older rhesus macaques showed decreased propensity to follow other's gaze compared to younger monkeys. However, older rhesus actually exhibited a 'negativity bias' with increasing relative attention to negative emotional stimuli, unlike humans. Finally, older rhesus maintained the ability to track reward values like younger adults. Comparisons with Barbary macaques further indicated that even closely-related species may differ in their patterns of cognitive aging, as Barbary macaques maintained robust gaze following during old age. These results indicate that some core cognitive features of human aging are shared with other primates, whereas others vary across species. These findings will be discussed in terms of relevance for life history evolution and patterns of comparative cognitive development across the lifespan.

This work was supported in part by NIMH (R01MH096875).

A complex genotype-phenotype map underlies the generation of genetic variation in murine molars

CHARLES C. ROSEMAN¹, REBECCA GREEN², AMANDA NEVES², CHRISTOPHER PERCIVAL³, LUCAS K. DELEZENE⁴, JAMES M. CHEVERUD⁵ and BENEDIKT HALLGRIMSSON²

¹Department of Animal Biology, University of Illinois, ²Department of Cell Biology and Anatomy, University of Calgary, ³Department of Anthropology, University at Stony Brook, ⁴Department of Anthropology, University of Arkansas, ⁵Department of Biology, Loyola University, Chicago

The Inhibitory Cascade (IC) model proposes that relative molar size in mammals is largely governed by the antagonistic action of activating and inhibiting factors during development. Here, we test hypotheses about the structure of the genotype-phenotype (GP) map for mandibular molar size in a large sample ($n = 1,100$) from the F_{34} generation of the Lg/Sm Advanced Intercross population genotyped for $\approx 2,400$ SNPs spaced evenly across the autosomes. Teeth show robust additive genetic covariation, heritability, and evolvability with no sign of strong variational constraint. The slopes of the additive genetic and environmental regressions of relative third molar size on relative second molar size both deviated from IC model expectations and the genetic correlation between the two was much weaker

than expected. We identified 47 quantitative trait loci (QTL) contributing to variation in absolute and relative molar size. The presence of QTL with unique (i.e. non-pleiotropic) or direct effects on the second and third molars run contrary to the expectations of the IC model. A minority of QTL contribute variation in a manner consistent with the IC model. While processes corresponding to those proposed in the IC model appear to have a role in producing evolvable variation, they appear to be insufficient to constrain evolutionary trajectories at microevolutionary scales. This adds further evidence to the notion that mechanisms that regulate the basic patterning of anatomical structures during development may be somewhat separate from those that produce variation on which evolutionary forces might act.

National Science and Engineering Council of Canada, University of Illinois Research Board, NIH (AR054224 and RR015116 to J.M.C.), and The McCaig Institute.

Facultative fatherhood? Parental and alloparental caretaking tradeoffs in Cebu, the Philippines

STACY ROSENBAUM¹, THOMAS W. MCDONALD^{1,2}, SONNY AGUSTIN³, CHRISTOPHER W. KUZAWA^{1,2} and LEE T. GETTLER^{4,5}

¹Anthropology, Northwestern University, ²Institute for Policy Research, Northwestern University, ³Office of Population Studies, University of San Carlos, ⁴Department of Anthropology, University of Notre Dame, ⁵Eck Institute for Global Health, University of Notre Dame

Cross-culturally, human children are raised by a flexible assortment of caretakers that can include mothers, fathers, grandparents, siblings, extended family, and even unrelated helpers. In virtually every culture, mothers are children's primary direct caregivers. Paternal roles, in contrast, are often variable, and it has been proposed that a father's level of involvement in direct care of his children will tend to be facultative, or particularly responsive to caregiving provided by other alloparental caregivers. Here, we examine the relationship between alloparental care and both maternal and paternal care among dual-parent households in metropolitan Cebu, Philippines. We hypothesized that participation by caretakers other than parents would predict lower paternal care, but not maternal care, as would be predicted by the hypothesis of facultative fathering. We compare caregivers in three domains that commonly occur on a daily basis, and are amenable to alloparents' assistance. According to reports provided by mothers, across households 95.8% of mothers and 59.8% of fathers gave children their meals, 96.9% of mothers and 66.5% of fathers watched over/cared for them, and 87.7% of mothers and 83.9% of fathers played with them. However contrary to our expectation, preliminary analyses indicate that in extended family households ($n=155$), where more adult caretakers were available

(mean=4.79, SD=2.07), incidences of paternal and maternal feeding, caring for, and playing fell by equal proportions relative to nuclear families ($n=289$). These findings in Cebu challenge the notion that fathers' caretaking will be more responsive than that of mothers to the level of assistance received from other alloparents.

This study was funded by the Wenner-Gren Foundation (7356; 8186) and the National Science Foundation (BCS-0962212; BCS-1317133)

Mechanisms for avoiding sand-laden foods in a population of coastal foraging monkeys (*Macaca fascicularis*)

JESSICA E. ROSIEN¹, NATHANIEL J. DOMINY¹, SUCHINDA MALAIWIJITNOND^{2,3} and AMANDA W. Y. TAN^{1,4}

¹Department of Anthropology, Dartmouth College, ²Primate Research Unit, Department of Biology, Faculty of Science, Chulalongkorn University, ³National Primate Research Center of Thailand, Chulalongkorn University, ⁴Department of Anthropology, Durham University

Prolonged consumption of dietary grit is hypothesized to damage teeth with deleterious effects on health and fitness. Primates perform wide variety of food-cleaning behaviors that have been conceived as behavioral mechanisms to avoid dietary grit. However, there has been little effort to quantify grit on food or explore whether differences in grittiness can explain variation in grit-avoidance mechanisms. To examine these questions, we conducted field experiments on a population of long-tailed macaques on Koram Island, Thailand, where food washing of sand-laden food during coastal feeding has been observed. We provided fruit with varying degrees of sand on the surface: low (mean: 0.17 mg mm⁻²), medium (mean: 0.86 mg mm⁻²), and high (mean: 1.83 mg mm⁻²), as measured with plastic peels that remove grit from the surface of each food item. We recorded the behavioral responses (brushing/rubbing, washing, peeling, or rejection) of 46 monkeys as a function of food grittiness. In total, we conducted 97 trials and 854 food-handling events. We found substantial variation in the food handling behavior of our study population; animals were progressively significantly more likely to manipulate, wash, or reject foods when grit levels were medium or high ($X^2 = 664.5$; $P < 0.0001$), indicating a strong behavioral aversion to grit. Our own simulations of these grit-induced food handling behaviors indicate removal rates of 60-90%. Taken together, our findings agree well with the long-standing presumption that food-washing exists to assiduously shed grit, and that grit in the oral cavity can influence dental wear with potential fitness costs.

This research was supported by the Claire Garber Goodman Fund, Department of Anthropology, Dartmouth College and the Mark A. Hansen Undergraduate Research, Scholarship, and Creativity Fund, Dartmouth College.

ABSTRACTS

Strain regimes in the ramus of *Macaca mulatta* estimated using finite element modeling

CALLUM F. ROSS¹, JOSE IRIARTE-DIAZ², ANDREA B. TAYLOR³, PAUL C. DECHOW⁴, SIMON WILSHIN⁵, HYAB MEHARI ABRAHA⁶ and OLGA PANAGIOTOPOULOU⁶

¹Department of Organismal Biology and Anatomy, University of Chicago, ²Department of Oral Biology, University of Illinois Chicago, ³Department of Basic Science, Touro University, ⁴Department of Biomedical Sciences, Texas A&M University College of Dentistry, ⁵Department of Comparative Biomedical Sciences, The Royal Veterinary College, ⁶Department of Anatomy and Developmental Biology, Monash University

The morphology of the mandibular ramus varies across primates, including fossil hominids, and has factored importantly in establishing phylogenetic relationships and feeding-system function in primates. However, the biomechanics of the mandibular ramus are under studied because the ramus is not amenable to *in vivo* strain gage recordings. Our validated finite element model of the mandible of *Macaca mulatta* facilitates testing of the hypothesis that the torus triangularis and endocondylar ridge function as the load path for forces from the tooth row to the condyle. Strain regimes in the finite element model during simulation of mastication reveal the balancing-side ramus experiences high magnitudes of: anteroposterior tensile strains extending posteriorly along the top of the torus triangularis and endocondylar ridge to the condylar neck; transverse tensile strains along the medial edge and inferior slope of torus triangularis and the endocondylar ridge; high positive transverse shear strains; and high negative sagittal shear strains along the top of torus triangularis and the endocondylar ridge. These high magnitude strain regimes in the ramus are posterior continuations of fields of similarly high strains in the lingual face and upper edge of the corpus, suggesting that the torus triangularis and endocondylar ridge constitute the primary load path from the corpus to the balancing-side condyle. Variation in these strain regimes across simulations of different feeding behaviors suggests that comparative morphological studies of the ramus may yield insight into form-function relationships of the ramus.

Funding was provided by: CIHR MOP-4918; NIH R01DE023816 and R24 HD050837-01; Brain Research Foundation; ERG-MACACA 267207; The University of Queensland, NSF BCS0962677.

Walking with hominins and chewing with lemurs in K-12 classrooms: Incorporating 3D digital repositories into state-specific lesson plans

AMANDA N. ROSSILLO¹, REBECCA W. COOK^{1,2} and ETHAN L. FULWOOD¹

¹Evolutionary Anthropology, Duke University, ²Department of Molecular Biomedical Sciences, North Carolina State University

Digitization of paleontological and zoological collections presents new opportunities to bring the primary data of biological anthropological research before non-academic audiences, including K-12 students. Detailed lesson plans, informed by education theory and drawing on the research expertise of biological anthropologists, maximize the usefulness of these materials to teachers in the classroom. We present lesson plans focused on the evolution of human bipedalism and on dietary adaptation in lemurs, tailored to North Carolina science standards for middle and high school biology. The first lesson asks students to compare regions of the skeleton associated with hominin bipedality in primate and non-primate species. Students use the morphology of these regions to formulate hypotheses about bipedal adaptations in fossil hominins. The second lesson asks students to formulate hypotheses as to the dietary adaptations and evolutionary relationships of ten lemur species from the shapes of their lower molars. Students are then evaluated on their ability to interpret the true lemur phylogenetic tree to test their hypotheses. Both lessons draw on 3D scans hosted on MorphoSource, an open-access repository for biological specimens, where they may be viewed on screens or downloaded and 3D printed. Lesson plans are distributed to North Carolina teachers through the Science Education Research Network (SciREN). This lesson plan model can be tailored to all grades and to alternate state and national standards frameworks, building on the hands-on nature of paleontology and functional morphology to cultivate K-12 interest in STEM.

The influence of anthropogenic forest edge on the social cohesion of mantled howler monkeys in Costa Rica

JESSE R. ROSSO^{1,2}, AMY L. SCHREIER^{1,2}, ELIZABETH M.C. COGGESHALL^{2,3}, CARRIE MERRIGAN-JOHNSON^{2,4} and LAURA M. BOLT^{2,5}

¹Department of Biology, Regis University, ²Maderas Rainforest Conservancy, ³Department of Anthropology, Central Washington University, ⁴Department of Anthropology, University of Toronto at Mississauga, ⁵Department of Anthropology, University of Toronto

Forest fragmentation is a persistent threat to primates across the world. The increase in forest edge has been shown to reduce the biomass of both plants and animals. Much research has

focused on the effects of edges on vegetation but our understanding of animals' responses to forest edge is still limited. We investigated how anthropogenic edge affects the social cohesion of mantled howler monkeys in a fragmented forest at the La Suerte Biological Research Station, Costa Rica. We predicted that howler monkeys would be more cohesive in the interior forest than the edge because of decreased average tree size and species richness in the edge. From May-August 2018, we used scan sampling on focal individuals to record the distance to their nearest neighbor and the number of individuals located within 5m of the focal primate. Contrary to predictions, there were significantly fewer individuals within 5m in the interior (average of 1.3 individuals) compared to the edge of the forest (1.6). Furthermore, the howler monkeys were significantly closer to their nearest neighbor in the edge (3.8m) than in the interior (4.3m). These results may be due to the limited space available in the edge, leading to monkeys congregating on the same tree rather than spreading out across trees. Understanding how edges affect mantled howler monkey social cohesion will contribute to our overall knowledge about the effects of edges on primates living in forest fragments; as deforestation and fragmentation are widespread globally, this research is imperative for ensuring the future of primates.

Paleoclimatic legacies structure present-day mammal communities in the global tropics

JOHN ROWAN¹, KAYE E. REED², LYDIA BEAUDROT^{3,4}, ANDREW ZAMORA¹, IRENE E. SMAIL² and JASON M. KAMILAR^{1,5}

¹Department of Anthropology, University of Massachusetts Amherst, ²Institute of Human Origins, Arizona State University, ³Department of Biosciences, Rice University, ⁴Program in Ecology and Evolution, Rice University, ⁵Program in Organismic and Evolutionary Biology, University of Massachusetts Amherst

A central goal of mammal biogeography is to understand the underlying environmental drivers of large-scale patterns of community diversity. Such studies are critical for understanding modern mammal diversity and feed directly into conservation efforts aimed at mitigating diversity loss in the face of anthropogenic climate and land-use change. Though much research has focused on present-day environmental drivers of community diversity, historical influences – such as late Quaternary climate fluctuations – may play an important role. Here, we use a database of phylogenetic and functional trait data for terrestrial large mammal communities (species > 500 g) in the global tropics (n=415) to test the relative influence of modern versus paleoclimates in structuring present-day patterns of tropical diversity. We used linear models to predict measures of community phylogenetic

ABSTRACTS

and functional trait structure from modern and paleo- temperature and precipitation variables. For the Afrotropical, Indo-Malay, and Neotropical realms, paleoclimates of the mid-Holocene and Last Glacial Maximum (LGM) are equally or more important predictors of community structure compared to present-day climates. Mammal community structure in Madagascar shows the strongest mid-Holocene and weakest LGM paleo- climate effect for any region. This pattern may be due to widespread Holocene extirpations and extinctions that fundamentally reshaped the present-day mammal communities on the island. Our study highlights the need to consider deep-time processes structuring contemporary patterns of community diversity, especially in the global tropics that are increasingly under threat but cradle the vast majority of the world's remaining primate diversity.

This research was funded by the National Science Foundation (NSF SBE Awards 1551799 and 1551810).

Shape analysis of the pubic symphyseal outline in a modern human sample

MEGAN J. RUE¹, CHELSEA C. CATALDO-RAMIREZ², RHIAN R. DUNN³ and HEATHER M. GARVIN⁴

¹Department of Chemistry, University of Southern Maine, ²Department of Anthropology, University of California, Davis, ³Department of Applied Forensic Sciences, Mercyhurst University, ⁴Department of Anatomy, Des Moines University

The human pubic bone is sexually dimorphic and the microtopography of the pubic symphyseal (PS) face is known to change with age. Although the overall shape of the PS face is often regarded as oval, variations in overall shape are not well-documented. This study utilized 214 CT scans of individuals of known sex, age, and ancestry to investigate variation in PS outline. Surface models were generated from CT scans and two-dimensional outlines of the symphyseal face were collected and subjected to elliptical Fourier and principal component analyses. Significant sex and ancestry differences were found on PC1 ($p < 0.001$), which explained 54% of the shape variation. Results indicate that males have a relatively broader symphyseal face than females. Individuals who self-identified as White displayed a relatively longer and narrower symphyseal face compared to Black and Hispanic/Latino individuals. There was no significant difference between Asian and White ancestries. Individuals of Asian ancestry have a more diamond-shaped symphyseal face relative to Black individuals (PC5, $p < 0.05$). Overall, age did not explain a high percentage of the shape variation (significant R^2 values all < 0.05). Further studies should include homogeneous age distributions of individuals from multiple ancestries and both sexes to determine the depth of variation in overall PS symphyseal shape. Increased understanding of the overall symphyseal shape

can be used to improve age estimation methodologies in forensics, better understand the biomechanics of the pelvis, and refine anatomical guidelines used to determine pathology of the PS joint.

The Evolution of Human Body Size and Shape

CHRISTOPHER B. RUFF

Functional Anatomy and Evolution, Johns Hopkins University School of Medicine

Reconstruction and interpretation of body size and shape variation among fossil hominins has been a major research interest of Erik Trinkaus for the past four decades. Here, new estimates of body mass in Plio-Pleistocene hominins are combined with long bone length data to investigate temporal and taxonomic patterns of variation in relative limb length, with comparisons to extant humans and African apes. The modern sample consists of 682 Holocene humans representing a wide variety of body sizes and shapes, with body mass estimated from reconstructed stature and maximum pelvic (bi-iliac) breadth, and 24 chimpanzees and gorillas of known body mass. Fossil hominin specimens include only those with relatively well-preserved limb bone elements.

Relative to body mass, femoral and tibial lengths are highly positively allometric in modern humans (RMA slopes of 0.46-0.47) but negatively allometric in nonhuman apes (slopes of 0.18-0.23). Thus, proportions are more similar in smaller-bodied humans and apes, but they don't completely converge. *Australopithecus afarensis* specimens (A.L. 288-1 and A.L. 827-1) have relative femoral lengths that fall below those of modern humans of similar body mass; however, relative tibia length is more human-like in *Au. afarensis* (KSD-VP-1/1) and *Ardipithecus ramidus* (ARA-VP-6/500). Thus, there is mixed evidence for relatively shorter lower limbs in these taxa. Relative bone lengths are within modern ranges for fossil *Homo*, but with some ecogeographic variation. When interpreting variation in body proportions among earlier hominins, it is important to consider all potential physiological influences, including not only locomotor behavior, but also thermoregulation and obstetrics.

Amylase copy number analysis in several mammalian lineages reveals convergent adaptive bursts shaped by diet

PETAR PAJIC^{1,2}, PAVLOS PAVLIDIS³, KIRSTEN DEAN², LUBOV NEZNANOVA¹, ERIN DAUGHERITY⁴, ROSE-ANNE ROMANO¹, DANIELLE GARNEAU⁵, ANJA GLOBIG⁶, OMER GOKCUMEN² and STEFAN RUHL¹

¹Department of Oral Biology, University at Buffalo, ²Department of Biological Sciences, University at Buffalo, ³Institute of Computer Science (ICS),

Foundation for Research and Technology – Hellas, Heraklion, Crete, Greece, ⁴Cornell Center for Animal Resources and Education, Cornell University, ⁵Center for Earth and Environmental Science, Plattsburgh State University, ⁶Friedrich-Löffler-Institut, Greifswald - Insel Riems, Germany

Diet has been a significant adaptive force in shaping human and nonhuman primate variation. One of the best-described examples is the expansion of the copy number of the amylase gene (*AMY*) in concordance with the increase of starch consumption in the human lineage. While the evolution of *AMY* is well described in the human lineage and similar *AMY* gene copy number gains have been described in dogs and mice, a comprehensive analysis of evolutionary dynamics shaping the amylase locus across mammals is missing. In the present study, we pursued a systematic investigation of the amylase gene copy number and salivary expression across multiple mammalian lineages. Our data demonstrate that *AMY* copy number amplifications evolved in multiple mammalian lineages independently. We could show that varied diets which include starch correlated with increased *AMY* copy number across mammals including several lineages of nonhuman primates. We also found that copy number amplifications were a prerequisite for expression of amylase enzymatic activity in the saliva of these species. Simulation-based analysis suggested that the observed copy number variation among mammals cannot be explained by neutral evolution alone. Thus, we argue that lineage-specific, convergent adaptive forces have shaped copy number variation of the amylase gene among mammalian species. Our findings underscore the overall importance of gene copy number amplification as a flexible and fast adaptive mechanism in evolution that can independently occur in different branches of the phylogeny.

This study was funded by The National Science Foundation NSF Grant No. 1714867 (OG) and National Institute of Dental and Craniofacial Research grants DE019807 and DE025826 (SR).

Macaque Y-chromosome introgression: Proteomic analysis of four Y-genes between rhesus (*Macaca mulatta*) and cynomolgus (*M. fascicularis*) macaques

CODY A. RUIZ, MORGAN E. CHANEY and ANTHONY J. TOSI

School of Biomedical Sciences, Department of Anthropology, Kent State University

Species in the genus *Macaca* typically live in multimale-multifemale social groups with male macaques exhibiting some of the largest testis:body weight ratios among primates. Males are believed to experience intense levels of sperm competition. Several spermatogenesis genes are located on the Y-chromosome and, interestingly, occasional hybridization between two

ABSTRACTS

species has led to the introgression of the rhesus macaque (*Macaca mulatta*) Y-chromosome deep into the range of the cynomolgus macaque (*M. fascicularis*). These observations have led to the hypothesis that the successful introgression of the rhesus Y-haplotype is due to selectively advantageous functional differences in spermatogenesis genes compared to those of the native cynomolgus Y-haplotype. The hypothesis is examined here at four Y-chromosomal loci – *RBYM*, *XKRY*, and two nearly identical copies of *CDY*. The genes were surveyed in representative animals from north of, south of, and within the rhesus-cynomolgus introgression zone. Our results show that non-synonymous amino acid substitutions were discovered between the two Y-haplotypes; however, statistical analyses did not detect a definite signal of positive selection (likely due to the close relatedness of the two species). Protein structure modeling via I-TASSER revealed different folding patterns between the two species' Y-proteins, and functional predictions via TreeSAAP further reveal physicochemical differences as a result of non-synonymous substitutions. The evolutionary implications, especially in the context of macaque Y-chromosome introgression as a model for early human x Neanderthal introgression, are discussed.

***Ateles* species differences in limb bone properties, body length, and sexual dimorphism**

JACQUELINE RUNESTAD CONNOUR¹, STEPHANIE L. CANINGTON² and KAYLA NIDA¹

¹Biological Sciences, Ohio Northern University,

²Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine

Ateles species are compared to evaluate similarities and sexual dimorphism using skeletal properties (NMNH and AMNH specimens), and body masses and linear measurements from the NMNH database (see below) and literature sources. Species include *belzebuth*, *chamek*, *hybridus*, *paniscus* and *geoffroyi*.

Species sample sizes range between four and thirty-one. Skeletal data include radiograph-derived humeral and femoral cortical area and length, and femoral head diameter for *paniscus* and *geoffroyi*. Linear dimensions include head-body, tail, and foot length for all species. Mann-Whitney tests are used to obtain p-values. For the NMNH database, information is provided with the permission of the National Museum of Natural History, Smithsonian Institution, 10th and Constitution Ave. N.W., Washington, DC 20560-0193. (<https://www.nmnh.si.edu>) Literature sources are available upon request.

Geoffroyi males have longer head-body lengths than females (p-value 0.035). Other species do not demonstrate clear sexual dimorphism.

No species differ in body mass. *Geoffroyi* have shorter humeri and femora, and smaller femoral heads than *paniscus* (0.014). *Geoffroyi* have shorter tails and feet than other species (0.00-0.03), and female *geoffroyi* are also shorter in head-body length (0.00-0.01). *Hybridus* and *chamek* are shorter in head-body length than *belzebuth* (0.00-0.02), and *hybridus* is shorter than *paniscus* (0.01).

In sum, *geoffroyi* are dimorphic and their limbs and tails are not as long as those of other species. Field data collected by Youlatos (2008) suggest *geoffroyi* use less bridging behavior and are more terrestrial than *belzebuth* and *paniscus*. These differences may correspond to less suspensory behavior in association with shorter appendages.

Reconstructing Mobility and Workload in Gule Populations from the Georgia Coast

C. KINLEY RUSSELL¹, CHRISTOPHER B. RUFF¹ and CLARK SPENCER LARSEN²

¹Center for Functional Anatomy & Evolution, Johns Hopkins University School of Medicine,

²Department of Anthropology, The Ohio State University

Long bone cross-sectional properties have been shown to vary in response to mechanical loadings in modern experimental samples and past populations. Here we apply this approach to reconstruct changing patterns of behavior in prehistoric and early historic Gule populations from the Georgia coast. These include a new sample from the recently discovered protohistoric, pre-mission Fallen Tree site on St. Catherines Island. Together with the previously analyzed temporal series from the region, this allows us to assess the effects of changing activity patterns on indigenous populations prior to and during early Spanish missionization.

Peripheral quantitative CT scans of 32 adult individuals from the Fallen Tree site were taken at the femoral midshaft, femoral subtrochanteric, and humeral mid-distal regions, and section properties determined using built-in software and the MomentMacro plug-in for ImageJ. Data were compared for prehistoric pre-agricultural, prehistoric agricultural, pre-mission contact-era, and early and late missionized population samples (total n=178).

Populations on the Georgia coast show a general temporal decline in both anteroposterior (midshaft) and maximum (subtrochanteric) bending rigidity in the femur, indicative of declining mobility and lower limb loading. However, Fallen Tree males are an exception to this trend, suggesting an unusual behavioral pattern just prior to missionization. Humeral rigidity declines through the earliest mission sample (including in Fallen Tree) and then increases in the later mission period, probably due to increased

workload imposed by the Spanish. These results enhance our understanding of Gule adaptations to changing environmental and behavioral demands over a period of several hundred years.

This research was supported by the St. Catherines Island Foundation, The Ohio State University, and Johns Hopkins University School of Medicine.

An ape partial postcranial skeleton from the Middle Miocene of Napudet, Turkana Basin, Kenya

GABRIELLE A. RUSSO¹, CAROL V. WARD², SHARON KUO², FAYE R. MCGECHIE² and ISAAH O. NENGO³

¹Department of Anthropology, Stony Brook University, ²Department of Pathology and Anatomical Sciences, University of Missouri, ³Turkana Basin Institute, Stony Brook University

We report a newly discovered partial postcranial skeleton from Middle Miocene deposits dated to ~13 mya at Napudet, West Lake Turkana Basin, Kenya. The postcranial skeleton (KNM-NP 64631) so far includes a glenoid fossa of the right scapula, right distal humerus, left radial head, some partial metapodials and phalanges, partial thoracic vertebral column, and rib fragments. We compared the Napudet postcranial material with that of extant nonhuman apes and cercopithecoids, and extinct Miocene primates. Overall, the skeleton appears similar in size to large-bodied taxa like *Nacholapithecus* and *Equatorius*, rather than to *Nyanzapithecus*, which is also known from Napudet. The scapular glenoid fossa is pear-shaped, similar to that of *Nacholapithecus*, *Ekembo*, and extant cercopithecoids, and unlike the more oval shape seen in extant nonhuman apes and *Morotopithecus*. However, the elbow complex shares derived shape aspects with living and extinct apes and suggests enhanced humeroradial joint mobility relative to extant cercopithecoids or earlier Miocene taxa like *Ekembo*. KNM-NP 64631 has a humeral trochlea well-separated from a globular capitulum and fairly well-developed zona conoidea on the humerus, and a strongly beveled radial head. The thoracic vertebral bodies appear small relative to the forelimb elements; in this way, they are reminiscent of *Nacholapithecus*. The phalanges are similar overall to those of other Kenyan Miocene hominoids, lacking the extreme length and curvature of later Miocene European taxa. KNM-NP 64631 provides important new information about the locomotor and geographic diversity of hominoids in the Middle Miocene of eastern Africa.

National Geographic Society, The Leakey Foundation (Gordon Getty)

Phylogenetic Affinities of Sivaladapidae within Adapoidea

KATHLEEN RUST

Sackler Educational Laboratory for Comparative Genomics and Human Origins, American Museum

ABSTRACTS

of Natural History, Department of Anthropology, Hunter College, City University of New York

Our understanding of primate evolutionary history has been fueled by invigorated paleontological efforts across the globe, resulting in the identification of new species and an ever-expanding fossil record. While these new discoveries highlight early primate morphological diversity, they have also generated competing hypotheses surrounding the phylogenetic affinities of adapoids and omomyoids. As a contribution to our current understanding of the evolutionary relationships among the earliest primate groups, this study presents the results of an 82 character phylogenetic analysis focusing on the family Sivaladapidae and its placement within the broader adapoid radiation. Previous hypotheses have proposed a close morphological relationship between sivaladapids and European adapoid families, North American notharctids, or the more recently described Asian asiadapids. To test these hypotheses, four independent phylogenetic analyses sampling 19 to 22 taxa were performed using parsimony methods. Qualitative and quantitative characters were taken from the cranium and dentition and focused on the earliest members of each of the commonly recognized adapoid families to avoid any issues of long-branch attraction. Resulting phylogenetic trees generally indicate that the earliest and most primitive sivaladapids share a closer evolutionary relationship with European adapoids rather than asiadapids or notharctids, although Sivaladapidae may be a paraphyletic group and support for a close relationship between all included sivaladapids and any other specific adapoid family is weak. The resulting trees also suggest that relationships among the major families of Eurasian adapoids are closely intertwined, with numerous biogeographic connections between Europe and Asia during the Eocene.

Mechanical stimulus vs. selection in determining entheses morphology in mice

AIDAN A. RUTH and KEVIN M. MIDDLETON

Pathology and Anatomical Sciences, University of Missouri School of Medicine

One of the central goals of biological anthropology is to interpret the life, culture, and activities of ancient humans. Physical activity plays a central role in all of these, and leaves distinct traces on the skeleton. Biological anthropologists frequently use ligament insertion sites, or entheses, as indicators of physical activity in order to study behaviors including tool use in hominins, labor intensity, division, and inequality in archaeological populations, and cultural transitions, among many others. Yet, little is known about genetic (evolutionary) or environmental (plastic) entheses responses to chronic mechanical stimuli.

We assessed differences in the microscopic anatomical structure of the biceps brachii and supraspinatus entheses in mice that have been artificially selected for high levels of voluntary running vs. randomly bred controls (linetype), and further divided those populations into experimental groups that were either allowed ($n=10, 10$) or denied ($n=10, 10$) access to wheels (activity). This experimental model allows us to statistically separate the plastic effects of exercise from those resulting from evolutionary change. Mineralized and unmineralized fibrocartilage thickness was measured using scaled photomicrographs in ImageJ.

Initial results of a linetype x activity Analysis of Covariance indicate no difference between mice of different lines whether given access to wheels or not. These results indicate that fibrocartilaginous entheses do not respond to mechanical stimuli by increasing either mineralized or unmineralized fibrocartilage thickness, but may accommodate these pressures by alternative means.

Support: Department of Pathology and Anatomical Sciences; MU School of Medicine

Genes, race and identity: a brief history

ADAM D. RUTHERFORD

Genes, Evolution and Environment, University College London/BBC

The history of human genetics is intrinsically entwined with scientific racism and eugenics. Francis Galton was one of the first people to apply robust biometric and novel statistical analyses to humans in large datasets, and in doing so, made significant contributions to the emerging fields of psychology, heredity, behavioural genetics, intelligence research and many other disciplines. He was also a racist, and some of his ideas congealed into the phenomenon of his own coinage, eugenics, which in the decades around the turn of the 19th century was not the toxic concept it is today, and was supported on both the political right and left.

Galton's legacy, both negative and positive, cannot be overstated. His ideas were enacted in many countries with longstanding policies of enforced sterilisation and genocide; yet he spawned a field that ultimately would demonstrate the speciousness of his prejudices. However, while genetics has revealed a picture of human variation and migration that does nothing to support traditional and popular views of race, ideas incorporating biological essentialism, determinism and race doggedly persist. The recent advent of direct-to-consumer genetic ancestry testing may also be bolstering a re-emergence of popular biological essentialism, from the trivial - the desire to discover ethnic ancestry, such as Viking or

Indigenous American - to giving succour to white supremacists and racists. This recapitulation of old ideas with new technology makes Galton a historical figure worth revisiting.

What goes around: Mothers' birth condition influences daughters' age at first pregnancy and uterine size in the common marmoset (*Calithrix jacchus*)

JULIENNE RUTHERFORD¹, CORINNA ROSS^{2,3}, DONNA LAYNE COLON³, AUBREY SILLS⁴, TONI ZIEGLER⁵ and SUZETTE TARDIF³

¹Women, Children, and Family Health Science, University of Illinois at Chicago, ²Biology, Texas A&M University, San Antonio, ³Southwest National Primate Research Center, Texas Biomedical Research Institute, ⁴Barshop Institute for Longevity and Aging Studies, University of Texas Health Science Center, San Antonio, ⁵Wisconsin National Primate Research Center, University of Wisconsin, Madison

Reproductive outcomes are incompletely defined as the result of adult health and "lifestyle choices." There is growing consensus across animal and human studies that a female's own birth weight and other aspects of her early life development have a lasting impact on her adult reproductive function. It is not yet established whether her mother's early life characteristics may also play a role. We asked whether age at first reproduction and uterine dimensions in adult female marmosets are influenced by their mother's birth condition. We assessed the impact of maternal (F0) birth condition on daughters' (F1) age at first pregnancy ($n=12$) and on nulliparous adult uterine width, measured via ultrasound ($n=8$). F1 lower birth weight and higher neonatal abdominal circumference each significantly predicted later age at first pregnancy; greater F0 (i.e. maternal) birth weight played an independent and significant role (model $r^2=0.86$, $p<0.0009$). F1 uterine width correlated with body weight only at months 8 ($r=0.88$, $p=0.05$) and 10 ($r=0.78$, $p=0.02$). At 14 months, a larger uterus was associated with lower birth weight ($r=-0.76$, $p=0.01$); additionally, being born to a triplet mother or one who was born at a lower weight was predictive of a larger uterus (model $r^2=0.83$, $p=0.01$). By 16 months, immediately after being paired with a male for the first time, these effects on the uterus had disappeared, possibly due to hormonal effects of ovarian function and/or pregnancy. We suggest that events preceding sexual maturity, both in the life of the individual and before, can shape reproductive parameters.

Funding: "Womb to womb: Programming reproductive development in female common marmoset monkeys" (NIH 1R01HD076018; Rutherford, PI)

ABSTRACTS

Germline epigenetic inheritance: Challenges and opportunities for linking paternal experience with offspring biology and health

CALLEN P. RYAN¹ and CHRISTOPHER W. KUZAWA^{1,2}
¹ANTHROPOLOGY, NORTHWESTERN UNIVERSITY,
²INSTITUTE FOR POLICY RESEARCH,
NORTHWESTERN UNIVERSITY

Recently, novel experimental approaches using model organisms and advanced molecular techniques have demonstrated that a father's experiences can be transmitted through the paternal germline via epigenetic processes. These findings suggest that paternal exposures might influence phenotypic variation and health across multiple generations. However, despite support for paternal germline epigenetic inheritance (GEI) in several species, evidence in humans remains largely unconvincing. Here, we will briefly review the evidence for paternal GEI in non-human animals, and the state of evidence for similar effects in humans. Drawing on epidemiological data, molecular embryology, and reproductive biology, we will outline a framework for the study of GEI in human populations, emphasizing some of the major challenges that researchers in this area still face.

CPR funded by the Natural Sciences and Engineering Research Council of Canada (NSERC).

Near-Infrared Spectroscopy to Predict Collagen Yield

CHRISTINA M. RYDER¹, MATT SPONHEIMER¹, SAHRA TALAMO², HELEN FEWLASS², ERIN SMITH¹ and WILLIAM J. PESTLE³

¹Department of Anthropology, University of Colorado, Boulder, ²Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology, ³Department of Anthropology, University of Miami

Researchers across anthropology's diverse subdisciplines use collagen, the protein component of bone, to answer an array of questions. Paleodietary studies and radiocarbon dating often use protocols dependent upon the presence of collagen. The chemical alteration of bone due to its interaction with the environment, known as diagenesis, presents a colossal problem for methods based on the organic tissue in bone. Here, we employ near-infrared spectroscopy to predict the collagen yields of unprocessed bone in a timely, cost-efficient, and non-destructive manner that can be used by researchers across anthropology and related fields. Near-infrared spectra span 780 – 2,500 nanometers and have wide and overlapping bands which require multivariate processing for chemometric analysis. We used a portable LabSpec 4 with a fiber optic probe to complete the measurements. The near-infrared device introduces a broad-spectrum light, and the absorbance pattern of the material reflects the molecular structure of

chemical functional groups. Here we show, the applications of near-infrared spectroscopy to collagen preservation in 88 ground and whole bone samples dating from 1750 AD to 49 KYA. A partial least squares regression on a calibration subset (n = 44) generated an R² value of 0.92, and a root mean square error of prediction of 2.0%. In the validation set, 24 of 25 specimens were accurately determined to preserve over 3% collagen. We anticipate our probe to be a starting point for more complex analyses including museum-wide surveys and in-field site surveys to monitor the preservation of collagen and other proteinaceous molecules.

1. Center to Advance Research and Teaching in the Social Sciences at the University of Colorado at Boulder
2. CU Boulder Anthropology Department Graduate Student Funding

Virtual Dissection of Complex Masticatory Muscles with DiceCT

RICHARD SAAVEDRA¹, RANGER KILE² and RACHEL A. MENEGAZ²

¹Department of Anthropology, Texas State University, ²Center for Anatomical Sciences, University of North Texas Health Science Center

Weaning is a critical stage in the life history of altricial mammals, with far-reaching impacts on growth trajectories and survival. Post-weaning diet(s) are known to affect craniofacial skeletal morphology as well as masticatory muscle volumes, PCSA, and fiber type ratios. These muscles and their subparts can be functionally grouped into vertical elevators, protractors, and retractors. However, the extent to which these functional groups differ in their responses to dietary changes is currently underappreciated, particularly where they are difficult to isolate through traditional dissection methods. Here we use diffusible iodine-based contrast-enhanced computed tomography (diceCT) to perform digital dissections of small, complex masticatory muscles to assess the effects of longitudinal variation in diet on the growth of functional groups of these muscles.

Sprague-Dawley rats were raised from weaning to adulthood (12 weeks), and randomly sorted into hard and/or soft dietary treatment groups. Post-sacrifice, cranial tissues were fixed in 4% PFM for 36 hours and stored in 70% EA at 4K. Specimens were stained in 11.25% Lugol's solution (I₂KI) for 48 hours before microCT scanning. In 3D Slicer, muscles were manually segmented every 10 slices, the "Fill Between Slices" function was applied, and volumes were quantified. Results suggest that, contrary to our expectations, animals raised on soft diets have larger temporalis and superficial masseter muscles than those raised on hard diets.

DiceCT is a promising method for soft tissue analysis that complements CT analyses of bone. Volumetric data can be obtained for small and/or complex musculature where limitations exist for traditional dissection methods.

Funding was provided by the NSF (BCS-1061368), the Wenner-Gren Foundation and the American Society of Mammalogists.

Sex differences in adrenal hormone production throughout development among Kanyawara chimpanzees (*Pan troglodytes schweinfurthii*) at Kibale National Park, Uganda

KRIS H. SABBI¹, MARTIN N. MULLER^{1,4}, ZARIN P. MACHANDA^{2,4}, EMILY OTALI⁴, RICHARD W. WRANGHAM^{3,4} and MELISSA EMERY THOMPSON^{1,4}

¹Anthropology, University of New Mexico, ²Anthropology, Tufts University, ³Human Evolutionary Biology, Harvard University, ⁴Co-Director, Kibale Chimpanzee Project

Adrenal hormones including cortisol and DHEA/S mediate individuals' responses to environmental conditions through their direct effects on metabolism and behavior. They may also help regulate the coordination of brain, somatic, and behavioral development (Wudy et al. 2007, Campbell 2011). In apes, extended development is associated with adrenarche, a unique developmental stage that marks the maturation of the adrenal gland accompanied by increasing DHEA/S production. Adrenal hormones therefore represent plausible mechanisms that structure critical stages of behavioral maturation before puberty. Small cross-sectional investigations among captive individuals established that chimpanzees experience adrenarche (Cutler et al. 1978, Smail 1982), but the timing and magnitude of developmental shifts in DHEA/S and cortisol have not been studied in wild populations. Here, we use noninvasively collected urine samples from chimpanzees (individuals: cortisol=76, f=48, m=28; DHEA-S=52, f=32, m=20) at Kanyawara in Kibale National Park, Uganda, between 1998 and 2017 to investigate changes in DHEA-S and cortisol production throughout development. Adrenarche, indicated by increasing DHEA-S (n=866), began prior to the typical weaning age in both sexes. Thereafter, males exhibited a steep increase in DHEA-S, plateauing in early adolescence. Female DHEA-S levels increased more gradually, continuing into adulthood. Surprisingly, cortisol (n=13,206) levels were at their minimum at approximately weaning age. Cortisol levels increased through the juvenile period, and males began exhibiting significantly higher levels than females during adolescence. Thus, social development is accompanied by

ABSTRACTS

dramatic shifts in adrenal hormone production that are also sexually dimorphic, revealing a candidate endocrine mechanism for diverging male and female social strategies prior to puberty.

This project was supported by NIH R01-AG045395, and NSF 1355014, 9807448, and 0416125, the Wenner-Gren Foundation, Nacey P. Maggioncalda Foundation, American Philosophical Society, and the Leakey Foundation.

Correlations between low resolution pQCT and high resolution μ CT scanning of trabecular bone: what are potential limits of inference from living people?

JACOBUS P.P. SAERS¹, LILY J. DOERSHUK², NICHOLAS B. STEPHENS², TEA JASHASHVILI^{3,4}, KRISTIAN J. CARLSON^{5,6}, ADAM D. GORDON⁷, TIMOTHY M. RYAN² and JAY T. STOCK^{1,8}

¹Department of Biological Anthropology, University of Cambridge, ²Department of Anthropology, Pennsylvania State University, ³Molecular Imaging Center, Department of Radiology, Keck School of Medicine, University of Southern California, ⁴Department of Geology and Paleontology, Georgian National Museum, ⁵Department of Integrative Anatomical Sciences, Keck School of Medicine, University of Southern California, ⁶Evolutionary Studies Institute, University of the Witwatersrand, ⁷Department of Anthropology, University at Albany, SUNY, ⁸Department of Anthropology, Western University

Trabecular bone variation may be useful as a tool to interpret behaviour in the past. It remains unknown how rapidly human trabecular bone adapts to loading conditions and whether there is variation in norms of reaction with sex or age. These questions are difficult to address in living humans due to the radiation required to image trabecular bone at high resolutions. Low-resolution pQCT imaging can be used but how well data derived from these low-resolution scans correlate to high resolution μ CT data is unknown. Here we compare low-resolution pQCT scans of dry bone to high-resolution μ CT scans to determine the potential amount of information obtainable using living humans to understand norms of reaction to varying experimental conditions.

Single slice pQCT images were taken at 4% bone length at the distal tibia in 50 dry tibiae and compared to standard trabecular properties from an analogous slice and a cubic trabecular bone volume of interest generated from μ CT.

Median pQCT-derived bone density correlates strongly with 2D μ CT BV/TV ($R^2=.95, p<.0001$) and volumetric BV/TV ($R^2=.82, p<.0001$). Correlations between pQCT and other 3D parameters are significant but less strong ($R^2: Tb.Th=.41, Tb.Sp=.60, Conn.D=.20$). Within-slice variation in pQCT bone density correlates with μ CT 2D BV/TV ($R^2=.70$) and 2D Tb.Sp ($R^2=.61$).

The problem of predicting volumetric BV/TV from pQCT density is not resolution but dimensionality and variation in BV/TV throughout the distal tibia. This demonstrates the limits of the level of detail that can be inferred from low-resolution scans of living people in future work.

RCUK/BBSRC grant BB/R01292X/1, NSF BCS-1719187, NSF BCS-1719140, European Research Council under the European Union's Seventh Framework Programme (FP/2007–2013)/ERC Grant Agreement n.617627

A haplotype-level analysis reveals adaptive polymorphic gene duplications in humans affecting pigmentation and hair morphology

MARIE SAITOU and OMER GOKCUMEN
Biological Sciences, University at Buffalo

Polymorphic gene duplications contribute to human phenotypic diversity. To detect potentially adaptive duplications across the genome, we developed a linkage-disequilibrium based method to locate insertion sites of polymorphic duplications. This method allowed us to revolve the haplotypes harboring the duplications for further evolutionary and phenotypic analyses. Using this method, we were able to conduct haplotype-level population genetic analysis of 22 common ($> 5\%$ allele frequency in CEU, YRI or CHB) duplications. To our surprise, we found that majority (15 out of 22) of these duplications are exonic and overlap with genes involved in human morphology, cognitive function, metabolism, detoxification and susceptibility to Huntington's disease. Based on population differentiation of allele frequencies, we focused a partial duplication of the pigmentation-related gene *HERC2* gene where duplicated haplotype reaches up to 75% allele frequency in East Asian populations, while remaining less than 3% allele frequency in European populations. We further showed signatures for non-neutral evolution based on the haplotype. This putatively adaptive *HERC2* duplication was inserted in the midst of its highly-expressed pseudogenes, *HERC2P9*, significantly lowering this pseudogene's expression. In parallel, we found the insertion site of the whole-gene duplication of *KRT34*, a member of the keratin gene family, which is associated with hair morphology. This duplication is common in African populations and increased the expression of *KRT34* in sun-exposed skin. Overall, our study provides a first look at the evolutionary impact of polymorphic gene duplications in human populations, and by doing so, provides several targets and a methodological framework for future studies.

This study is supported by MS's fund from Astellas Foundation for Research on Metabolic Disorders, Graduate Program for Leaders in Life Innovation.

Stable isotope analysis reveals nutritional impacts of anthropogenic food sources in a group of dumpster-feeding Barbary macaques (*Macaca sylvanus*)

SANA T. SAIYED, NOEMI E. TOROCZKAI, MARK R. SCHURR, LEE T. GETTLER and AGUSTIN FUENTES
Anthropology, University of Notre Dame

Anthropogenic impacts on nonhuman primate populations are of growing interest in primate studies. Perturbation of nonhuman primates' local ecologies can lead to resource reduction and increased energetic stress, while increased consumption of anthropogenic foods can contribute to energetic excess and result in conflicts with humans. Because isotope compositions reflect dietary differences, stable isotope analyses can inform comparisons of feeding ecology between populations with varying levels of human interaction. In a previous study, we compared $\delta^{13}C$ and $\delta^{15}N$ values of five groups of Barbary macaques (*Macaca sylvanus*) from the Upper Rock Nature Reserve, Gibraltar, and found significant differences in both stable isotope values amongst groups related to their interaction patterns with humans. In this study, we analyzed hair samples from an additional 11 individuals ($N = 146$). We compared $\delta^{15}N$ and $\delta^{13}C$ values between groups categorized into three ecological niches, reflecting varying exposures to anthropogenic interactions and foods. These analyses include a new group that resides in and around a garbage dump. While $\delta^{13}C$ values did not significantly differ across groups, we found significant differences in $\delta^{15}N$ values, using groups with frequent tourist exposure as the comparison (p -values < 0.05). Two groups in particular, both with low-to-no tourist interactions, reflected significantly higher $\delta^{15}N$ values than the other groups on average, suggesting an anthropogenic effect on macaque foraging ecology. Using these results, in addition to behavioral and ranging data, we argue that stable isotope analyses expand our understanding of anthropogenic influences on primate feeding ecology in specific and beneficial manners.

The Effects of Orthopedic Pathologies on the Prevalence of Hip Osteoarthritis

AUBRIE M. SANCHEZ¹ and SEAN D. TALLMAN^{1,2}
¹Department of Anatomy & Neurobiology, Boston University School of Medicine, ²Department of Anthropology, Boston University

Osteoarthritis (OA) is a degenerative joint disease estimated to be the fourth leading cause of disability (Zampetti et al. 2016). In the U.S., over 2.5 million individuals live with total hip arthroplasties (Kremers et al. 2015), of which 70% attribute OA as the cause (AJRR 2016). Because the majority of anthropological OA research excludes pathological individuals, little is known about how prostheses and pathologies impact OA. This project adds to the research surrounding OA by

ABSTRACTS

investigating its relationship with age, disease and prostheses. The proximal femora of 179 individuals (25-95 years old), from the Edmonds Orthopedic Pathology Collection at the National Museum of Health and Medicine from the Armed Forces Institute of Pathology were analyzed. OA was scored using Jurmain's (1990) method, which employs an ordinal four-point scale to categorize the changes as none/slight, moderate, severe, and ankylosis. It is hypothesized that osteoarthritic hip changes are positively correlated with age and presence of a prosthesis, and that systemic diseases, such as cancer, will increase the likelihood of OA in an individual.

The multifactorial etiology of OA suggests that different populations exhibit different patterns of OA. Results from Chi-square tests show that there is a statistically significant relationship ($p < 0.000$) between degree of OA, recorded disease and evidence of previous injury or prostheses. These results help researchers better understand the etiology and contemporary risk factors of OA, as well as contribute data to OA research on an underrepresented sample.

Funded through thesis research budget of the Forensic Anthropology Program at Boston University's School of Medicine, Department of Anatomy & Neurobiology

Skeletal growth in wild chimpanzees: urinary bone biomarkers capture age variation in bone turnover

AARON A. SANDEL^{1,2}, MILJA ARPONEN³, ISABELLE R. CLARK², SUVI-KUKKA TUOMI³ and KAISA K. IVASKA³

¹Department of Anthropology, University of Texas at Austin, ²Ngogo Chimpanzee Project, ³Institute of Biomedicine, University of Turku

When do animals stop growing and shift energy to reproduction? How unique is the human pattern of development, including the adolescent growth spurt? Despite the importance of growth for life history theory, few studies have investigated growth in primates due to the difficulty of assessing it non-invasively. One innovative solution is urinary biomarkers of bone turnover, which have been used to assess growth in humans, but have not been used in nonhuman primates. Here we present data on two urinary bone biomarkers in a cross-sectional sample of wild chimpanzees: aminoterminal crosslinked telopeptides of type I collagen ("collagen"), a measure of bone resorption, and osteocalcin, a measure of bone formation. Both are high during growth and plateau at skeletal maturity in humans. We collected urine from 10 juvenile (5-9 yrs), 10 adolescent (9-12 yrs), 11 adult (27-37 yrs), and 8 elderly (40-66 yrs) chimpanzees at Ngogo, Kibale National Park, Uganda. We ran mixed models to assess variation in biomarkers based on age class, controlling for urine concentration with creatinine. For both biomarkers, juvenile and adolescent chimpanzees exhibited higher levels

than did adults. Adolescents did not differ significantly from juveniles, but adolescents tended to exhibit higher levels of collagen than did juveniles. These findings confirm that urinary bone biomarkers are a useful method of assessing skeletal growth in wild primates. Future studies should investigate subtler aspects of growth. Importantly, longitudinal data will elucidate the ontogeny of growth, including whether primates exhibit an adolescent growth spurt, as do humans.

The Leakey Foundation, the University of Michigan, the Nacey-Maggioncalda Foundation, the National Science Foundation Doctoral Dissertation Research Improvement Grant (1540259), and the National Science Foundation Graduate Research Fellowship (F031543).

A Comparison of Gunshot Wound Trauma between Physical Crania and 3D Printed Models

JESSICA E. SANGER and ELIZABETH A. DIGANGI
Anthropology, Binghamton University

Computed tomography (CT) data is often utilized in the assessment of skeletal trauma, providing a comprehensive view of injury. In conjunction with three-dimensional (3D) technology, the researcher is granted access with a virtual model to an unaltered perspective that may further provide substantial forensic evidence. In the context of gunshot wound trauma, information such as the location and dimensions of the gunshot wound(s) and in situ fragments are illustrated with a 3D model created using CT scanned data. By utilizing 3D printing, this study assesses cranial gunshot wound trauma to determine the replicability and accuracy of 3D printed models. This research was conducted using CT data for 45 donated fleshed human heads with experimentally-produced gunshot wound trauma. To determine the accuracy of the 3D printed models with regard to entrance wound dimensions, the 3D models were evaluated alongside the original specimens to account for variability and observer error. The results of this study indicate that there is less than a 2-millimeter difference in the entrance wound diameter between the original crania and 3D printed models. Additional statistical analysis using multiple t-tests further suggests that there is no significant difference between the original crania and the 3D printed models ($p > .05$). CT scans along with 3D replication of skeletal trauma provide multiple advantages: reproducibility, objectivity in analysis, as well as the localization of bullet and skeletal fragments in situ. The possibility of 3D modeling and printing models provides a researcher with a non-destructive approach to replicate trauma for research purposes.

This research was supported by a grant from the National Institute of Justice: 2016-DN-BX-0155.

Biogeographic study of human gut associated crAssphage suggests impacts from industrialization and recent expansion

KRITHIVASAN SANKARANARAYANAN^{1,2}, TANVI HONAP^{1,3}, STEPHANIE SCHNORR^{1,3}, ANDREW OZGA^{1,3}, CHRISTINA WARINNER^{1,3} and CECIL LEWIS JR.^{1,3}

¹Laboratories of Molecular Anthropology and Microbiome Research, University of Oklahoma, ²Department of Microbiology and Plant Biology, University of Oklahoma, ³Department of Anthropology, University of Oklahoma

CrAssphage (cross-assembly phage) is a bacteriophage that was first discovered in human gut metagenomic data. CrAssphage belongs to a diverse family of crAss-like bacteriophages thought to infect gut commensal bacteria belonging to *Bacteroides* genus. However, not much is known about the biogeography of crAssphage and whether certain strains are associated with specific human populations. Gut metagenomic data for a total of 3,263 samples from ten studies were *de novo* assembled. Of these, 755 samples contained open reading frames (ORFs) with matches to $\geq 50\%$ of crAssphage reference proteins and were considered positive for crAssphage. For these studies, we find that crAssphage prevalence is low in traditional, hunter-gatherer populations as compared to industrialized, urban populations. Within the same individual, crAssphage sequences show persistence over time. Statistical comparisons showed no association of crAssphage prevalence with host variables such as age, sex, body mass index, and health status. Phylogenetic analysis using a subset of 366 samples demonstrating the presence of a single crAssphage genotype showed a lack of biogeographic structuring. An average linkage clustering approach using 98% pairwise sequence similarity identified 33 crAssphage sequence clusters, one of which is observed across populations in Europe, the Middle East, and the Americas, and a second cluster that is predominantly observed in Asia. We hypothesize that this structuring is suggestive of a recent expansion event within a major crAssphage clade. Overall, we determined that crAssphage presence is primarily associated with an industrialized lifestyle/diet, exhibits limited phylogeographic structure, and its major clade likely underwent a recent global expansion.

This study was supported by the National Institutes of Health (NIH R01 GM089886).

Exploring Provincial Interactions in the Tiwanaku State (C.E. 500-1100) Using Paleodiet Reconstruction

JULIANNA SANTILLAN GOODE¹, ALLISEN C. DAHLSTEDT², PAUL GOLDSTEIN¹, MARGARET SCHOENINGER¹ and KELLY J. KNUDSON²

¹Anthropology, University of California, San Diego, ²Anthropology, Arizona State University

ABSTRACTS

Investigation of multifaceted identities in frontier contexts advances our understanding of relationships between the Andean Tiwanaku state (C.E. 500-1100) and coeval populations. In the Middle Moquegua Valley of southern Peru, relations between Tiwanaku colonists, indigenous mid-valley Huaracane, and coastal peoples remains unclear. It has been argued that Tiwanaku settlement in the Middle Moquegua Valley was almost entirely isolationist. The present study hypothesizes that some individuals interred at the Middle Moquegua Valley Tiwanaku provincial center of Omo M10 engaged in non-Tiwanaku dietary practices during life. New stable isotope data for six individuals buried there is compared with published paleodiet data for Omo M10, a Huaracane site, and two coastal sites. Five Omo M10 individuals had a dietary profile typical of Tiwanaku colonists. Young adult female M10A-7 (buried in an isolated group of tombs) had stable isotope ratios outside the range of the other Tiwanaku individuals and within the ranges of the Huaracane and the two coastal sites, suggesting the need for further research to better understand this anomalous Omo M10 tomb and cemetery context. One hypothesis for M10A-7 is that she was a Huaracane individual who married into the Tiwanaku group. Perhaps she was not considered a full member of the Tiwanaku community who merited burial in a proper cemetery. In conclusion, this study contributes to a deeper anthropological understanding of peripheral contexts as dynamic sites of interaction and exchange rather than static cultural borders.

Validation of the auricular surface method for sex estimation in non-adult human remains

ANA LUISA SANTOS¹, ÁLVARO M. MONGE CALLEJA¹, CLAUDIA M. ARANDA² and LEANDRO H. LUNA³

¹Life Sciences, CIAS, University of Coimbra, Portugal, ²Faculty of Odontology, University of Buenos Aires, Argentina, ³IMHICIHU, CONICET, Argentina

Sex of non-adult individuals is usually not estimated in bioarchaeological and forensic studies because it is argued that skeletal sexual dimorphism is minimal before puberty. However, several methods have been developed to address this issue. In 2017, a new approach based on the shape of the auricular surface of the ilium was proposed by Luna and co-authors after the analysis of the Coimbra skeletal Collection. The present study aims to test if the sexual dimorphic variables obtained in that research are equally accurate in another sample that includes younger ages. Sixty-one individuals (30 males, 31 females) from the Lisbon Collection, aged between 1 day and 18 years-old, were analyzed by two observers without previous knowledge of the sex of the individuals. Data shows a low interobserver error

(ICC>0.92; K>0.74). The discriminant function classified correctly 86.7% of the males and 71% of the females, and the logistic regression, 80.0% and 74.2%. The percentage of accuracy of both the overall and apex morphology was found to be 76.7% for males and 80.6% for females, and the morphometric ratios provide correct results in at least 76.7% of males. The method was equally reliable in younger (0-12y.o.) and older (13-18y.o.) individuals and slightly more accurate in males. The percentages of correct estimations are not influenced by the cause of death (e.g. infectious, heart problems) of the individuals. This study confirms the usefulness of auricular surface shape for sexual estimation of non-adult individuals. Additional validation tests in documented individuals from other geographic regions are suggested.

Research Centre for Anthropology and Health—UID/ANT/00283/2013—FCT

Detecting shifts in the trophic niches of sympatric Verreaux's sifaka (*Propithecus verreauxi*) and ring-tailed lemurs (*Lemur catta*) using stable isotope analyses

NORA W. SAWYER¹, JAMES E. LOUDON¹, RYAN SCHACHT¹, MICHELLE L. SAUTHER² and MATT SPONHEIMER²

¹Department of Anthropology, East Carolina University, ²Department of Anthropology, University of Colorado, Boulder

Behavioral observations have revealed that primate dietary patterns are flexible and reflect phenological and seasonal changes. Throughout the year, primates readily consume their preferred plants species and organs when they become available. These food resources are partitioned differently among primates living in communities. We examined how sympatric Verreaux's sifaka (*Propithecus verreauxi*) and ring-tailed lemurs (*Lemur catta*) co-exist within a small forest by their differing reliance on the plants available to them. We collected fecal matter and behavioral observations from collared individuals during a nine-month period. To examine trophic niches, we analyzed the fecal stable carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) isotope values of lemurs and sifaka (n=224), and the $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values of the plants they consumed (n=128). Fecal stable isotope values represent the undigested portions of diet and should agree with our feeding observations and plant isotope values. We then transformed the $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values into two-dimensional space to represent each species' δ -space as a proxy of their trophic niche. The δ -space of the lemurs was large, encompassing the δ -space of the sifaka. The δ -space of each primate overlapped with the $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values of the plants they consumed and agreed largely with our observations. The fecal $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values and δ -space for each species revealed significant differences between groups, habitat,

and seasons ($P < 0.05$). Our data also revealed intragroup differences demonstrating individual feeding decisions on a month-to-month basis. Overall, the use of isotopic analyses provides a powerful tool for assessing niche space in wild primates.

This project was funded by the National Science Foundation (BCS 0525109).

Sensory cues related to short distance foraging choices in a nocturnal, folivorous primate

RACHEL SAWYER¹, TOLOTRA RANAIVOSON⁵, DAVID WALKER², STEFANO VAGLIO^{2,3}, K A I NEKARIS^{1,4} and GIUSEPPE DONATI¹

¹Nocturnal Primate Research Group, Anthropology and Geography Department, Oxford Brookes University, ²Faculty of Science & Engineering, School of Sciences, University of Wolverhampton, ³Department of Anthropology, Durham University, ⁴Little Fireface Project, Indonesia, ⁵Departement Biologie Animale, Universite d'Antananarivo

Primates have a keen spatial and temporal memory which helps them locate food. Upon detection of a potential food patch, other external senses are required to assess the edibility of potential feeding items. As small-bodied, nocturnal, folivores, *Avahi meridionalis* must be selective in the leaves they eat to avoid over-ingesting harmful plant secondary metabolites. Here we investigate the sensory foraging methods used to locate food and the differences in food sensory cues. We collected behavioral data on sensory foraging methods and used dynamic headspace sampling to collect the volatile organic compounds (VOCs) of feeding and non-feeding leaves of *A. meridionalis*. We analyzed leaf VOCs using thermal desorption and GC-MS. *Avahi meridionalis* used visual scanning in 55% of foraging attempts (FAs) and olfaction in 44% of FAs. We found a significant difference in the use of sensory foraging methods among the top three feeding species, *Harungana madagascariensis*, *Cynometra* sp. and *Canephora madagascariensis* ($X^2=29.2$, $df=6$, $p < 0.0001$). The frequency of olfactory investigation was higher in tree species with fewer VOCs per sample, including *Cynometra* sp. (mean VOC=5.0) and *Canephora madagascariensis* (mean VOC=3.7), compared to *Harungana madagascariensis* (mean VOC=11.3), where visual scanning was used more frequently when foraging. *Avahi meridionalis* rely on both vision and olfaction when foraging for leaves. When foraging on tree species with visually conspicuous differences in leaf morphs (*H. madagascariensis*), *A. meridionalis* appear to rely on vision, whereas on species with less conspicuous leaf differences (*Cynometra* sp., *C. madagascariensis*), olfaction is more important in making foraging decisions.

ABSTRACTS

How to save anthropology: Lessons from primatology and human origins research

KEN SAYERS

Southwest National Primate Research Center,
Texas Biomedical Research Institute

Most early workers interested in human evolution were broadly-trained naturalists. In the early 20th century, authors warned of the perils of academic overspecialization and narrow definitions concerning what constituted an anthropological study of humankind. A historical survey of the literature, including edited volumes, suggests that modern workers have generally, although not absolutely, overlooked these admonitions. The purvey of study is limited: using hand-held tools to skin an antelope, for example, is considered more “anthropological” than using hippocampus-enabled memory to locate a social partner, which is considered more “psychological.” A direction forward is suggested, with illustrations that, if followed in spirit, could help countervail these trends. Studies of langur monkeys on mountains, chimpanzees in fields, and rhesus monkeys on computers illustrate the ecological and behavioral flexibility that underlies everyday primate life; abilities which served as a precursor for the evolution of hominids. Recent fossil evidence from the Miocene and Pliocene, in combination with data from extant forms, suggest those features of niche expansion, social bonding, and information processing that best explain our divergence from apes. Of particular note is that few of these are typically “anthropological” research foci. It is argued that anthropology should constitute a holistic natural history of humankind, progressive in its inclusion of disparate data, and unfettered by the straightjacket of disciplinary boundaries.

This work was funded in part by grants from the Leakey Foundation, National Science Foundation, and National Institutes of Health.

Influence of physical activity on aging and frailty in human foragers

M. KATHERINE SAYRE¹, HERMAN PONTZER², BRIAN A. WOOD³, GENE A. ALEXANDER^{4,5,6,7,8,9} and DAVID A. RAICHLEN¹

¹Department of Anthropology, University of Arizona, ²Department of Evolutionary Anthropology, Duke University, ³Department of Anthropology, University of California Los Angeles, ⁴Departments of Psychology and Psychiatry, University of Arizona, ⁵Evelyn F. McKnight Brain Institute, University of Arizona, ⁶Neuroscience Graduate Interdisciplinary Program, University of Arizona, ⁷Physiological Sciences Graduate Interdisciplinary Program, University of Arizona, ⁸BIO5 Institute, University of Arizona, ⁹Arizona Alzheimer's Consortium

Frailty, a health condition associated with age-related decline in physical function, is a major public health concern in the US. Physical activity (PA) can help mediate functional decline and improve frailty status among older adults by improving

strength, balance, and endurance. Among US adults, PA levels are low and may contribute to high frailty incidence during aging. Individuals living in small scale societies display higher PA levels, but frailty has not yet been assessed in these populations. In this study, we examined PA among the Hadza hunter-gatherers of Tanzania, and assessed the impact of PA level on performance on two common tests of physical frailty: grip strength and the 2-minute walk test. We recruited 54 Hadza participants ($n_{\text{female}}=24$, $n_{\text{male}}=30$, age=11-84), who wore a wrist-worn accelerometer for eight days and completed a grip strength test to assess PA and muscle strength respectively. A subset of participants ($n=31$, age=22-84) also completed a 2-minute walk test to assess physical endurance. Sex and age, but not PA, were significantly associated with grip strength, with males and younger participants displaying greater strength (sex: $p<0.001$, age: $p<0.05$). Sex and PA level was significantly related to performance on the walk test, with males and more active participants achieving greater distances (sex: $p<0.01$, PA level: $p<0.01$). Activity levels are high among the Hadza, and while PA level predicts endurance, PA does not predict muscle strength. In a population with overall higher levels of activity, PA may impact frailty measures differently than what is typically seen in the US.

Supported by NSF Awards 1440867 (Raichlen) and 1440671 (Wood) and the Max Planck Institute for Evolutionary Anthropology, Department of Human Behavior, Ecology, and Culture.

Violence and Geographic Fluidity: Using Incremental Strontium Isotopes to Track Geographic Residence Throughout the Life Course in Prehistoric Arequipa, Peru

CASSANDRA K. SCAFFIDI¹, GEORGE KAMENOV², GWYNETH GORDON³, CRISTINA TICA⁴, REBECCA ULLOA⁵, KELLY KNUDSON⁶ and JOHN KRIGBAUM⁷

¹Archaeological Chemistry Laboratory, Arizona State University, ²Geological Sciences, University of Florida, ³School of Earth and Space Exploration, Arizona State University, ⁴Anthropology, University of Nevada Las Vegas, ⁵Archaeological Chemistry Laboratory, Arizona State University, ⁶Archaeological Chemistry Laboratory, Arizona State University, ⁷Anthropology, University of Florida

Endemic violence can incentivize populations to migrate to safety, or dig in their heels to maintain access to ancestral lands. This study examines the impact of a period of intense violent conflict on migration patterns and assesses how lifetime residential histories varied depending on the absence or nature of cranial trauma. ⁸⁷Sr/⁸⁶Sr measurements ($n = 91$) were taken from incrementally-forming tooth and bone from 59 individuals from the Uraca cemetery (200 – 700 AD); most experienced antemortem or perimortem cranial trauma. Powdered enamel, bone, and cementum were mechanically and

chemically cleaned, digested, and measured for trace element concentrations and strontium isotope ratios. The local (2σ) range is 0.70818 – 0.70832 (mean = 0.70825, SD = 0.00032). All decapitated “trophy heads” were outside the local range, and 58% (7/12) were statistical outliers. Of the non-decapitated population, 23% (11/47) fell outside the 2σ range, with four statistical outliers: two fatally injured males, one uninjured female, and one male with antemortem cranial trauma. Trophy heads had greater ⁸⁷Sr/⁸⁶Sr variance than the non-decapitated (F-test, $f = 0.23$, $p < 0.01$), as did the injured or killed compared to the uninjured (F-test, $f = 83.95$, $p < 0.01$). Mean intra-lifetime ranges were greater for trophy heads than the rest of the population (T-test, $t = 1.79$, $p < 0.04$). The low percentage of outliers, narrow variance, and small intra-lifetime range for women, subadults, and uninjured men compared to fatally injured and decapitated men suggest intra-lifetime geographic fluidity predisposed men to fatal injuries and violent post-mortem dismemberment.

Isotope analysis was funded by Sigma Xi Grants-in-Aid, Research-in-Residence (Integrated Training for Continental Scale Ecology, NSF award #1137336), and the Nell I. Mondy Fellowship, Graduate Women in Science.

Sex differences in behavioral coordination in white-bellied spider monkeys

CLARA J. SCARRY¹, ANDRÉS LINK^{2,3,4} and ANTHONY DI FIORE⁵

¹Department of Anthropology, Sacramento State University, ²Department of Biological Sciences, Universidad Nacional de los Andes, ³School of Management, Universidad Nacional de los Andes, ⁴Fundación Proyecto Primates, Fundación Proyecto Primates, ⁵Department of Anthropology, University of Texas at Austin

Within groups, individuals may differ in their assessment of the relative benefits of alternative activities, making it challenging to achieve coordination and maintain spatial cohesion. Among spider monkeys (*Ateles belzebuth*) in Amazonian Ecuador, males and females differ in both their daily and annual ranging patterns, suggesting potential conflicts of interest over mutually exclusive activities. Male spider monkeys collectively monitor and defend a community range, which requires long daily movements, whereas females occupy smaller core areas and cover shorter distances daily. The fluid association patterns that characterize this species allow individuals to fission into subgroups rather than requiring groups to reach a consensus decision regarding movements. Here, we examine whether individuals coordinate activities and preferentially follow same-sex individuals to maintain cohesion with partners with whom consensus decisions involve lower costs. Between 2010 and 2016, we collected focal animal follows of all adult members of one community, recording the behavior of both the focal animal and its nearest neighbor at 5-min

ABSTRACTS

intervals. We fitted generalized linear mixed-effects models to examine whether behavioral synchrony was affected by the sex composition of focal-neighbor dyads and explored whether there was a sex difference in success at initiating behavioral changes. Overall, same-sex dyads were more synchronized in their activities than mixed-sex dyads. There was no sex difference in ability to successfully initiate a change in behavioral state; rather, individuals were more likely to "follow" same-sex nearest neighbors. These results point to a behavioral mechanism that may make membership in mixed-sex parties less stable than same-sex associations.

Funded by NSF (BCS 0726133, 1062540, 1638822), the L.S.B. Leakey Foundation, the Wenner-Gren Foundation, the Harry Frank Guggenheim Foundation, the National Geographic Society, and the University of Texas at Austin.

Husband, Lover, Pater, Genitor: Concurrency and Paternity in Himba Pastoralists

BROOKE SCENZA¹, SEAN PRALL¹, NATALIE SWINFORD², SHYAMALIKA GOPALAN³, ELIZABETH ATKINSON^{3,4,5}, RICHARD MCELREATH⁶, JACOB SHEEHAMA⁷ and BRENNAN HENN^{2,3}

¹Anthropology, UCLA, ²Anthropology, UC Davis, ³Ecology and Evolution, SUNY Stony Brook, ⁴Analytical and Translational Genetics, Harvard Medical School, ⁵Stanley Center for Psychiatric Research, Broad Institute of Harvard and MIT, ⁶Human Behavior, Ecology and Culture, Max Planck Institute for Evolutionary Anthropology, ⁷School of Medicine, University of Namibia

There is general consensus among researchers that nonpaternity rates in humans are negligible, hovering around 1%. However, these data are in conflict with the anthropological literature, which has documented much more variable rates of concurrent partnerships around the world. This conflict occurs in part because the nonpaternity data that is available comes almost exclusively from western nations where the costs of misallocated investment by fathers is high and the benefits to women of engaging in concurrent partnerships relatively low. Furthermore, we have almost no data matching men's and women's assertions about paternity with genetic paternity data, which is critical to understanding decision-making about paternal investment. Here we match demographic and genetic data from a population of Namibian agropastoralists who regularly practice socially sanctioned concurrency and present rates of nonpaternity among married couples and paternity confidence for both husbands and wives. The nonpaternity rate is 49%, significantly higher than any previously reported rate. Paternity confidence, the percent of time that men and women are accurate in their assertions, is high for both men and women (71% and 76% respectively). These data demonstrate the importance of studying nonpaternity

in a broader suite of populations and opens the door to future studies that can use genetic data to shed light on the roles of social and biological fatherhood. We end by discussing some of the ethical and practical implications of doing nonpaternity research in diverse populations and the importance of community involvement and consent throughout the process.

This material is based upon work supported by the National Science Foundation under Grant No. (BCS-1534682)

Community Outreach: Engaging the Public While Hosting a World Lemur Festival Event at Salt Lake Community College

MELISSA S. SCHAEFER
Anthropology, Salt Lake Community College

Primatology students at Salt Lake Community College (SLCC) engage in community outreach as they plan and host a local event in conjunction with the World Lemur Festival. This is an international festival with local events held worldwide to raise awareness for lemur conservation. The SLCC event is open to the public and features lemur-themed games, activities, and educational materials. Hosting the festival uses multiple High Impact Practices (HIPs) including community-based learning, common intellectual experiences, and collaborative projects; HIPs are known to increase rates of student learning, retention, and success. For the festival, students engage with the community before and during the event. Before the event, each student collects donations for use as festival prizes and silent auction items. This requires that they effectively explain the reasons for the festival to local business owners. During the event, students interact with the guests as they welcome them to the event, run the games and activities, and answer questions. At all stages of the event, students must engage with the community and, among other things, explain to them the importance of lemur conservation. I will present details on the planning and hosting a World Lemur Festival community event as well as preliminary data regarding student learning through participation in the event itself (e.g. 92% of students were able to successfully explain the importance of conservation on a subsequent assignment scoring a 3 or better on a modified 1-4 Likert scale). Results from this experience can serve as a model for other community events.

Response to selection on facial coloration in *Mandrillus sphinx*

JERRED K. SCHAFER¹, ADAM D. GORDON¹, BARTHELEMY NGOUBANGOYE² and JOANNA M. SETCHELL³

¹Anthropology, University at Albany-SUNY, ²Centre de Primatologie, Centre International de Recherches Médicales, ³Anthropology, Behaviour

Ecology and Evolution Research (BEER) Centre, Durham University

Sexual selection theory predicts differential responses to selection in secondary sexual traits, but this is difficult to measure in natural primate populations due to their long lifespans. Mandrills (*Mandrillus sphinx*) provide one of the best examples of sexual selection in the order Primates due to their high levels of sexual dichromatism and size dimorphism, and data are available for 96 pedigreed individuals from a semi-free-ranging colony at the Centre International de Recherches Médicales, Franceville, Gabon. This study examines the response to selection of facial coloration in this species. The sample consists of annual reproductive success (fitness) measurements and repeated measures of luminosity and redness over 17 years. We calculate response to selection using the Price-Robertson equation, which estimates the response as the additive genetic covariance between the traits and fitness. We include individual animal and mother IDs as random effects, and modeled sex, age, and rank as fixed effects. Results show significant ($\alpha = 0.05$) additive genetic variance in coloration traits and fitness measurements in both sexes. Results show a positive response to selection in male redness but not in female redness, or luminosity in either sex. Given the positive response to selection in male redness and previously documented moderate intersexual genetic correlations, these results suggest female redness is at least partially a correlated response to intersexual selection via female choice. However, we cannot rule out that body size or other variables not included in this analysis might also be targets of selection in either sex that influence these patterns.

Microhaplotypes: New markers in Anthropological Genetics

MOSES S. SCHANFIELD¹, REBECCA HART¹, KELLY LONG¹, KATRINA MADDELLA¹, C WOOTEN², ROBERT LAGACE², JOSEPH CHANG², FABIO OLDONI¹, KENNETH KIDD³ and DANIELE PODINI¹

¹Forensic Science, The George Washington University, ²Genetics, Thermo Fisher Scientific, ³Department of Genetics, Yale University School of Medicine

The introduction of Massive Parallel Sequencing (MPS) (Next Generation Sequencing (NGS) can reproduce SNP and STR based testing, but has also lead to the development of new marker types. Though the cost and time for analysis are increased because of the large number of tests performed, the cost per test has decreased.

Originally developed by Kenneth Kidd at Yale. Microhaplotypes (mh) are two or more SNPs in a short sequence of DNA (<300 BP). As part of a forensic science project 28 mh with two, three or four SNPs yielding on average 4, 6 or 9 haplotypes and a maximum of 10, 21 or 45 genotypes

ABSTRACTS

were tested in four populations (European Americans [N=104], African Americans [N=100], Southwestern Hispanics [N=90] and Southeast Asian [N=37]).

Ten of the 28 loci had an *Fst* of less than 0.05 (35.7%) (Considered to be the threshold of significance [Wright]) and none had a significant Chi-square after Bonferroni correction. In contrast, 18 of the 28 loci had *Fst* greater than 0.05 (0.051- 0.278, mean 0.103)(64.3%), and 12/18 (66.7%) had significant Chi-square after Bonferroni correction (*Fst* = 0.099 – 0.278). There were no significant differences in *Fst* significance among populations. African American populations (proxy for African populations) had significant *Fst* 78.6% compared to 50% for the other 3 populations in total, supporting the out of Africa hypothesis

Previous forensic studies have shown that microhaplotypes are useful in calculating the likelihood of population affinity indicating that they maybe of anthropological use

Research was funded through NIJ grant 2017-DN-BX-0164

Species distribution models at different scales: Predicting the chimpanzee geographical distribution at continental and country levels

BENJAMIN J. SCHIERY¹, STACY M. LINDSHIELD¹, PAPA IBNOU NDIAYE², JILL PRUETZ³, STEPHANIE BOGART⁴ and ERIK R. OTAROLA-CASTILLO¹

¹Anthropology, Purdue University, ²Département de Biologie Animale, Université Cheikh Anta Diop, ³Anthropology, Texas State University, ⁴Anthropology, University of Florida

Species distribution (niche) models explain a species' geographical occurrence and are broadly applicable to evolutionary and ecological research. Prior to the emergence of open-access, geo-referenced datasets, chimpanzee niche modeling was limited by the high costs of field surveys. Several chimpanzee niche models have been generated and validated using now-common modeling frameworks across large geographic areas. Meanwhile, less is known about model performance while scaling down to high-resolutions, despite the need for localized niche maps in conservation and management programs. Here, we modeled the occurrence probability of chimpanzees (*Pan troglodytes*) across the African continent, and compared its predictive performance to small-scale data from Senegal. To create the model, we used presence/absence locational data for chimpanzees across Africa, and variables representing the physical environment. We obtained the smaller-scale Senegal data from a 2014 national survey of *P. t. verus* in unprotected areas. Furthermore, we compared 15 modeling methodologies from traditional and Machine Learning frameworks.

We compared predictions using 16 performance diagnostics (e.g., Matthews correlation coefficient; MCC). Results showed that at large scales, the best performing algorithms were Random Forest (MCC = 0.828), Recursive Partitioning (MCC = 0.796), and Multilayer Perceptron (MCC = 0.79). At the smaller scale, the independent Senegal data was best predicted using Random Forest (MCC = 0.88) and Recursive Partitioning (MCC = 0.86). These results indicate that environmental variables are excellent predictors of the chimpanzee range at the local scale. However, these techniques involve diagnostics-dependent trade-offs and users should be familiar with the diagnostic tools best reflecting modeling goals.

Funding for this research was provided by Purdue University's Department of Anthropology (SML) and College of Liberal Arts Exploratory Research in the Social Sciences Grant (EOC).

Missing identities: Identifying burned and cremated remains in bioarchaeological and forensic settings

CHRISTOPHER W. SCHMIDT¹ and ROBIN L. QUATAERT²

¹Anthropology, University of Indianapolis, ²Anthropology, SUNY Buffalo

At times, gathering osteological data from cremains is overlooked because of the challenges introduced by thermal alterations to bone's composition, color, size, and integrity. But neglecting cremains risks having certain populations underrepresented in bioarchaeology. Data collection has improved due to recent advances in methodology and technology that enable greater standardization and more quantitative data. Examples of these advances include efforts to distinguish burned from unburned bone via histology, organic from thermal discoloration via light microscopy, and cut marks from thermal fractures via profilometry. The following archaeological case study exemplifies the value of studying burned bones in that it provides insight into a group that is nearly missing from the osteological record of Indiana: the 8,000-10,000 year-old people of the Early Archaic. Respectively, the sites of Jerger and Steele produced 10.8 and 4.3 kg of highly fragmented and commingled cremains, averaging around 1.4 cm in length. The minimum number of individuals was 14 for Jerger (5 adults and 9 subadults) and 5 for Steele (2 adults and 3 subadults). About 80% of the bone fragments were calcined. But, Steele had significantly more warping and delamination, which indicates its remains had higher soft tissue content at the time of burning. It appears the Steele remains were curated for a shorter period of time than those at Jerger, which also may explain why it had fewer people. In the end, the analysis of human cremains yielded cultural and biological data that would otherwise go undetected.

Forelimb and hindlimb peak forces in *Gorilla*

DANIEL SCHMITT¹, ROSHNA E. WUNDERLICH^{1,2} and ANGEL ZEININGER¹

¹Evolutionary Anthropology, Duke University, ²Department of Biology, James Madison University

Almost all primates experience higher vertical peak forces (Vpk) on their hindlimbs compared to their forelimbs during quadrupedal walking. This pattern, which takes an extreme form in *Pongo* and *Pan*, has stimulated discussion about the role of posterior weight shift in the evolution of hominin bipedalism. The potential mechanisms, including high degrees of hindlimb protraction and forelimb compliance, that drive this forelimb-hindlimb differentiation are currently debated, the resolution of which has implications for models of an arboreal vs. terrestrial evolution of bipedalism. Currently no data exist on the Vpk forelimb/hindlimb ratios for *Gorilla*. We predicted that gorillas would show the same pattern of Vpk distribution as all other primates. We collected vertical peak forces on the forelimb and hindlimb of seven gorillas ranging in age from 5 to 34 years at the North Carolina Zoo. Force and video data were collected as animals walked at self-selected speeds along a long outdoor runway embedded with two force platforms. Gorillas were variable in the degree to which they had higher hindlimb than forelimb Vpk and impulse (F/H Vpk ratio = 84% ± 14%), with younger animals being the most variable. Overall, *Gorilla* showed a more even distribution of forelimb/hindlimb peak and impulse values compared to other great apes. This may reflect terrestrial locomotor behavior and reduced forelimb compliance, lower hindlimb protraction, and more extended knees compared to more arboreal apes, reinforcing the idea that functional differentiation of the forelimb and hindlimb reflect arboreal locomotor habits even among hominoids.

Research supported by the National Science Foundation Grant BCS-1517561

Intra-Population Dietary Variation at Himerá

AUTUMN SCHMITZ¹, LAURIE J. REITSEMA², KATHERINE L. REINBERGER³, STEFANO VASALLO³ and BRITNEY KYLE⁴

¹Department of Anthropology, University of Michigan, Ann Arbor, MI 48109, ²Department of Anthropology, University of Georgia, Athens, GA 30602, ³Regional Archaeological Superintendence, Palermo, Italy, ⁴Department of Anthropology, University of Northern Colorado, Greeley, CO 80639

Social status is closely linked to occupation in complex societies. In ancient Greek society, high levels of physical activity were associated with occupations of lower social classes, and types of physical activity varied dramatically between the sexes. We investigate the relationship between sex, osteoarthritis (OA), and stable carbon ($\delta^{13}C$)

ABSTRACTS

and nitrogen isotope indicators ($\delta^{15}\text{N}$) of dietary protein intake during the 6th-5th century BCE at the Greek colony Himera to examine the relationship between physical activity and diet. We test the hypothesis that OA is associated with diets low in animal protein. Bones of 13 individuals with OA present at two or more joints (7 male, 5 female, 1 unidentified), and 11 individuals observed to have no OA at any joint (7 male, 4 female), were isotopically analyzed. Only adults aged 15-50 years were included, as OA development is positively correlated with age. Mann-Whitney U tests revealed no statistically significant isotopic differences between OA and non-OA groups ($p=0.9547$ for $\delta^{13}\text{C}$, $p=0.6085$ for $\delta^{15}\text{N}$). Although three males exhibit outlying $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values, there are no statistically significant isotopic differences between the sexes ($p=1.0000$ for $\delta^{13}\text{C}$, $p=0.4389$ for $\delta^{15}\text{N}$). This study shows that activity levels, sex, and by extension, status may not have heavily influenced individuals' diets at Himera, at least in terms of access to animal protein. This study therefore supports interpretations that ancient Greeks may have mainly consumed animal protein in religious and sacrificial contexts, with these sacrifices equalizing individuals' access to animal protein, regardless of social or occupational divisions.

This research was funded by National Science Foundation Research Experience for Undergraduates award numbers 1560227 and 1560158, the University of Georgia, and the University of Northern Colorado.

Absolute brain size correlates very strongly with social group size in Primates

P. THOMAS SCHOENEMANN

Cognitive Science and Anthropology, Indiana University

Two recent research reports assessed the "social intelligence" hypothesis in Primates using the largest datasets to date and concluded that ecological variables are more important than social variables in explaining the evolution of larger brains (DeCasien et al., 2017; Powell et al., 2017). However, both exclusively analyzed relative brain size, not absolute brain size. It is not legitimate to use relative brain size unless one can show body size has a direct, independent, causal effect on sociality. It has been argued that larger bodies might simply *allow* for larger brains, and don't have a direct causal influence on the functioning of brains. Empirically, absolute brain size correlates with behavioral ability across primates much better than relative brain size, which is consistent with how we think brains work. Therefore, it is critical to assess the strength of the association between absolute brain size and social group size. For the Powell et al. dataset ($n=155$), log endocranial volume correlates $r=.68$ ($p<.001$) with log group size, but only $r=.16$ ($p<.05$) with percent-fruit-in-diet (phylogeny accounted for using independent contrasts). In addition,

adding log body size into a multiple regression predicting log endocranial volume removes the association with percent-fruit-in-diet ($p=.69$), but maintains a strong association with social group size ($p<.001$; phylogeny accounted for using independent contrasts), suggesting that the contrary conclusions from these recent studies are simply due to peculiarities of their phylogenetic generalized least-squares regression methods. Thus, the social intelligence hypothesis is actually very strongly supported by these new datasets.

This research was supported in part by grant 52935 from the Templeton Foundation titled: "What Drives Human Cognitive Evolution?"

Tibial torsion and patterns of metatarsal robusticity in humans: an osteometric study

MCKENZIE A. SCHRANK^{1,2}, JESSICA S. WOLLMANN¹, AUBREE S. MARSHALL^{1,2} and LAURA T. GRUSS²

¹Anthropological Sciences, Radford University,

²Biology, Radford University

Here we use osteometric data from a modern human sample to test the hypothesis that the very low degree of tibial torsion in the Dmanisi D3901 *H. erectus* individual (1°; modern humans average 15-20°) is related to its unusual pattern of metatarsal robusticity (Pontzer et al., 2010). Anatomically, a lower degree of tibial torsion may be expected to produce a more medial orientation of the foot, with greater stresses engendered in the more central rays of the foot during locomotion. This may explain the relatively greater robusticity in the Dmanisi MT III and IV compared to modern humans. Here we compare tibial torsion and MT robusticity in a sample of 40 young male human individuals from the Robert J. Terry Anatomical Skeletal Collection at the Smithsonian Institution. Tibiae were photographed and the resulting images were used to calculate tibial torsion. MT robusticity (dorso-plantar and medio-lateral bending strength and axial strength) was estimated from external measurements and biplanar x-rays. We found no relationship between tibial torsion and the pattern of robusticity (either bending or axial strength) among the metatarsals. Our results suggest that tibial torsion alone is not adequate to explain MT robusticity patterns in D3901. The extent to which tibial torsion actually influences foot orientation during locomotion is unclear, but our separate experimental study has so far failed to reveal relationships between tibial torsion, foot orientation, and stress patterns in the foot in living human subjects, which corroborates these osteometric results.

Brain size, body size, and time allocation strategies in primates

JOSHUA M. SCHROCK, LAWRENCE S. SUGIYAMA and J. JOSH SNODGRASS

Department of Anthropology, University of Oregon

Diurnal primates spend most of their daytime hours in three categories of activity: resting, foraging, and locomotion. Discovering how different components of species-typical time budgets relate to one another may offer insight on the evolution of primate time allocation strategies. Here, we test the relative strength of time spent in each of these activities in predicting one another. The time budget percentages in our dataset are drawn from published data in focal follow and scan sampling studies of wild non-human primates and represent mean species-level values, averaged between sexes and studies ($n=47$ species). Using phylogenetic least squares regression, we find that resting is much stronger than foraging as a predictor of locomotion ($\Delta\text{BIC}=26.03$), and resting is much stronger than locomotion as a predictor of foraging ($\Delta\text{BIC}=34.49$). These patterns persist after controlling for log brain size, log body size, percent folivory, group size, and mean ambient temperature. Brain size and body size, when adjusting for one another, are the strongest non-time budget predictors of time spent resting. Larger brain size is associated with less resting and larger body size is associated with more resting. Entering resting time into models attenuates the effects of brain and body size on locomotion and foraging, which suggests that resting may mediate the effects of brain and body size on foraging and locomotion. These results suggest that brain and body size may coevolve with relative resting time, and tradeoffs between resting and other more energetically expensive behaviors may influence the structure of species-typical time allocation strategies.

The path to *Homo*, revisited

LAUREN SCHROEDER^{1,2} and REBECCA R. ACKERMANN^{2,3}

¹Department of Anthropology, University of Toronto Mississauga, ²Human Evolution Research Institute, University of Cape Town, ³Department of Archaeology, University of Cape Town

The transition from *Australopithecus* to *Homo* was not straightforward. Exploration of this divergence is complicated by the diverse morphology that characterizes the genus *Homo* at this transition, the existence of coexisting taxa, and their wide geographic distribution. The likely ancestor of *Homo* is also uncertain. Recent studies have indicated that multiple evolutionary forces have been acting on our lineage, contributing to the complex evolution of our genus. Here we build on a previous study, providing an expanded analysis (both in terms of fossils and data points) of the evolutionary processes that have driven the

ABSTRACTS

emergence of the diverse cranial and mandibular morphology of our genus. We apply statistical tests developed from evolutionary quantitative genetics theory to investigate whether the differences between late *Australopithecus* and early *Homo* across eastern and southern Africa can be explained by natural selection or genetic drift. In cases where selection was detected, further tests were conducted to identify the specific traits that were under strong selective pressures. Results are consistent with previous findings that a scenario involving selection is necessary to explain a transition from an *Au. africanus*–*Au. sediba*–*Homo*, while transitions from *Au. africanus* to various early *Homo* groups that exclude *Au. sediba* can be achieved through drift alone. Interestingly, when *Au. afarensis* is included in the analyses we find that selection needs to be invoked to explain any transition from *Au. afarensis* to early *Homo*. This may support a simpler (non-adaptive) path to early *Homo* in a southern African context.

Reappearance Diversity: Quantifying Musicality in Primate Vocalizations

DAVID SCHRUTH¹, CHRIS TEMPLETON² and DARRYL HOLMAN¹

¹Anthropology, University of Washington, ²Biology, Pacific University

Musical behavior predates the emergence of *Homo sapiens* and primitive song could have evolved in primates 65 MYA, convergent with and independent of its emergence in Aves and Cetaceans. The avian literature uses quantitative metrics such as *trill rate*, *consistency*, *repertoire size*, *song bout length*, and *complexity* to evaluate song quality. There have been few analogous efforts to quantify the aesthetic qualities of primate vocalizations. We developed a novel method to quantify the elaborateness of acoustic displays using published spectrograms of primate vocalizations ($n=832$ calls). These spectrograms (plots of acoustic energy across both frequency and time) were visually scored along the following ethnomusicologically universal acoustic parameters: *tone*, *interval*, *transposition*, *repetition*, *rhythm*, and *syllabic diversity*. Principal components analysis was used to reduce the scores to a single univariate measure of musical elaborateness. The resulting index is mathematically defined as the expected number of syllables reappearing within a call. Specifically it is the count of unique syllables multiplied by the probability that any given unit reoccurs over time or at different frequencies. This “*reappearance diversity*” correlated well with vocal display contexts. To test the general utility of the index we explored popular co-evolutionary theories on the function of song such as group and pair level signaling as well as the acoustic [habitat] adaptation hypothesis. Species that live in monogamous family

units (2-5 individuals) had higher index values. Reappearance diversity was not related to habitat as would have been consistent with the acoustic adaptation hypothesis.

Historic *Treponema pallidum* genomes: Towards a reconstruction of the evolution of treponemal diseases using ancient DNA

VERENA J. SCHUENEMANN

Institute of Evolutionary Medicine, University of Zurich, Institute for Archaeological Sciences, University of Tuebingen

Among the worldwide prevalent treponemal diseases, syphilis appears as a global threat that is currently re-emerging. However, the origins of syphilis and other treponemal diseases are so far unresolved and are subject to an intensive scholarly debate. Until now, assumptions on its origins and evolutionary history could only be drawn from osteological analyses of past cases and genetic analysis of contemporary *T. pallidum* genomes; contributions from ancient DNA are very rare and have, until now, failed to provide genome-level data.

Recently, the first historic *T. pallidum* genomes (two from *T. pallidum* ssp. *pallidum* and one from *T. pallidum* ssp. *pertenue*) were recovered from skeletons interred at the Convent of Santa Isabel in Mexico City, operational between the 17th and 19th centuries. Our analyses indicate that different *T. pallidum* subspecies caused similar diagnostic presentations that are normally associated with syphilis in infants, and potential evidence of a congenital infection of *T. pallidum* ssp. *pertenue*, the causative agent of yaws. Contemporaneous newly sequenced genomes from historic Europe further elucidate *T. pallidum*'s past and can contribute to the understanding of the global distribution of different *T. pallidum* strains in the early modern times.

Altogether, the recovery of *T. pallidum* genomes from archaeological material opens the possibility of studying its evolutionary history at a resolution previously assumed to be out of reach and thereby establishes a new method that could greatly contribute to uncovering the mystery regarding the origins of treponemal diseases.

Periodical increase of dust load reduces chewing efficiency in forest dwelling Western chimpanzees (*Pan troglodytes verus*)

ELLEN SCHULZ-KORNAS¹, JULIA STUHLTRÄGER¹, MARCUS CLAUSS², ROMAN M. WITTIG^{3,4} and KORNELIUS KUPCZIK¹

¹Max Planck Weizmann Center for Integrative Archaeology and Anthropology, Max Planck Institute for Evolutionary Anthropology, ²Clinic for Zoo Animals, Exotic Pets and Wildlife, Vetsuisse Faculty, University of Zurich, ³Department of Primatology, Max Planck Institute for Evolutionary

Anthropology, ⁴Tai Chimpanzee Project, Centre Suisse de Recherches Scientifiques

It has been debated to what extent dust contributes to volume loss of the tooth crown and chewing efficiency. While the findings of controlled feeding studies in ungulates have suggested that dusts does not result in tooth wear, it is unknown to what extent primates in the wild are affected by dust as potential stressor of the digestive system. Here, we collected fecal samples from 13 Western chimpanzees (*Pan troglodytes verus*) from the Tai forest (Ivory Coast) during a six month sampling period covering both a dry period with trade wind-borne dusts accumulating on plant foods and a wet period when the dust is washed off. Fecal particle size was measured as an indicator of chewing efficiency and compared with feeding ecological data of the sampled population. Both were matched to 3D surface texture data measured on molar facets of 26 skulls from the same population. During the dry period the mean fecal particle size was larger, indicating a reduced chewing efficiency compared to the rest of the observation period. Similar to the changes in chewing efficiency, the dust particles led to increased abrasive wear evidenced by smaller texture features and a higher density of fine furrows. Our findings indicate that a periodical increase in dust loads places a dietary-physiological stress on the digestive system of chimpanzees. We suggest that this climatic phenomenon represents a constraint underestimated in paleo-environmental reconstructions in fossil hominins so far and we propose new ways to account for this in future studies.

This research was funded by the Max Planck Society.

Genetic History of Los Floridanos, Florida's First Spanish Families

THEODORE G. SCHURR¹, CRYSTAL B. SOLANO², CLARE SUPER¹ and RAQUEL E. FLESKES¹

¹Anthropology, University of Pennsylvania, ²Cultural Heritage, Los Floridanos

In this project, we explored the genetic ancestry of Los Floridanos and attempted to trace their connections to different populations who contributed to their formation in the New World. Working with 127 members of the Los Floridanos community, we characterized the uniparentally-inherited portions of the human genome (mtDNA and Y-chromosome) to determine female and male lineages, and used phylogeographic methods to trace their ancestral connections to different regions of the world, including the Americas and Europe. We also employed the GenoChip to investigate autosomal SNP diversity in these individuals, hence, the genetic contributions of ancestors from various parts of the world. We observed an array of West Eurasian mtDNA haplogroups (H, HV, I, J, K, N1a, T, U2, U4, U5, W) in Los Floridanos participants that commonly

ABSTRACTS

appear in Europe and the Near East, with haplogroup H being the most frequent lineage. Y-chromosome data also largely confirmed this pattern, with most male lineages appearing in Los Floridanos men (E1b1b, I1, I2, J, R1a, R1b) also occurring in European populations. At the autosomal level, Los Floridanos members showed a strongly European ancestry. On average, some 60-85% of their biparental markers came from European source areas (British Isles, Western Europe, Southern Europe, etc.), with a mixture of ancestries from other geographic locations also being identified, except for the Americas. In the context of historical and genealogical evidence, we are using these genetic data to investigate the Spanish colonization of North America, and in particular the establishment of the first colony in Florida.

This research was supported by University Research Funds and Faculty Research Funds to T.G.S., and by Los Floridanos.

Through thick and thin: Tooth crown strength and enamel thickness variation in apes and fossil hominins

GARY T. SCHWARTZ¹, AMANDA MCGROSKY¹ and DAVID S. STRAIT²

¹Institute of Human Origins, Arizona State University, ²Department of Anthropology, Washington University in St. Louis

Measures of relative enamel thickness (RET) are used extensively as key features in hominin systematics and in functional interpretations of hominin tooth design. Here, we provide a novel perspective on enamel thickness (ET) variation as it relates to fracture mechanics theory. Recent studies have elucidated the behavior of "ribbon" fractures (both radial and marginal) that propagate through the enamel cap and can result in catastrophic abfraction. Fracture theory predicts that ET does not confer equal resistance to radial vs. margin fractures: ET strengthens the crown against radial fractures as thickness^{3/2} but only strengthens the crown against margin fractures as thickness^{1/2}. Thus, "summary" measures of ET likely only provide coarse information about tooth strength. Therefore, we tested (1) whether RET is significant predictor of tooth strength, and (2) whether teeth are designed such that they are equally strong against radial vs. margin fractures. ET data were collected from published microCT crown sections in various ape and fossil hominin species to evaluate the relationship among both radial and marginal fracture resistance and RET. Correlations between RET and the force to propagate radial and margin fractures (Prf and Pmf, respectively) are modest, suggesting that RET is of limited utility for understanding tooth function. Prf scales with significant positive allometry relative to Pmf indicating that teeth are structurally

asymmetric with regard to fracture resistance. These results are discussed within the broader context of current knowledge of hominin masticatory configuration and dietary ecology.

Colonial urbanism: A comparative exploration of skeletal stress in two 18th century North American French colonies

AMY B. SCOTT¹, MARIE DANFORTH², SARAH MACINNES³, NICOLE HUGHES¹ and MATTIA FONZO¹

¹Anthropology, University of New Brunswick, ²Anthropology and Sociology, University of Southern Mississippi, ³Fortress of Louisbourg National Historic Site, Parks Canada

In the early 18th century, French colonial expansion into North America was well underway with urban centers developing quickly across the landscape. Two such colonies, separated by the bulk of the continent, were the Fortress of Louisbourg along the north Atlantic coast and New Biloxi along the Gulf of Mexico. Established in 1713, the Fortress of Louisbourg was the seat of the French cod fishery and a military stronghold before it was destroyed in the 1760s. In contrast, New Biloxi was an important staging region for French inland expansion into the Louisiana territory in the 1720s. For this research, 27 individuals (20 males, 3 females) from the Moran cemetery at New Biloxi were compared to 26 individuals (18 males, 3 females) from the Block 3 (1713-1723) cemetery at the Fortress of Louisbourg to assess patterns of skeletal stress in French colonial North America. In general, the Moran individuals showed increased evidence of antemortem tooth loss, and dental caries, whereas the Block 3 individuals showed more evidence of trauma, enthesal changes, and childhood indicators of stress. While both sites represent early French colonies, the military function of Louisbourg versus the administrative function of New Biloxi no doubt contributed to the skeletal differences observed. Despite the relatively short period of occupation at both sites, this early colonial period provides significant insight into the lived experience of the 18th century French and the many challenges they faced with rising urbanism on the new frontier.

This research is supported by a SSHRC Partnership Development Grant (#890-2017-0049) (AS).

Dental morphology of fossil *Homo sapiens*

G RICHARD SCOTT¹ and MARIA MARTINON-TORRES²

¹Anthropology, University of Nevada Reno, ²National Research Center on Human Evolution, Museum of Human Evolution, Burgos, Spain

The definition of the "modern dental complex" for fossil *Homo sapiens* includes: (1) traits that may be unique to *H. sapiens*, such as the full absence of shovel shape and/or labial convexity, winging,

round lower premolars without accessory cusps and specific groove patterns; (2) traits that, with some exceptions, are only found in *H. sapiens*, such as three-cusped and four-cusped upper and lower molars, respectively; and (3) traits that are not usually found in modern humans, such as cingulum-like Carabelli and protostylid forms and high middle trigonid crests. While the general morphology of Late Pleistocene *Homo sapiens* can be framed in the variability of contemporary modern groups, "fossil *Homo sapiens*" often display primitive retentions that are mostly lost in recent groups, such as higher degrees of incisor labial convexity, vestigial labial and buccal cingular derivatives in the anterior teeth, more robust root systems, and more complex occlusal surfaces in posterior teeth. Here we present examples that illustrate the variability of crown and root morphology in fossil versus contemporaneous modern human teeth.

Trophic shifts, diversification, and the adaptive origins of crown primates

JEREMIAH E. SCOTT

Department of Medical Anatomical Sciences, Western University of Health Sciences

The visual-predation hypothesis proposes that certain derived features shared by crown primates reflect an insectivorous ancestry. Critics of this idea have argued that because insectivory is uncommon among extant primates it is unlikely to have been a major influence on early primate evolution. The present study tests two alternative hypotheses for the low frequency of insectivory that are compatible with an insectivorous ancestor: (1) that trophic evolution was biased, such that herbivory evolved repeatedly with few shifts back to insectivory, and (2) that insectivorous lineages have diversified at a lower rate than herbivorous lineages. Model-based analysis conducted using trait data for 307 primate species indicates that transition rates into and out of insectivory are similar, rejecting the hypothesis of biased trophic evolution. On the other hand, the hypothesis of asymmetric diversification is supported, with insectivorous lineages having a lower rate of diversification than herbivorous lineages. This correlation is mediated by activity pattern, however: insectivory occurs mostly in nocturnal lineages, which have diversified more slowly than diurnal lineages. The frequency of insectivory also appears to have been shaped by numerous transitions out of, but few transitions into, the range of body sizes at which primate insectivory is biologically feasible. These findings suggest that the current distribution of trophic strategies among extant primates is the result of macroevolutionary processes that have favored the proliferation and persistence

ABSTRACTS

of herbivory relative to insectivory. Thus, the low frequency of insectivory is not necessarily an indicator of its adaptive importance at the origin of the clade.

Assessment of dental microwear formation using a capuchin model: grit versus diet

ROBERT S. SCOTT¹, OLIVIA BOSS¹, LARISA R. G. DESANTIS², CLAIRE MARCIL¹, CALLUM ROSS³, ANDREW SCHWARTZ², BARTH W. WRIGHT⁴, KRISTIN A. WRIGHT⁴, ADAM VAN CASTEREN⁵ and DAVID S. STRAIT⁵

¹Anthropology, Rutgers, The State University of New Jersey, ²Earth and Environmental Sciences, Vanderbilt University, ³Organismal Biology & Anatomy, University of Chicago, ⁴Biomedical Graduate Studies, Kansas City University of Medicine and Biosciences, ⁵Anthropology, Washington University in St. Louis

Despite decades of work, the precise causes of dental microwear patterns remain uncertain. A long-standing prevalent view links dental microwear patterns with the mechanical properties of foods consumed. More recently, environmental grit has been implicated as a principal causal agent in microwear formation and as a possible source of complex dental microwear textures. Recent work on quantifying the actual food mechanical properties of primate diets has also opened the door to a more precise assessment of the relationship between specific food mechanical properties and dental microwear textures. Here we report on a large sample of dental microwear textures from robust and gracile capuchins consuming a range of foods and including robust capuchins exposed to high levels of grit. Our sample includes 126 molar casts scanned using white-light confocal profilometry including *Sapajus nigritus*, *Sapajus libidinosus*, *Sapajus apella*, *Sapajus cay*, and *Cebus olivaceus* drawn from collections at the American Museum of Natural History, Field Museum of Natural History, and the National Museum of Natural History. No correlation was evident between food mechanical properties and dental microwear textures for a comparison of *Cebus olivaceus* to *Sapajus apella*. High grit loads for the robust capuchin species *Sapajus libidinosus* and *Sapajus nigritus* noted elsewhere remain a possible explanation for the complex dental microwear textures noted for these species.

Research supported by NSF awards BCS 1440541, 1627206, 1440545, and 1440542.

Resource preference of a female aye-aye (*Daubentonia madagascariensis*) in Torotorofotsy, Madagascar

TIMOTHY M. SEFCZEK¹, DOMENICO R. RANDIMBIHARINIRINA², OLIVIER RANDRIANARISON³ and EDWARD E. LOUIS^{1,3}

¹Conservation Genetics, Omaha's Henry Doorly Zoo and Aquarium, ²Mention Anthropobiologie et Developpement Durable, Ecole Doctorale Sciences de la Vie et de l'Environnement, University of Antananarivo, ³Research, Madagascar Biodiversity Partnership

The extreme morphological adaptations of aye-ayes (*Daubentonia madagascariensis*) include continuously growing incisors, elongated, clawed digits and a unique metacarpophalangeal joint in the third digit. Aye-ayes use these features to extract insect larvae from woody substrates, known as percussive foraging. However, aye-ayes are thought to be too large-bodied to sustain themselves on invertebrates. Several studies have suggested alternative resources as the aye-aye's main food, including *Canarium* sp. seeds and *Ravenala madagascariensis* nectar. Insect larvae were essentially said to be a fallback food, consumed when other resources were unavailable. More recently, invertebrates were described as the most frequently consumed resource over the course of a year in Kianjavato. While dietary composition has been determined in several aye-aye populations, food preference has not. We examined the feeding preference of an adult female aye-aye for two years in the undisturbed eastern rainforest of Torotorofotsy, Madagascar. Our goal was to determine a preference index for aye-aye foods. We conducted six-hour follows using continuous focal-animal sampling. We also collected monthly phenological data along 20 transects to estimate availability of *Canarium* seeds, *Ravenala* flowers and invertebrates. A negative binomial regression ($\alpha=0.05$) indicated that the aye-aye consumed significantly more invertebrates than *Canarium* seeds overall ($z=-13.79$; $df=47$; $p<0.001$). Additionally, based on consumption and abundance estimates, invertebrates were the aye-aye's preferred resource. At no point did we witness the aye-aye consume nectar from *Ravenala* flowers. Our findings indicate that invertebrates are the aye-aye's preferred food and that aye-aye can persist on an insectivorous diet, despite their large body size.

Omaha's Henry Doorly Zoo and Aquarium, Columbus Zoo and Aquarium, Primate Conservation Inc., Cleveland Metroparks Zoo, Sacramento Zoo, Margot Marsh Biodiversity Foundation, OSU Alumni Grant, OSU Larsen Research Grant

Understanding Canine Cranial Morphology: The Impact of Selection for Facial Reduction in Dogs

MOLLY C. SELBA¹, GERHARD U. OECHTERING², HOCK GAN HENG³ and VALERIE B. DELEON¹

¹Department of Anthropology, University of Florida, ²Small Animal Department, University of Leipzig, ³Department of Veterinary Clinical Sciences, Purdue University

Through artificial selection, humans have altered the morphology of domestic dogs and created the range of physical traits present in dog breeds today. The purpose of this study was to analyze the effects of breeding on facial reduction in domestic dogs (*Canis lupus familiaris*). The study of these dogs allows for a natural experiment on facial reduction and can provide additional insight into this previously recognized phenomenon, which has been associated with the morphological evolution of animals such as primates. Using clinically obtained CT scans, we established two groups of dogs based on skull shape. In both groups, we recorded a total of 62 cranial and mandibular landmarks. Through geometric morphometric analysis, we determined that cephalic index is associated with nearly all cranial shape differences in dogs. The shape changes in the crania and mandibles co-vary, and are both associated with cephalic index. Within the hard palate, there appears to be modularity associated with the pre-maxilla, maxilla, and palatines. The majority of the shape change in the hard palate is centered on the maxilla, specifically at the carnassials. Whereas the shape change seen in the mandible is mainly a uniform anterior-posterior shortening and a medial-lateral widening, the shape change seen on the hard palate includes a unique anterior projection and rotation of the maxillary carnassials resulting in disruption of the functionally important carnassial complex. These results help us better understand facial reduction as a result of artificial selection and highlight the deleterious effects of these morphological changes in domestic dogs.

Is the locomotor diversity in odd-nosed monkeys reflected in their olecranon size or orientation?

MICHAEL S. SELBY

Biomedical Sciences, Georgia Campus-Philadelphia College of Osteopathic Medicine

More suspensory anthropoids typically have relatively short and posteriorly oriented olecranon processes. Odd-nosed monkeys perform more suspensory locomotor behavior than other colobines and have been shown to have a lower olecranon to ulna ratio, however, their olecranon lengths relative to body size and olecranon orientations have not been described. Here, odd-nosed monkeys are compared to a broad sample of anthropoids to see if their olecranon length and orientation resemble apes or

ABSTRACTS

spider monkeys more so than other colobines. Olecranon and distal ulna lengths were measured from the center of rotation at the trochlear notch, with olecranon orientation defined as the angle between these two lines. Size was corrected by a geometric mean of limb joint surfaces. Angles and ratios were compared by ANOVA with Bonferroni *post hoc* adjustment. Olecranon/distal ulna length ratio is lowest in highly suspensory anthropoids: hylobatids, *Pongo*, and *Ateles*. Odd-nosed monkeys and *Presbytis* have the next lowest ratios. Relative olecranon length is shortest among hominoids; odd-nosed monkeys, *Ateles*, *Presbytis* and *Ptilocolobus* have the next lowest ratios. Hylobatids have the longest distal ulnae, while *Pygathrix*, *Ateles*, *Presbytis*, and *Erythrocebus* have the next longest, followed by *Pongo*, *Nasalis*, *Mandrillus*, and *Theropithecus*. Hominoids have the most posteriorly oriented olecranons, but olecranon angle does not significantly differ between odd-nosed monkeys and other arboreal cercopithecines. Odd-nosed monkeys, therefore, are intermediate to hominoids and other colobines in olecranon length, but not orientation. Whether this reflects current differences in locomotor behaviors or nascent suspensory adaptations requires further investigation.

Supported by PCOM.

Investigating variation in euarchontan dental topography as a signal of dietary breadth

KEEGAN R. SELIG¹, MALCOLM S. RAMSAY^{2,3} and MARY T. SILCOX¹

¹Anthropology, University of Toronto Scarborough, ON, ²Anthropology, University of Toronto, ON,

³Institute of Zoology, University of Veterinary Medicine, Hanover, Germany

Sympatric animals may reduce interspecific competition by consuming diets of differing breadths (i.e. generalists versus specialists). Dental topographic metrics have proven useful for comparing occlusal form, providing a quantitative means for examining euarchontan dietary adaptations. What remains unexplored is the degree to which these metrics relate to dietary breadth. In particular, are animals that exploit a broad diet characterized by more varied dental morphology compared to specialists? Our study examines the dental topography of three pairs of sympatric euarchontan species that vary in dietary breadth to explore the relationship between dietary and morphological variability.

We measured occlusal curvature (DNE), complexity (3D-OPCR), and relief (RFI) of the lower m2 in sympatric samples of *Alouatta palliata* (n = 8) and *Ateles geoffroyi* (n = 14); *Eulemur fulvus* (n = 5) and *Haplemur griseus* (n = 3); and *Tupaia tana* (n = 5) and *Tupaia gracilis* (n = 4). Each pair of species represents a generalist and a specialist, respectively. We scored dental

wear for each specimen based on the relative degree of occlusal dentine exposure. We used principal component analysis and Fligner-Killeen tests to examine patterns of variation.

Our results show that generalists are characterized by greater variability in topography and wear compared to specialists. Furthermore, variability in occlusal topography is taxon dependent, with species showing different amounts of variability depending on which metrics are considered. Overall, our study indicates that dental topography is useful for examining dietary breadth and may also be useful for examining niche partitioning in extinct euarchontans.

This research was supported by an NSERC Discovery Grant to MTS and a Pilot Research Grant from the Department of Anthropology at the University of Toronto to KRS.

Heat increases IGF-I uptake in growth plate and perichondrium of mouse hindlimbs: Implications for human evolution

MARIA A. SERRAT, GABRIELA ION and DOMINIC THOMAS

Department of Biomedical Sciences, Marshall University School of Medicine

Research into the molecular regulation of bone elongation has identified multiple potential targets for limb length evolution. However, it is still unclear how these processes are altered by the environment. We previously demonstrated that heat increases limb length and vascular supply to skeletal growth plates. Here we use in vivo multiphoton microscopy to measure uptake of the growth-promoting hormone IGF-I in growth plate and surrounding perichondrium at temperatures within a physiological range of healthy human knees measured during normal outdoor activities. We tested the hypothesis that heat increases uptake of IGF-I in growth plate cartilage. Hindlimbs of 5-week old male and female C57BL/6 mice (N=10) were cooled (22C) or warmed (36C) and fluorescently labeled, biologically active IGF-I (~6 µg/g) was visualized in the proximal tibial growth plate and perichondrium by multiphoton imaging at consistent depths and times as we have previously described. Data were collected in standardized regions. Statistical analysis was performed using ANOVA and t-tests in SPSS. There was >1.5 times more IGF-I in the superficial perichondrium at 36C relative to 22C (t=2.0, p<0.05), and more than twice as much at the deepest edge of the perichondrium immediately adjacent to the growth plate (t=2.49, p<0.05), as well as in the growth plate itself (t=2.41, p<0.05). Our results support the hypothesis that heat increases IGF-I uptake in the proximal tibial

growth plate and perichondrium of young mice. This study is relevant for understanding limb development and evolution in humans living at climate extremes.

Funding Information: National Institute of Arthritis and Musculoskeletal and Skin Diseases of the National Institutes of Health (1R15AR067451-01)

Bovid paleocommunities and *Australopithecus* environments in the lower Awash Valley, Ethiopia, from ~3.8-2.95 Ma

CHALACHEW M. SEYOUM¹, JOHN ROWAN², KAYE E. REED¹ and WILLIAM H. KIMBEL¹

¹Institute of Human Origins, School of Human origin and Social Change, Arizona State University, Tempe AZ 85281, USA, ²Department of Anthropology, University of Massachusetts Amherst, Amherst, MA 01003, USA

The lower Awash Valley (LAV) of Ethiopia has produced a rich Pliocene record of *Australopithecus* and associated mammalian faunas. Bovidae numerically dominate LAV assemblages in terms of both species richness and absolute abundance. Here, we combine bovid mesowear and abundance data for seven temporally well-constrained assemblages from Woranso-Mille (~3.8-3.3 Ma) and Hadar/Dikika (~3.5-2.95 Ma) to infer patterns of environmental change through time. Bovid mesowear data (n=458 specimens) consisted of cusp relief and shape and were scored together on a 0-4 rank scale from collections housed at the National Museum of Ethiopia. Abundance data come from previously published literature and were analyzed at the tribal level. We show moderate shifts in mesowear through the LAV from ~3.8-3.3 Ma: specimens from Woranso-Mille show wear indicative of mixed-feeding (average across three assemblages=40.7%), whereas the lower portions of the Hadar Formation contain significantly more browsers (Basal Member=33.3%; Sidi Hakoma=38.8%) than all other assemblages. Despite being roughly contemporaneous in time, the Burtele and Waytaleyta assemblages from Woranso-Mille significantly differ from those of the Sidi Hakoma and Denen Dora members at Hadar/Dikika, with the latter having fewer grazers. One striking abundance difference is the scarcity of Reduncini at Woranso-Mille compared to Hadar/Dikika. Reduncini favor water-logged floodbank environments and their commonness at Hadar/Dikika may reflect the persistent fluvio-lacustrine system associated with paleolake Hadar. Collectively, these results suggest that *Australopithecus* environments in the LAV

ABSTRACTS

varied both temporally and spatially. The latter is an important consideration when assessing regional patterns of hominin biogeography and diversity.

This research was funded by a Leakey Foundation Baldwin Fellowship and Elizabeth Harmon and Donald C. Johanson Dissertation Grants from the Institute of Human Origins to C.S.

Skeletal element independence and implications for quantification

VALERIE SGHEIZA

Anthropology, University of Illinois Urbana-Champaign

This work was undertaken to test skeletal element types for independence of recovery. This informs the accurate representation of uncertainty in existing estimators of number of individuals, such as Most Likely Number of Individuals. Calculations based on elements that have dependent recovery probability will underestimate uncertainty. Appendicular skeletal inventories were collected from two forensic and two archaeological collections of individuated remains ($n = 160$). Analyses were performed in R. The binary inventory file was converted to a correlation matrix of 24 left and right element types. Using eigen-decomposition, eigenvector 1 showed differences in probability of recovery, rather than relationships between elements. According to a distance matrix of standardized eigenvectors 2-5, relationships in element recovery were nonrandom with respect to anatomical position. The left and right ossa coxae grouped with each other and with the shoulder girdle. The femur and the long bones of the upper limb showed unrelated recovery between the right and left side. The lower leg and foot grouped together, including elements from opposite sides. When distance values were aggregated by side, the shortest distances were between the radius and ulna, tibia and fibula, and calcaneus and talus. These results were corroborated by cluster analysis of eigenvectors 2-5 and angular arccosine representation of correlation values. The results indicate that best results in skeletal quantification would be achieved by treating the shoulder and pelvis, upper limb and femur, and lower limb and foot as dependent units, taking particular care to avoid including anatomically adjacent elements in the same calculation.

Neandertal-Upper Paleolithic *H. sapiens* population dynamics

LAURA L. SHACKELFORD¹ and SHEELA G. ATHREYA²

¹Anthropology, University of Illinois Urbana-Champaign, ²Anthropology, Texas A&M University

In his seminal 2005 work on early modern humans, Erik Trinkaus cautioned that the question of *Homo sapiens*' origins had shifted from

seeking to understand Late Pleistocene population dynamics to one of searching for evidence of gene flow in an effort to determine the "purity of living humanity." In doing so, he influenced a field-wide course correction for a generation of scholars who have reconfigured the study of Late Pleistocene hominins to be more than simply a study of "archaic" vs. "modern." Here, we share our research on early *Homo sapiens* in South and Southeast Asia to show how the study of our evolutionary history can move past questions of the purity of modern humans and address the evolutionary forces that have shaped human phylogeny during this time period. We reflect on the ambiguities inherent in interpreting human phylogeny with the perspective gained from the mentorship and wisdom that Erik has shared with us over the years. Specifically, we address the utility of moving beyond typological questions and reevaluating traditional taxonomic narratives to accommodate the increasingly complex fossil record. By abandoning an archaic vs. modern evaluation of the evolution of our species, we examine the influence of environmental dynamics on human migration and adaptation during OIS 5-3, and we consider the behavioral, chronological, and biological changes that occurred in the context of regional populations of the Late Pleistocene.

An Ethnographic Approach to Characterizing Zoonotic Disease Risk from Primate Hunting in an Indigenous Reserve in Guyana

MARISSA S. MILSTEIN¹, CHRISTOPHER A. SHAFFER², TIFFANY M. WOLF¹ and DOMINIC A. TRAVIS¹

¹Department of Veterinary Population Medicine, College of Veterinary Medicine, University of Minnesota, ²Department of Anthropology, Grand Valley State University

Primate hunting is a particularly important interface for zoonotic disease transmission, and many highly virulent diseases have emerged through the butchery and consumption of primate bushmeat. While an increasing number of researchers have sought to understand how human behaviors influence zoonotic disease emergence from bushmeat in Africa and Asia, the topic remains little studied in Amazonia. In this study, we used an ethnographic approach to characterize zoonotic disease risk from primate hunting among indigenous Waiwai in Guyana, South America. During three, 3 month study periods from 2015 to 2017, we combined structured, semi-structured, and unstructured interviews with hunter self-monitoring and participant observation to address the following research question: how does the hunting, preparation, and consumption of primates put the Waiwai at risk for acquiring zoonotic disease? The majority of Waiwai ate bushmeat 2-3 times/week and primates were

among the most frequently harvested prey. Primate hunting was also integral to Waiwai identity and they exhibited a cultural aversion to meat from domestic animals. While the Waiwai engaged in several behaviors that mitigate the risk of exposure to zoonotic pathogens, including discarding entrails, avoiding the consumption of animals that appear diseased, and always thoroughly cooking meat, we also identified activities that may perpetuate disease risk. For example, individuals frequently cut themselves during butchery and village dogs often consumed discarded entrails. Our study is one of the first to focus on the association between bushmeat hunting and disease in Amazonia and demonstrates the importance of ethnographic methods for characterizing and mitigating zoonotic disease risk.

Funded by the National Geographic Society, Veterinary Pioneers in Public Health Fund of the University of Minnesota's Center for Animal Health and Food Safety, and the American Association of Physical Anthropologists

Mitochondrial DNA Analysis of M21 Xiongnu Tomb in Hulaha Valley of Mongolia

XINYUE SHAO, NAIFAN ZHANG and YAQI GUO
School of Archaeology, Jilin University

Xiongnu was an ancient nomad in North China. Xiongnu rose to great power in the 3rd century B.C. (Eastern Zhou), and began to decline in the 1st century B.C. (Eastern Han Dynasty), ruling the Mongolian Plateau for about three hundred years. The generation, existence and development of Xiongnu played an important role in the history of China, producing profound and far-reaching effects. However, the race type of the main body of Xiongnu remain in dispute.

In order to answer this question at molecular level, we performed ancient mtDNA analysis of M21 Xiongnu tomb in Hulaha Valley of Mongolia. A 393bp fragment (nucleotides 16017-16409) of the mtDNA Hypervariable Region₁ was amplified by using two sets of overlapping primers. And to identify the gender, we used a pair of primers to amplify the AMG gene.

The results indicated that M21 belonged to the Europe Haplogroup T2a1b1. Previous studies showed that only European haplogroups U and J were found in Xiongnu, it was the first time that T was present in Xiongnu. Combined with the previous ancient DNA analysis of Xiongnu populations, we suggested that the main body of the Xiongnu belong to Mongoloid. As for the Europoid found in Xiongnu, may be absorbed into Xiongnu during the rapid expansion and the conquest of Xiongnu power.

ABSTRACTS

Exploring biological anthropology content on popular science YouTube channels

DARSHANA SHAPIRO

Center for Human Evolutionary Studies,
Anthropology, Rutgers, The State University of New Jersey

YouTube is a popular social media platform that hosts >700 channels categorized as science/technology or education with 500k+ subscribers. This suggests there is interest in science among YouTube users, making them a potential audience for science communication about biological anthropology (BA), and making the site a valuable teaching resource and tool for combating misinformation. This project examined popular science/technology and education channels to determine if they were making BA-focused videos and, if so, how often, on what topics, and how many views were they getting. The aim was to characterize the current YouTube BA landscape, and investigate the problems and potential it has for science communication. ChannelCrawler.com was used to identify relevant science/technology (N=15) and education (N=20) YouTube channels with 500k+ subscribers. Relevance was based on whether a channel created science- or education-focused content in a variety of fields for a general audience. The science/technology channels ranged from having 0-53 BA videos (0-3.22% of their content). The education channels ranged from having 0-26 BA videos (0-4.15% of their content). Some common topics (3 or more channels) included new discoveries, whether humans are evolving, monogamy, and 23andMe. Videos were opportunistically sampled for content quality and attempts were made to determine the qualifications of the creator(s); both of these things varied. This study suggests that YouTube has both pitfalls, in that content is generally created by non-experts and is not reviewed, and potential opportunities for anthropologists to create content or partner with existing channels to improve the quality of their BA videos.

Assessing the determinants of primate gait kinematics in an ecological and phylogenetic framework, Part II: Platyrrhine quadrupedalism

LIZA J. SHAPIRO¹, TOBIN L. HIERONYMOUS², NOAH T. DUNHAM², ALLISON MCNAMARA¹ and JESSE W. YOUNG²

¹Anthropology, University of Texas at Austin,
²Anatomy and Neurobiology, Northeast Ohio Medical University

Lab-based studies of primate locomotor kinematics are limited in substrate complexity and species availability. Here, we use video data gathered on wild primates to explore ecological and phylogenetic influences on quadrupedal locomotor kinematics. We quantified locomotor kinematics for eleven platyrrhine species at field sites in Ecuador and Costa Rica (n = 1,233 strides)

and remotely measured the orientation and diameter of locomotor substrates. The effects of substrate variation (ecology) and phylogenetic history on locomotor kinematics were explored in multivariate space using redundancy analysis combined with variation partitioning. Results indicate a strong phylogenetic signal influencing locomotion among the eleven species, accounting for 58% of the total kinematic variation. Callitrichines were maximally divergent, driven by their preferred use of higher speeds and asymmetrical gaits. Pitheciids were also unusual in their use of lower limb phases within symmetrical gaits (including lateral sequence gaits). Controlling for phylogeny, limb phase was strongly correlated with substrate declination, leading to more frequent use of lateral sequence gaits. Substrate inclination was positively correlated with limb phase as well as hindlimb duty factor. Functionally, the effects of substrate condition on kinematics are consistent with previous analyses that indicate small primates moving on large substrates prefer higher speeds and asymmetrical gaits, whereas larger taxa prefer symmetrical gaits and adjust limb phase and/or duty factors as gravitational components shift with substrate orientation. Broadly, our results suggest that phylogenetic and kinematic divergence may have been strongly correlated during primate evolution.

Research supported by NSF BCS-1640552 and BCS-1640453.

Comparing Sleep Segmentation Between Traditional and Western Populations: a Test of the Sentinel Hypothesis

ERIC C. SHATTUCK¹ and DAVID R. SAMSON²

¹Institute for Health Disparities Research, University of Texas at San Antonio, ²Department of Anthropology, University of Toronto, Mississauga

The sentinel hypothesis proposes that sleep characterized by repeated bouts of nighttime wakefulness (i.e., segmented sleep) may be an adaptive response to dangerous or unpredictable environments. Wakefulness, combined with staggered sleep patterns, ensures that some members of the group are alert to threats throughout the night, as described in the Hadza, thereby contributing to group survival. Using actigraphic data from Tanzania and Madagascar and secondary data from the Midlife in the United States (MIDUS) dataset, we explored the presence of sentinel-type sleep patterns in three distinct populations (n = 2150; 1,203 USA, 33 Hadza, 54 Malagasy). Linear mixed models found greater WASO values in Hadza and Malagasy individuals ($\beta = 0.61$ and 0.5 , respectively; $p < 0.0001$) compared to US Caucasians, indicating a strong sentinelized sleep pattern. No significant WASO differences between ethnic groups in the US were found. Decreased sleep efficiency was found in the Hadza and Malagasy as well ($\beta =$

-0.51 and -0.4 , respectively; $p < 0.0001$). Taken together, these results suggest that the relative safety of Western sleep environments permits longer bouts of continuous sleep. Intriguingly, however, African-Americans had the shortest sleep time of any group at ~ 5 hours/night (SD = 1.05; $\beta = -0.08$, $p = 0.03$). Although ethnic differences in sleep quality in the US have been widely noted, actigraphic data are limited. Further use of these devices in the US and in natural sleeping populations will result in greater understanding of the social, environmental, and genetic drivers of sleep variability across the globe.

Missing anthropologists: The lack of minority representation in bioanthropology

AGUSTIN FUENTES and SUSAN GUISE. SHERIDAN
Anthropology, University of Notre Dame

Substantive analyses suggest that a multitude of voices are absent or in the extreme minority in biological anthropology theory and practice. The "view" from a relatively homogeneous racial, sexual and experiential background remains the dominant paradigm in research and teaching on and about past populations. At the same time there is increasing evidence that diverse voices, life experiences and perspectives enrich and alter the shape, content and impact of biological anthropological research and theory, making it more inclusive and better representing the range of human experience and variation. Increasing attention to underrepresented groups of the past, enhanced by new analytical, statistical methods, and theoretical approaches has provided a glimpse of the potential diverse perspectives to reconstructions of daily life in antiquity. What, then, as scholars are we to make of the lack of diversity in bioarcheological, paleoanthropological, and human biological practice? How do we enhance our practice so that it is more inclusive and how might that change our interpretations and representations of human bodies and context of the past? Here we offer an overview of where substantive gaps in diversity influence our analyses and elaborate on possible remediation and its potential impacts on practice, theory, and teaching.

Deconstructing genetic influence: evolution of the primate craniodental complex

RICHARD J. SHERWOOD^{1,2}, ANNA M. HARDIN¹, RYAN P. KNIGGE^{1,2}, DANA L. DUREN^{1,2}, JANARDAN SUBEDI³, SARAH WILLIAMS-BLANGERO⁴ and MICHAEL C. MAHANEY⁴

¹Pathology and Anatomical Sciences, University of Missouri School of Medicine, ²Orthopaedic Surgery, University of Missouri School of Medicine, ³Sociology and Gerontology, Miami University, ⁴Human Genetics and South Texas Diabetes and Obesity Institute, University of Texas Rio Grande Valley School of Medicine

ABSTRACTS

The dentition and jaws are the most frequently used elements in assessments of the phylogenetic status of fossil primates. However, the fundamental genetic architecture underlying variation in dentognathic traits is still poorly understood. Demonstration of genetic influence on trait variation is necessary to eliminate biases resulting from trait redundancy and to identify independent trait sets for use in phylogenetic analyses.

To examine the genetic architecture of dentognathic traits, dental impressions were taken from 993 members of the Jirel population (Nepal) aged 18-76 years. We captured numerous quantitative phenotypes describing morphology from high-resolution dental casts. A maximum-likelihood variance components-based method was used to estimate the heritability of each trait and the genetic correlation of each trait pair. All measures were significantly heritable ($p < 0.05$). Heritability of tooth crown areas were high (~0.70 - 0.90) with arch dimensions more moderate (~0.35-0.60). The strongest genetic correlations are found between tooth crown areas, and between arch width and lengths within and between the maxilla and mandible. Molar crown areas and jaw arch lengths are highly correlated; however, crown areas are not highly correlated with jaw width measurements.

The Jirel pedigree provides an unparalleled opportunity to investigate fundamental aspects of dentognathic genetic architecture in a population with minimal access to dental care. Future work will combine these findings with our genetic epidemiological work on the craniofacial complex. The net result will be a set of synergistic studies that complement and inform each other, allowing us to explore the mechanisms responsible for craniofacial evolution in novel ways.

Supported by NIH R01 DE018497, and NIH R01 AI037091, NIH R01 AI044406

Urbanization and Ancient Parasitism

DONG HOON SHIN¹, SANG-YUCK SHIM², HWA YOUNG LEE², YONGJUN KIM¹, JONG HA HONG¹ and MIN SEO³

¹Department of Anatomy, Seoul National University College of Medicine, ²Department of Archaeology, The Baekje Culture Foundation, ³Department of Parasitology, Dankook University College of Medicine

The impact of urbanization on human civilization, especially on the health status and disease states of ancient populations, is very large, because different kinds of infectious diseases newly emerged, became endemic or sometimes disappeared as urbanization progressed in human history. Archaeoparasitologists presumed that a similar phenomenon has been occurring in parasitism during urbanization, as the infection rates of soil transmitted helminths doubtless increased when large numbers of people came

to congregate and live progressively sedentary lifestyles in limited spaces. Whereas this conjecture is reasonable with reference to modern clinical reports, it has not been supported by bioarchaeological evidence so far. In this sense, our archaeoparasitological studies of the last 10 years, performed on specimens collected at excavation sites in South Korea, are meaningful to concerned researchers. In this presentation, we will introduce our studies on archaeological specimens of the ancient Baekje Kingdom: samples from Buyeo, the capital city of the Kingdom, and others from outlying counties. We found that soil-transmitted helminth eggs were evident mostly in the capital city samples, with very few in the county specimens. This strongly suggests that parasitism in ancient Korean society was closely related to population density, in that the counties of the Baekje Kingdom were so sparsely populated that there was a significantly lesser probability of soil-transmitted parasite infection relative to the capital city. Our series of studies shows that parasitism, especially in the form of soil-transmitted helminth infections, might have been seriously influenced by urbanization in human history.

This work was supported by a National Research Foundation of Korea (NRF) grant funded by the Korean government (MSIP) (NRF-2016R1A2B4015669).

SNPs discovered in European GWAS shape worldwide facial diversity

MARK D. SHRIVER¹, JULIE D. WHITE¹, TINA LASISI¹, RYAN J. ELLER², TOMÁS GONZÁLEZ-ZARZAR¹, KARLIJNE INDENCLEEF^{3,4}, JIARUI LI^{3,4}, HANNE HOSKENS^{3,4}, ALEJANDRA ORTEGA-CASTRILLÓN^{3,4}, ARSLAN ZAIDI⁵, SETH M. WEINBERG⁶, JOANNA WYSOCKA⁷, SUSAN WALSH², JOSHUA M. AKEY⁸ and PETER CLAES^{3,4}

¹Anthropology, Penn State University, ²Biology, Indiana University-Purdue University Indianapolis, ³Electrical Engineering, Katholic University Leuven, ⁴Medical Imaging Research Center, UZ Leuven, ⁵Biology, Penn State University, ⁶Oral Biology, University of Pittsburgh, ⁷Developmental Biology, Stanford University School of Medicine, ⁸Ecology and Evolution, Princeton University

Recent discoveries of genes shaping facial variation are helping us address questions about patterns of facial variation in humans. For example, how much of the genetic architecture underlying facial shape is shared across populations? We propose a framework for determining the extent to which global facial variation is driven by variants discovered in European cohorts: We examined 218 SNP peaks resulting from a meta-analysis GWAS of two large cohorts of European ancestry (N = 7,632) for allele frequency correlations among 26 population groups from the 1000 Genomes Project (1KGP). Using diverse facial and genetic databases, we constructed population-specific ancestry consensus faces for the 1KGP population groups. We quantified

the effect size of SNPs discovered in a European GWAS on 1KGP consensus faces and compared these average facial effects to the allele frequencies. We identified 53 loci (24.3%) passing the False Discovery Rate threshold of 0.0019 and 29 loci (13.3%) passing the Bonferroni threshold of 0.00023, including *ALX1*, *FGF8*, *SIX1*, and *TRPS1*. These results suggest that contemporary global patterns of craniofacial diversity are shaped by clinal variation in allele frequency for loci that are shared across populations. Several of these loci also show signatures of selection and are enriched for archaic alleles. This suggests that selection and archaic introgression played an important role in shaping human craniofacial diversity. While our study demonstrates the utility of SNPs discovered in European cohorts, GWAS in diverse, underrepresented populations will further advance our understanding of the evolutionary history of facial form.

PSU Center for Human Evolution and Diversity (CHED)

Post-mortem Birth, Death in Childbirth, or Mortuary Practices? A Case Study From Bronze Age China

ASHLEY SHULTS¹, RUILIN MAO², HUI WANG², IVY YEH-HUI YUAN³ and SARA JUENGST¹

¹Department of Anthropology, University of North Carolina at Charlotte, ²Department of Archaeology, Gansu Provincial Institute of Cultural Relics and Archaeology, ³School of Humanities, Nanyang Technological University

Analyzing fetal remains in relation to adult burials can contribute to research on maternal health and the possible cause of death of the mother and child. Post-mortem birth, death in childbirth, and mortuary practices are difficult to interpret in the archaeological record, as they often have similar bioarchaeological signatures. In the instance of post-mortem death, the fetus is expelled from the womb by built up bodily gasses after the burial, and is typically found inferior to, and in line with the mother's pelvis. Obstructed births may result in infant remains associated with the lower pelvic girdle; however, this may be confused with mortuary treatment that places a deceased infant over a woman's abdomen. This poster uses a case study from the cemetery site, Mogou, in the Gansu Province of China, dated to 1750-1100 BCE. In laboratory data analysis conducted in Summer 2018, we analyzed a 32 week old neonate (M1650 R4) excavated from between the femurs of a 12-15 year old female (M1650 R3), inside the side chamber of the grave. Over 75% of the female and 25% of the fetal skeletons were preserved, and neither individual presented any signs of skeletal pathology. This case study demonstrates the difficulty of differentiating between these possibilities, and the importance of archaeological context when assessing the burial of infants and mothers.

ABSTRACTS

Morphological Analysis of Human Skeletal Remains from a Late Neolithic Dolmen, Switzerland

INGA SIEBKE¹, ANJA FURTWÄNGLER², NOAH STEURI³, GABRIELE ARENZ¹, MARIANNE RAMSTEIN⁴, JOHANNES KRAUSE^{2,5,6} and SANDRA LÖSCH¹

¹Department of Physical Anthropology, Institute for Forensic Medicine, University of Bern, Switzerland,

²Department of Archaeo- and Palaeogenetics, Institute for Archaeological Sciences, University of Tübingen, Germany, ³Department of Prehistory, Institute for Archaeological Sciences, University of Bern, Switzerland, ⁴Archaeological Service Bern, Switzerland, ⁵Max Planck Institute for the Science of Human History, Jena, Germany,

⁶Senckenberg Centre for Human Evolution and Palaeoenvironment, University of Tübingen, Germany

The inhumations from the dolmen burial in Oberbipp represent a unique ensemble to study Late Neolithic population structures and lifeways in the area of today's Switzerland. Radiocarbon dating was used to evaluate the occupation of the dolmen. The recovered fragmented and commingled inhumations formed the basis of this morphological study. A minimal number of individuals, age-at-death, sex, stature and pathologies were evaluated. Additionally, the sex was determined by aDNA analysis. Skeletal elements of the entire human skeleton were recovered with at least 42 individuals based on the femora. Age classes from neonate to adult (43% subadults, 57% adults) with 7% children below six years were buried within the dolmen. Slightly more males than females (44% males, 35% females, 22% id) were recovered. Stature was estimated from femora (n=3) indicating an average body height between 154-157cm. The caries intensity is 7.9% (49/618 teeth). Two occupation phases could be reconstructed between 3550-2650BCE and at least three generations (aDNA) were primary buried in the dolmen. No indications for fatal interpersonal violence were observed. However, unspecific pathological alterations, age related degenerations, and healed fractures were recorded. A possible separation of burial areas for males and females within the dolmen is hypothesized. Based on the analysis it is concluded that the individuals buried within the dolmen are representative for a farming population of the late Neolithic.

This Project is funded by the Swiss National Science Foundation (CR3113L_157024) and the Deutsche Forschungsgemeinschaft (KR4015/4-1)

Trabecular ontogeny of the mandibular condyle in callitrichids

NICOLE D. SIEGEL and CHRISTOPHER J. VINYARD
Anatomy and Neurobiology, NEOMED

Several bony and soft tissue structures of the callitrichid masticatory apparatus have been studied to understand how gouging behavior in

marmosets is facilitated by specific morphologies. While marmoset craniofacial anatomy indicates features that likely enable relatively wider gapes compared to non-gouging tamarins, these studies have largely failed to demonstrate morphologies that assist in generating or resisting relatively large bite forces. A previous comparison of condylar trabeculae between adult gouging and non-gouging platyrrhines found that marmoset condylar trabeculae may be less robust than non-gougers. We extend this work by comparing the ontogeny of condylar trabecular morphology in gouging marmosets versus non-gouging tamarins.

We collected μ CT images of the mandibular condyles of 13 adult and 7 neonatal common marmosets (*Callithrix jacchus*) and 9 adult and 6 neonatal cotton-top tamarins (*Saguinus oedipus*) at a voxel resolution of 20.5 μ m. We processed the entire condylar trabecular volume in Avizo 8.0 and measured several trabecular metrics in BoneJ. We compared trabecular features across ontogeny and between species.

We found that *C. jacchus* undergoes a marked decrease in bone volume fraction during ontogeny, while *S. oedipus* experiences a slight increase. Both species lose connectivity with age; *C. jacchus* more markedly than *S. oedipus*. While trabeculae in both species are more spaced in adults, this change is more marked in *C. jacchus*. Collectively, we see little evidence in marmosets for age-related increases in load-resistance abilities in the condylar trabeculae further supporting the argument that marmosets are not adapted for generating relatively large bite forces during gouging.

NSF BCS-0959438, BCS-0412153

A Systematic Review of Palaeoepidemiological Investigations in Neoplastic Disease

THOMAS SIEK

Institute of Archaeology, University College London

There are claims in the palaeopathological literature that the prevalence of neoplastic disease began to increase during the Medieval period. However, these claims are rarely supported with any in-depth explanation or comparative studies, and consequently, evidence for an increase in neoplastic prevalence is scant. To explore whether in fact there was an increase (or simply why palaeopathologists think there was an increase), a systematic review of published, palaeoepidemiological data was undertaken. While filling a gap in the bioarchaeological literature, this review aimed to determine if a noticeable rise in neoplastic prevalence could be detected over time. A suite of search criteria was established to filter and isolate palaeoepidemiological studies from palaeopathological case reports. The systematic review identified less than ten

investigations regarding neoplastic disease. Unfortunately, these previous studies did not use effective methods to interpret their results and, as they did not provide enough detail regarding the skeletal assemblage's demographic profile, these studies precluded themselves from any in-depth comparison. Despite this, it was possible to use the reported data to perform an approximation of neoplastic prevalence. The results did not indicate a drastic increase in neoplastic disease over time. However, these results must be viewed with extreme caution due to the low number of investigations and the overlapping and wide time-spans they cover. The findings from this systematic review indicate that the palaeoepidemiology of neoplastic disease requires much more investigation, beginning with the establishment of better, standardized practices.

Chronic diseases in Amazonian populations: Socioepidemiology and biocultural perspectives

ARIANA KELLY SILVA¹, LÍGIA A. FIGUEIRAS², ROSEANE B. TAVARES³ and HILTON P. SILVA⁴

¹Secretariat of Education of Para and Anthropology

Department, SEDUC and Federal University of Para,

²Center for Social Sciences and Education,

University of the State of Pará, ³Anthropology

Department, Federal University of Para,

⁴Anthropology Department, Federal University of Para

In Brazil, the African-derived groups have been historically discriminated. Even though there is a National Policy for the Health of the Black Population (PNSIPN) there is still a dearth of actions for its implementation. Especially among the Quilombola populations, hypertension, type 2 diabetes and Sickle Cell Disease (SCD) are not adequately identified. This work analyzes the links between socioepidemiologic and biocultural aspects of these rural afroderived groups and the main challenges faced in their search for health. Data comes from projects conducted between 2008 and 2016 with the participation of over 2500 people, of 24 Quilombola communities, and 60 SCD patients from Pará State. In general the most prevalent diseases among children are related to the respiratory and digestive tracts, dermatitis and dermatosis. In relation to the weight patterns there is a simultaneous occurrence of undernourished (up to 4%) and overweight (up to 10%) in 0 to 10 year old children, and the women present a high prevalence of overweight and obesity (21%). Men present a high frequency of hypertension (18%). Among the patients, 65% live in poverty, in periurban and urban areas, 83% consider themselves "Black" or "Brown", and the majority indicates having suffered some form of discrimination throughout their lives. In general, the harsh conditions of life, low economic status, environmental situation and social vulnerability of the rural Amazonian populations have strong

ABSTRACTS

impacts on their well-being. The work of biological anthropologists in Brazil is fundamental to help empower the Black populations in their struggle for health rights.

Biological anthropology in Brazil: Past and present perspectives

HILTON P. SILVA

Anthropology, Universidade Federal do Pará

In Brazil, Physical Anthropology has been a recognized field of studies since the end of the 19th Century. Nevertheless, starting in the 1950's until the early 1990's, this field almost disappeared from academic institutions, even though some individual researchers continued to work with themes related. As a holistic and dynamic field, throughout its history, Biological Anthropology has proven its importance. Nevertheless, until 2010 there was no formal training, whether at the undergraduate or graduate level, in Physical/Biological Anthropology in the country. In 2010 the Graduate Program in Anthropology of the Universidade Federal do Pará (PPGA/UFPA) was inaugurated as the first training program involving the four traditional fields: Archeology, Bioanthropology, Linguistics and Sociocultural Anthropology, becoming the only one in the nation to offer training at the Master's and Doctoral levels specifically in Biological Anthropology. This initiative helped to increase the creation of joint Anthropology and Archeology programs throughout the country, and the expectation that, as the number of Biological Anthropology graduates increase, there will be other programs created in the Four Fields, Boasian, model. Faculty from PPGA has engaged in transdisciplinary research, some of it in partnership with colleagues from USA and other countries, in a broad spectrum of themes. The program is helping to forge a new generation of anthropologists, able to investigate issues from pre-historic to contemporary populations, demonstrating that the field can have an important role in the comprehension of the distinct problems faced by the Brazilian society, from its past to the present.

Middle meningeal arteriovenous and dural sinus variation in 6-8.0 year old humans

ISABELLE B. REICH¹, PINA S. SIMONE¹, CORTNEY M. CONNOR², CHLOE LEE³, TIFFANY W. SHIEN¹, REBECCA S. JABBOUR⁴ and GARY D. RICHARDS⁵

¹Department of Molecular and Cell Biology, University of California Berkeley, ²Department of Integrative Biology, University of California Berkeley, ³Department of Public Health, University of California Berkeley, ⁴Department of Biology, Saint Mary's College of California, ⁵Department of Biomedical Sciences, A.A. Dugoni School of Dentistry, University of the Pacific

The meningeal arteriovenous system supplies or drains blood from the dura mater and bone while the dural sinuses drain blood from the brain, dura, and bone. Assessment of these systems, based on patterns exhibited on endocranial casts, has a long history in the study of primate brain evolution. However, recent reviews demonstrate a significant need for new data and investigative procedures. We address some of the issues by analyzing a large ontogenetic sample in three dimensions.

We CT-scanned 40 crania developmentally aged from 5.8-7.9 years. Ages derive solely from tooth calcification patterns. Meningeal and dural sinus systems were reconstructed in 3D on isosurfaces. Various-sized 3D markers were placed to map relative sizes and patterns.

Using the traditional Adachi types for the meningeal system resulted in 45%, 15% and 40% of Types I, II, and III, respectively. Right/left differences in these types occurred in 65% of the sample. Alternatively, looking at the 3D complexity of branching and anastomoses, right/left differences were observed in 60% of individuals, with right-dominance and left-dominance equally represented. Middle meningeal branches crossed the coronal suture in 95% of individuals. The frequency and number of such branches were higher on the left side. The right transverse dural sinus was dominant in 55% of cases, with 30% showing left dominance and 15% having equal drainage. Only 25% of cases showed occipital marginal drainage. Three-dimensional mapping of the arteriovenous and dural sinus drainage systems has the potential to reveal their relationships to the developing neural contents and functional cranial regions.

Funding provided by Undergraduate Opportunity Fund Grants to Isabelle Reich, Pina S. Simone, Cortney M. Connor, Chloe Lee, and Tiffany Shien.

Ontogenetic allometry in catarrhine crania: scaled variants or variance in scaling?

EVAN A. SIMONS and STEPHEN R. FROST

Anthropology, University of Oregon

Some have argued that size divergence in catarrhines has produced several examples of scaled variants in cranial shape. These putative scaled variants are often posited to be the product of ontogenetic scaling, the extension/truncation of common growth allometries. Here, we use multivariate shape data to examine if ontogenetic scaling is a common pattern in catarrhines, or if other factors are driving cranial morphological evolution.

Forty-three 3D landmarks, digitized from an ontogenetic series of 1,304 crania representing 30 catarrhine species, were superimposed using generalized Procrustes analysis. We performed Homogeneity of Slopes tests to determine if allometric trajectories varied among species within

each of three clades (Cercopithecinae, Colobinae, Hominoidea). As each clade was found to have a significant interaction effect between LnCS and species ($p < 0.0001$), Procrustes ANOVA was used to parse which species differed, and if this was due to allometric trajectory rate, direction, or both. Trajectories were then compared using Phenotypic Trajectory Analysis (PTA).

Procrustes ANOVA showed shape difference per unit LnCS (magnitude) is conserved among catarrhines and variation among allometric trajectories is largely due to differences in trajectory orientation (pattern). Likewise, the PTA showed that the orientation of ontogenetic trajectories (pattern) rather than amount of shape change (magnitude) is most influential in producing differences in adult crania. As allometric patterns vary among taxa, ontogenetic scaling *sensu stricto* does not often account for most morphological differences, i.e., large and small taxa within clades are generally not scaled variants. Support for scaled variants was found within *Papio* and between *Hylobates* and *Symphalangus*.

This research was funded by a National Science Foundation DDRIG (BCS-1751885).

The Lower Limb of *Ardipithecus ramidus*

SCOTT W. SIMPSON¹, NAOMI E. LEVIN², JAY QUADE³, MICHAEL ROGERS⁴ and SILESHI SEMAW^{5,6}

¹Anatomy, Case Western Reserve University School of Medicine, ²Earth & Environmental Sciences, University of Michigan, ³Geosciences, University of Arizona, ⁴Anthropology, Southern Connecticut State University, ⁵Paleolithic Archaeology, Centro Nacional de Investigación sobre la Evolución Humana, ⁶Paleolithic Archaeology, Stone Age Institute & CRAFT

The Early Pliocene hominid *Ardipithecus ramidus* recovered from the Middle Awash, Ethiopia study area had a mixed locomotor anatomy that retained a capacity for arboreal clambering and adaptations to terrestrial bipedality. The first functional analyses of the *Ar. ramidus* (Lovejoy et al., 2009a-b, *Science*, v. 326) lower limb identified an ape-like talo-crural orientation and the foot's elongated and rigid midtarsus, dorsiflexion at the lateral metatarsophalangeal joints, and an abducent great toe that lacked evidence of hallucal fulcrumation.

Here, we review the lower limb anatomy of the ca. 4.5 Ma *Ardipithecus ramidus* partial skeleton from Gona, Ethiopia and how it broadens our understanding of the locomotion in this species. This includes anatomical regions not previously known for *Ar. ramidus* including the proximal femur and distal fibula. The Gona fossil has many similarities with the Middle Awash sample including overall size, but exhibits notable functional differences – such as a more vertical talocrural orientation and regular recruitment of

ABSTRACTS

the hallux during bipedal propulsion in the Gona individual – that document notable variation in the locomotion adaptations of this early hominin despite occupation of a similar landscape.

Funding provided by Leakey Foundation (SS), NSF HOMINID-RH01 BCS-0321893 (T. White & C. Howell), National Geographic Society (SS, JQ), and Wenner-Gren Foundation (SS).

Experimental animal models for domestication: insights into modern human craniofacial evolution

NANDINI SINGH¹ and KATERINA HARVAT^{1,2,3}

¹Anthropology, California State University, Sacramento, ²Paleoanthropology, Senckenberg Center for Human Evolution & Paleoenvironment, Eberhard Karls Universität Tübingen, ³DFG Centre for Advanced Studies 'Words, Bones, Genes, Tools: Tracking linguistic, cultural and biological trajectories of the human past, Eberhard Karls Universität Tübingen,

Dmitri Belyaev's domestication experiments conducted on silver foxes and rats have established that selecting for tame behaviors was the precursor to all genotypic and phenotypic traits associated with domestication. It has also been proposed that humans are a "self-domesticated" species. In fact, gracilization of the modern human face since the Middle Pleistocene is associated with behavioral changes towards increased social tolerance, i.e. "tameness". Our previous study examining the relationship between behavior and craniofacial morphology in Belyaev's rats selected for tameness and defensive aggression showed that not all domesticated phenotypes are necessarily present in experimental animal models for domestication. Here we expand our previous work to include a comparative sample of wild caught rats to further examine the effects of selected behaviors (both tameness and aggression) on the craniofacial skeleton as it relates to domesticated traits. Our objective is to determine whether the aggressive strain is a "true" representation of the "non-domesticated" phenotype. We hypothesize that both the aggressive and tame rats will be different in shape and size from the wild caught sample. We used 3D geometric morphometric methods to quantify and analyze the craniofacial shape of all three groups of rats. Results show group-specific craniofacial size and shape differences. The wild caught sample also exhibits size-related changes associated with sexual dimorphism. This study will help to assess the role of experimental animal models when examining the morphological consequences of domestication and its implications for modern human craniofacial evolution.

Supported by California State University, Sacramento, "Research and Creative Activity Faculty Grant" (2018-19); and the Deutsche Forschungsgemeinschaft (DFG INST 37/706, FOR 2237)

Household exposure to allomaternal care improves early cognitive outcomes in older female infants

BRITT SINGLETARY

School of Anthropology, University of Arizona

Allomaternal care (AMC: care from someone other than the mother) is known to reduce energetic stress for moms and developing infants. Yet, AMC provides opportunities for infants to learn from various informal teachers, and may enhance cognitive skills. To test this, I collected data from mothers and infants in Tucson, AZ during May 2017-September 2018, including 27 females and 31 males aged 13-15 months, and 28 females and 25 males aged 16-18 months. Cognitive skills were assessed via in-lab administration of the Bayley III Screening Cognitive Subtest (Bayley), while daily diaries and questionnaires were used to obtain AMC data from the mother. Pearson's correlation coefficients were used to determine whether infants who receive more AMC per day, interact with a greater number of caregivers engaged in learning-oriented or play behaviors, or have a larger number of residential caregivers received cognitive benefits. Cognitive benefits were quantified by achievement of higher overall scores on the Bayley, completion of more successful trials of finding a hidden object (Task 18) or obtaining an object from an enclosed space (Task 20), and a higher number of total successful peg placements (Tasks 19 and 21). While several relationships approached significance, there were no uniform predictors of cognitive benefits across age and sex categories ($p > 0.05$). Notably, in older females (aged 16-18 months), an increase in older siblings and total household residents was correlated with higher overall Bayley scores ($p < 0.001$). Further analyses considering residential and nonresidential AMC separately may further clarify these relationships across age and sex categories.

Funding received from the National Science Foundation (BCS-1752542), International Chapter of the P.E.O. Sisterhood, and University of Arizona's School of Anthropology, SBSRI, GPSC, and Conflucenter for Creative Inquiry.

Impact of the 1854 cholera epidemic at the Erie County Poorhouse, Buffalo, New York

ROSANNE L. HIGGINS and JOYCE E. SIRIANNI

Anthropology, SUNY Buffalo

Buffalo, New York was severely impacted by the 1854 cholera epidemic. Both city residents and inmates of the Erie County Poorhouse (ECPH) including, the Insane Department were affected. This research investigates the incidence of mortality in the city compared to that of the poorhouse to determine if the poorhouse was successful in buffering the inmates from the high mortality associated with that disease.

ECPH Inmate Records for 1854 were examined. Between April and October, 1854, the institution housed 279 inmates: 226 in the poorhouse proper and 53 in the insane department. During this period, 63 poorhouse inmates contracted cholera, 26 males, 33 females and 4 of unknown sex. In the poorhouse, 34 of 43 infected inmates died (79%). In the insane residence, 19 of 20 infected inmates died (95%).

The average age at death was 36 years for insane inmates and 38 for poorhouse inmates. The mean length of stay in the institution was 207 days for insane inmates and 182 days for poorhouse inmates.

The City Health Physician reported 1034 cholera cases in the city. Of these 569 died (55%). The higher mortality at the poorhouse indicates that conditions there did not offer protection from cholera. In fact, poor diet, improper waste disposal and inadequate privies reported by city officials probably were the major factors. Furthermore, the increased length of stay may have compromised insane inmates, leaving them more vulnerable to the disease. Other aspects of life between the insane department and the poorhouse are also explored.

Uncertainties Regarding the Physical Basis of Lamellar Bone Periodicity in Secondary Osteons Suggest that Surrogates Based on Infilling/Periodicity Should be Considered

JOHN G. SKEDROS and MADISON S. DOUTRÉ

Orthopaedics, University of Utah

Periodicity with which enamel layers form (Retzius periodicity) is a manifestation of a biorhythm that is also expressed in lamellar bone. This idea is being investigated in anthropoids as the Havers-Halberg Oscillation hypothesis (Mahoney et al.). However, defining 'lamellar bone periodicity' (LBP) is difficult because: 1. its physical basis is poorly understood/controversial; 2. LBP can be established by different ultrastructural motifs that might be interpreted as having differences in 'formation period' duration. These motifs include: 1. layered patterns of predominant collagen fiber orientation - the classical Gebhardt-like models; eg, orthogonal plywood design (OrthoP-D) and twisted plywood design (TwistP-D), and 2. Marotti model = alternating dense and loose lamellae (AltD-L-La). In the perspective of a literature review and examinations of computer-assisted and synthetic models, we demonstrate how these motifs can lead to different interpretations of formation periods, hence LBP, in polarized-light images of secondary osteons. Results: the AltD-L-L motif could be interpreted as one or two formation periods. But if the AltD-L-La is actually an artifact of harsh etching (Yamamoto et al.) and LBP is actually created by 180-degree twists of the TwistP-D, then each full twist might be

ABSTRACTS

considered as three formation periods. Additional confusion arises if some osteons have OthoP-D. However, the infilling rate of two similar-sized osteons is equivalent regardless if OthoP-D or TwistP-D motif. Consequently, when the physical basis for LBP is unclear, then it seems appropriate to use surrogates for Retzius-like periodicity in lamellar bone; for example, averaged osteon infilling rate or the osteon wall thickness normalized to osteon area.

N/A

It's getting better all the time: A look at the contributions of G. Richard Scott to dental anthropology

CASSIE E. SKIPPER, ROSE L. PERASH, LAURA E. CIRILLO, VICTORIA M. SWENSON, DONOVAN M. ADAMS, REBECCA L. GEORGE, STEPHANIE J. COLE, CORTNEY N. HULSE, TATIANA VLEMINCQ-MENDIETA, DORI KENESSEY, SAVANNAH HAY and MARIN A. PILLOUD

Anthropology, University of Nevada, Reno

Dental anthropology has experienced significant changes over the last half century, including the development of the widely used Turner-Scott dental morphological trait scoring method (formerly the Arizona State University Dental Anthropology System). G. Richard Scott has played a key role in the advancement of dental anthropological research. Specifically, he has made improvements to scoring dental crown and root morphology with special attention given to shoveling, Carabelli's trait, and two-rooted lower canines. Scott is currently a Foundation Professor of Anthropology at the University of Nevada, Reno, but he also achieved full professor status at the University of Alaska, Fairbanks.

Throughout his 40-year research career, Scott has authored three books, edited two books, and authored over 70 articles and book chapters. Specifically, his contributions to dental anthropology through *The Anthropology of Modern Human Teeth* and the Turner-Scott method represent fundamental sources of information required to perform research on dental morphological traits. Additionally, Scott collaborates internationally and has co-authored publications with researchers from nine countries, including England, Portugal, Spain, Denmark, Croatia, Australia, Brazil, Colombia, and Chile. He was the first president of the Alaska Anthropological Association, and he currently serves as co-editor of the *Dental Anthropology* journal and associate editor for the *American Journal of Physical Anthropology*. Scott also helped to develop the biological anthropology graduate program at the University of Nevada, Reno. His dedication to his graduate students, colleagues, and research endeavors will continue to advance dental morphological research and make a significant impact to the scientific community in decades to come.

Archaic encounters: Retracing interactions between Neandertals and Denisovans

VIVIANE SLON

Department of Evolutionary Genetics, Max Planck Institute for Evolutionary Anthropology

Denisovans and Neandertals separated from each other at least 390,000 years ago. Skeletal remains of individuals from both groups have been discovered at Denisova Cave (Russia). To date, nuclear DNA has been retrieved from five of these individuals – four Denisovans and one Neandertal. Traces of Neandertal DNA in the genome of one of the Denisovans demonstrated that Neandertals and Denisovans admixed at least once in the past.

"*Denisova 11*" is an additional individual from Denisova Cave, represented by a single bone fragment identified using collagen fingerprinting, whose genome has now been sequenced. This individual had both Neandertal and Denisovan ancestry, in nearly equal extents. To explore this signal of mixed ancestry, comparisons between the distribution of Neandertal-like and Denisovan-like genetic variants across her genome, and theoretical expectations under different genealogical scenarios, were carried out. These indicated that she was the daughter of a Neandertal mother and a Denisovan father, and that her Denisovan father had at least one distant Neandertal ancestor.

The genome of *Denisova 11* provides direct evidence for multiple admixture events between Neandertals and Denisovans, occurring ~300,000 years after the separation of the two groups. Added to previous evidence for admixture between Denisovans and early modern humans, and between Neandertals and early modern humans, this suggests that individuals from different Late Pleistocene hominin groups mixed often when they encountered one another.

The Max Planck Society; the Max Planck Foundation (grant 31-12LMP Pääbo); the European Research Council (grant agreements No. 694707, 324139 and 715069); and the Russian Science Foundation (project No. 14-50-00036).

Comparative biomechanics of the Hominidae mandible

AMANDA L. SMITH¹, CALLUM F. ROSS¹, ZERAY ALEMSEGED¹, ANDREA B. TAYLOR², CHRIS ROBINSON³, CAROL V. WARD⁴, PHILIPP GUNZ⁵ and BILL KIMBEL⁶

¹Organismal Biology and Anatomy, University of Chicago, ²Department of Basic Sciences, Touro University California, ³Department of Biological Sciences, City University of New York Bronx Community College, ⁴Department of Pathology and Anatomical Sciences, University of Missouri, ⁵Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology, ⁶Institute of Human Origins, Arizona State University

Intra- and interspecific variation in the shape of the hominid mandible has been documented, but the mechanical consequences of these variations remain unclear. Specific shape metrics including symphyseal depth and inclination, corpus thickness, the height and orientation of the rami and the divergence of the posterior dental row have all been hypothesized to be functionally related to feeding. According to previous work, these features should either serve to reduce bone strains or increase biting efficiency or both. However, whether these features function together to produce species-specific patterns of deformation or strain patterns has not yet been evaluated. This study uses finite element analysis (FEA) to examine the biomechanical implications of mandibular shape variation within and across species of extant great apes.

Geometric morphometric methods were used to analyze shape variation in the mandibles of four extant hominid species (26 *Pan troglodytes*, 18 *Pongo pygmaeus*, 22 *Gorilla gorilla*, 37 *Homo sapiens*) based on 504 Procrustes coordinates. Shape-space principal coordinates analysis (PCA) was used to identify the mean female and male specimens for each species and eight total finite element models (FEMs) were constructed from the CT scans of the selected specimens. The FEMs were assigned the material properties of bone, loaded with equivalent muscle forces and constrained to simulate maximal bites at multiple locations across the tooth row.

Preliminary results indicate variation in strain magnitude but some broad similarities in strain regime and deformation patterns across taxa.

This research was funded by NSF BSC 1515270

The Use of Laser Scanning Confocal Microscopy in Detecting Bone Microstructure Using Basic Fuchsin and Toluidine Blue Stains

ASHLEY C. SMITH

Department of Anthropology, University of Toronto

The use of laser scanning confocal microscopy to develop a three-dimensional imaging of bone is still relatively novel in the field of human osteology. The purpose of this project is to demonstrate the usefulness of using basic fuchsin stain and toluidine blue to develop a three-dimensional image of bone microstructure using a laser-scanning confocal microscope. This project used 3 human femora, three human ribs, and three pig ilia damaged fragments to examine the microstructure using basic fuchsin and toluidine blue stains. Testing was done using a Carl Zeiss LSM800 at the 10x, 20x, and 64x magnification, with an emission wavelength setting of 543nm and 653nm; the emissions wavelength best used to view the two stains. Using the elements described, the results of this project found that it is possible to develop three-dimensional imaging of lamellar

ABSTRACTS

interactions within osteons, as well as develop edge geometry of fracture sites. Additionally, when used with Slow-Fade Gold, we can visualize proteins and their degradation. Lastly, this project found that the LSM800 is better at higher magnifications such as 64x magnification than at 10x or 20x to view the microstructure. Lower level magnification was better able to demonstrate the relationship between collagen and bone mineral, while the higher-level magnification demonstrated lamellar band interaction and the inter-lamellar space.

This project was funded by the author.

Working with Low Income Students: Ideas and concepts to create a more inclusive classroom

B. KATHERINE SMITH¹, CARA PACE², MARC KISSEL² and KAREN RUSSO²

¹Anthropology and Sociology, University of Southern Mississippi, ²Anthropology, Appalachian State University

Universities are currently serving a diverse population of students with different races, ethnicities, gender identities, religious affiliations, and socioeconomic statuses. As anthropologists we are ideal for creating an inclusive space for students in our classroom, and have worked hard to address many of the above mentioned items. However, previous research has shown that lower socioeconomic students are still under-represented at the university level, whether in representation through faculty, or representation in materials and scholars covered in class (Holley and Gardner 2012). We analyzed publicly available syllabi being taught in all fields of anthropology across universities in the U.S. We examined every time a syllabus discussed services available to low income students, such as food banks, the content covered in class, and assumptions of the cultural capital necessary to succeed in class. Using text mining and sentiment analysis in R (using the tidytext package) we calculated the tone of a syllabus. Preliminary analysis suggests that many scholars do not explicitly take socioeconomic class into account (though the majority do refer to other forms of discrimination). Using data from the Equality of Opportunity Project we show how place of birth and family income level significantly affects a student's chance of success in college. Using these two datasets we discuss recent research into educational theory that will allow teachers to better address these concerns. We also discuss how anthropology can be more open to lower-income students and ways in which we can avoid gatekeeping and promote a more inclusive classroom.

The localized environment of early *Homo erectus* at East Turkana, northern Kenya

CHRISTOPHER D. SMITH^{1,2,3}, MARYSE D. BIERNAT⁴, DAVID B. PATTERSON^{5,6} and ASHLEY S. HAMMOND^{3,7}

¹The Graduate Center, City University of New York, ²Center for Anatomy and Functional Morphology, Icahn School of Medicine at Mount Sinai, ³New York Consortium of Evolutionary Primatology, ⁴Institute of Human Origins, School of Human Evolution and Social Change, Arizona State University, ⁵Department of Biology, University of North Georgia, ⁶Center for the Advanced Study of Human Paleobiology, George Washington University, ⁷Division of Anthropology, American Museum of Natural History

The environment that facilitated the emergence of *Homo erectus* in eastern Africa remains unresolved. One of the earliest (~1.87 Ma) fossils attributed to *H. erectus* in Africa is KNM-ER 2598, a partial occipital bone from Upper Burgi Member (UBM) deposits at East Turkana, Kenya. Although paleoenvironmental data exist for the UBM more broadly, we do not know much about the localized ancient environment associated with KNM-ER 2598.

In this study, we compare the mammalian faunal community represented in the entire UBM of the Koobi Fora Formation with that of the area around where KNM-ER 2598 was discovered (i.e., Collection Areas 13, 14 and 15). We focused on taxa indicative of either grassland or forested environments. Faunal abundance data were obtained by combining the Turkana Basin Paleontology Database (TBPD) with fossils collected in 2017-2018. We calculated faunal abundance of each species per member as well as within the combined Collection Areas of 13, 14, and 15. We use a Pearson's chi-squared test with Bonferroni post-hoc correction to determine significant differences between faunal proportions per member.

Results indicate a significant difference ($p=0.014$) between faunal families associated with the KNM-ER 2598 sample relative to the rest of the UBM. This difference includes an increased proportion of equids (11.82% versus 6.59%, respectively), suggesting the region around the KNM-ER 2598 site of discovery may have exhibited a more open habitat than other portions of the UBM. Future work should include isotopic studies of mammalian enamel and soils to reconstruct the environment in this region.

This research was supported by the National Science Foundation (IRES-OISE 1358178) and would not be possible without the support of the National Museums of Kenya.

Sociopolitical patterns in treponemal disease prevalence in the pre-Columbian eastern United States

MARIA O. SMITH¹ and TRACY K. BETSINGER²

¹Sociology and Anthropology, Illinois State University, ²Anthropology, State University of New York, Oneonta

Various studies have determined that non-venereal treponemal disease has a considerable antiquity in the pre-Columbian site samples of the Eastern United States. The earliest evidence for the skeletally visible tertiary stage dates to (at least) the Late Archaic period (circa 1500-1000 BCE). The pathognomonic and diagnostic manifestations have evidently remained stable across the millennia, although these reactive changes have not always been uniformly applied in the identification of treponemal cases. Nevertheless, it has long been evident that there is an increase in the prevalence of treponemal disease with sedentism and aggregated village settlement. This co-associates with the temporal transition from transient hunter/forager (Archaic Period) to sedentary maize-intensive agriculture (Mississippian Period, post-1000 CE). By controlling case prevalence with different levels of diagnostic reliability (i.e., pathognomonic, diagnostic, consistent with), the authors have detected how nuanced treponemal disease prevalence can be. Using multiple site samples from the same geographic area (e.g., Tennessee River Valley, Mississippi River Valley) and the same cultural context, social status/role differences have been detected as well as patterned differences between samples that vary in the degree of sedentism and size of settlement. Although the synergistic relationship between individual health status and treponemal disease progression is still unclear, these prevalence patterns may eventually allow scholars to predict the subsistence and settlement context for mortuary samples without a firm archaeological context.

There was no independent funding for this project.

Unwinding the Triple Helix: Race, Sex, and History in Population Genomics

RICK W. A. SMITH

William H. Neukom Institute for Computational Science, Dartmouth College, Anthropology, Dartmouth College

Recent public debates in genomics have turned again to the question of race. Central to these discourses is the salience of race for illuminating medically-relevant genetic differences between populations. These discourses also raise binary sex differences as support for the existence of genetic, morphological, and behavioral distinctions between racial groups. Drawing these kinds of connections is by no means original, as the concepts of race, sex, and disease have long relied on one another for their mutual intelligibility.

ABSTRACTS

These concepts have a long history of being built in and through one another, and their interconnectedness is often a forgotten subtext underlying contemporary debates about race in genomics. We need new models of genetic research that do not make sense of race by reifying sex, and are increasingly attuned to the historical processes in which race and the biological effects of racism have emerged. In this presentation, I challenge the usage of sex and disease in recent advocations for racial genomics. I present genetic data challenging the existence of binary sex differences, demonstrating that sex is not uncontested ground for the production of race. I also present new epigenomic data that challenges the innateness and genetic underpinnings for complex diseases. Collected in collaboration with indigenous peoples in the US Southeast, these data show that histories of forced relocations, and not genetic ancestry, are strong predictors of medically-relevant epigenomic variation.

This research was funded by the Neukom Institute for Computational Science at Dartmouth College.

Tales teeth tell: Wintertime stress, nursing, and lead exposure in Neanderthal children

TANYA M. SMITH¹, CHRISTINE AUSTIN², DANIEL R. GREEN^{3,4}, RENAUD JOANNES-BOYAU⁵, SHARA BAILEY⁶, DANI DUMITRIU⁷, STEWART FALLON⁸, RAINER GRÜN^{1,8}, HANNAH F. JAMES⁹, MARIE-HÉLÈNE MONCEL⁹, IAN S. WILLIAMS⁹, RACHEL WOOD⁹ and MANISH ARORA²

¹Australian Research Centre for Human Evolution, Griffith University, ²Department of Environmental Medicine and Public Health, Icahn School of Medicine at Mount Sinai, ³Forsyth Institute, Forsyth Institute, ⁴Department of Human Evolutionary Biology, Harvard University, ⁵Southern Cross GeoScience, Southern Cross University, ⁶Department of Anthropology, New York University, ⁷Department of Neuroscience, Icahn School of Medicine at Mount Sinai, ⁸Research School of Earth Sciences, Australian National University, ⁹Département de Préhistoire, Institut de Paléontologie Humaine

Paleoanthropologists have highlighted increasing climate variation 300,000 years ago as a key factor in the evolution of our species, as well as the more recent demise of Neanderthals. One difficulty in testing these ideas is that it has not been possible to recover ancient climate records over the scale of a human lifespan, as most environmental estimates are derived from large-scale records such as ice cores. While many scientists have sampled teeth for paleoenvironmental reconstruction, concerns about the timing of elemental incorporation during tooth mineralization and the fidelity of oxygen isotopes in teeth have hindered direct investigations of the fossil record. We employ two mass spectrometry methods, addressing these methodological concerns and quantifying oxygen isotopes, trace element distributions, and tooth development

in two Neanderthals and one modern human from Payre, an archeological site in the Rhone Valley. The 250,000 year-old Neanderthals inhabited cooler and more seasonal periods than the modern human, evincing childhood development stress during wintertime. In one instance this may have included skeletal mobilization of elemental stores and weight loss; this individual was born in the spring and appears to have weaned 2.5 years later. Both Neanderthals were exposed to lead at least twice during the deep winter and/or early spring. While diagenetic modification may prohibit characterizations of teeth interred near naturally occurring metal sources, the quantification of oxygen isotopes provides complementary insights into the lives of young hominins. This approach reveals patterns of seasonal variation, Neanderthal life history, and exposure to potential environmental hazards with unprecedented detail.

DBS 2.0: Renewed investment in methods development of biomarkers from dried blood spots

J. JOSH SNODGRASS¹, GEETA EICK¹ and SAMUEL S. URLACHER²

¹Anthropology, University of Oregon, ²Evolutionary Anthropology, Duke University

In biological anthropology and sister disciplines, biomarkers collected through “field-friendly” techniques have provided an important tool to monitor physiological processes and thereby investigate human adaptation and the pathways through which aspects of the social environment are embodied. Blood is the biological substance of choice or necessity for many analytes, and the use of capillary whole blood from finger prick collected onto filter paper (dried blood spots [DBS]) has opened field-friendly possibilities. However, despite significant advancements in the development of DBS-based biomarkers, several serious challenges have impeded progress and left initial predictions for widespread adoption unfulfilled. First, use of DBS assays requires modification and validation of commercially available assays designed for serum/plasma or development of novel assays with follow-up validation; this process is time-consuming, expensive, requires numerous matched samples, and necessitates project staff with extensive molecular biology training. Second, there is no overarching plan for the development of DBS assays, so individual labs must themselves secure funding to develop assays; as a result, many potentially valuable biomarkers remain unavailable for DBS. Third, only limited effort has been made to harmonize results across labs and little consideration has been given to addressing inter-lab variability. This poster summarizes the state-of-the-science with DBS, using recent validations in the Global Health Biomarker Laboratory of two analytes—Epstein-Barr Virus (EBV) antibodies and TRACP-5b

(tartrate-resistant acid phosphatase 5b)—to outline a rigorous approach to assay evaluation and modification, thus rebuilding the DBS foundation and setting the standard for future DBS biomarker development.

NSF BCS-1638786

Shifting Spaces: short-term home range patterns in white-handed gibbons in mosaic habitat in western Thailand

MARGARET SOBASZEK and LYDIA E. O. LIGHT
Anthropology, University of North Carolina at Charlotte

The small apes are increasingly endangered due to habitat degradation and climate change. Therefore, it is critical to understand how they alter their activities when living in lower-quality habitat areas. Our project focused on white-handed gibbons (*Hylobates lar*) living in two neighboring but distinct habitat types in western Thailand. Because of the differences in food resource availability between the evergreen forest and savannah habitats at this site, we hypothesize that gibbons will use their home ranges (HR) differently with savannah groups using less of their HR each week compared to evergreen forest groups. We followed two social groups over six weeks during the rainy season from July-October 2018. We then compared overall HR area and used a Minta Index to calculate week-by-week consistency of use estimates. Overall HR area differed considerably with Group D occupying a range twice as large as group B (Group B: 7.04 hectares; Group D: 15.96 hectares). Average Minta Index values were higher in group B (66.3%) compared to Group D (58.8%); however, this difference was not significant (Mann-Whitney $U = 0.4286, p > 0.05$). While limited by sample size, our results do not support our hypotheses. Weekly ranging patterns vary, yet this does not appear to be habitat-specific as both groups shifted locations across weeks. We conclude that habitat type is not the primary factor driving ranging patterns in this population and suggest that gibbons may adjust their ranging patterns to respond to availability of specific food resources, location of neighboring groups, or other factors.

Research in Thailand was supported by the American Society of Primatologists and the University of North Carolina at Charlotte.

Patterns of land use in the early urban centers of the Near East: bioarchaeological evidence

ARKADIUSZ SOŁTYSIAK
Department of Bioarchaeology, University of Warsaw

Proportions of stable nitrogen (and carbon) isotopes have been traditionally used to assess the composition of diet, but recently they proved

ABSTRACTS

to be also indicators of land use patterns. Especially combining nitrogen and strontium isotopic data may produce insight into spatial distribution of food resources. $^{86}\text{Sr}/^{87}\text{Sr}$ and $\delta^{15}\text{N}$ values have been obtained for human teeth representing three important early urban centers: Tell Brak (NE Syria, Late Chalcolithic and Early Bronze Age), Tepe Sialk (Central Iran, Transitional Chalcolithic) and Tepe Challow (NE Iran, Late Chalcolithic and Early/Middle Bronze Age). At Tell Brak along with rapid population growth in the Late Chalcolithic, decrease of average $^{86}\text{Sr}/^{87}\text{Sr}$ values together with their higher dispersion indicate extension of the area under cultivation. During the crisis of the 23rd century BCE, $\delta^{15}\text{N}$ values decreased significantly, indicating a shift from more intensive to extensive agriculture. At Tepe Challow, population growth between the Late Chalcolithic and Middle Bronze Age was related to decrease in the $^{86}\text{Sr}/^{87}\text{Sr}$ value dispersion, most likely the consequence of centralized grain storage and distribution. At all three sites, migration rate, estimated using both $^{86}\text{Sr}/^{87}\text{Sr}$ and $\delta^{15}\text{N}$ distributions, was low suggesting demographic growth in a local population as the main factor contributing to the development of large urban centers. Observed temporal and regional patterns suggest that the process of urbanization was paralleled by complex changes in agricultural practices, triggered not only by demographic growth, but also by specific environmental settings in semi-arid zones with high inter-annual variability of precipitation.

Research funded by National Science Centre (NCN), grant No. 2016/22/M/HS3/00353.

Capstone Projects: Combining Critical Thinking and Creativity

K. ELIZABETH SOLURI

Anthropology, Cabrillo College

Introductory biological anthropology students often complete final papers or projects where they explore a course topic in greater depth by synthesizing relevant scholarly literature and, on rare occasions where circumstances permit, conducting original research. While these assignment formats mimic the work product of professional biological anthropologists, many of our introductory students are not anthropology majors and will instead need to apply course concepts and skillsets to a wide range of professional contexts beyond our classrooms. With this in mind, I redesigned the final project in my introductory course. Students now complete a capstone project where they research the realities behind a popular misunderstanding about evolution and then design public education materials that creatively teach these realities to a general audience. In doing so, students practice a broad set of library research skills, critically explore and synthesize course content in a way that is accessible for their target audience, and

correct their own lingering misunderstandings about human evolution. Using between-subjects T-tests, I have detected no statistically significant differences when comparing student performance on the previous assignment ($M = 91.1$, $SD = 0.57$) with student performance on the new project ($M = 91.6$, $SD = 0.81$, $p = 0.64$). However, qualitative data compiled from student survey responses indicate students are meaningfully engaging with course themes and may be developing higher quality knowledge. This preliminary study suggests the new capstone project may be particularly well-suited for helping introductory students actively participate in constructing and correcting their knowledge of human evolution.

Estimation of Bullet Construction from Cranial Entrance and Exit Wound Diameters

TESSA SOMOGYI, ELIZABETH A. EVANGELOU, KEVIN E. SHERIDAN and ELIZABETH A. DIGANGI
Anthropology, Binghamton University

Cranial gunshot analysis is an essential part of the forensic anthropologist's toolkit. This study tests whether entrance and exit wound diameters can be used to estimate bullet construction. A sample of 45 donated human heads obtained from an anatomical supply company were placed on a stand designed to simulate the height of an adult male and shot using a 0.38 caliber revolver from a distance of 3 yards. The shot locations were either through the frontal bone or through the temporal and/or parietal bones and the bullet constructions were full metal jacket and jacketed hollow point. Full metal jacket ammunition is designed to exit the body while jacketed hollow points are designed to expand and therefore not exit. The two variables (shot location and bullet construction) were distributed randomly yet evenly throughout the sample. After being shot, the specimens were autopsied and processed using standard maceration methods. Diameters of the entrance and exit wounds were measured using digital sliding calipers and rounded to the nearest tenth of a millimeter. These data were then subjected to independent sample t-tests with significance set at $p=.05$. Results revealed a significant difference in entrance wound diameters ($p=.002$), but not exit wounds ($p=.188$), indicating that bullet construction has a significant impact on the diameter of entrance wounds, but not exit wounds. This has implications for our ability to interpret ballistic trauma and highlights the potentially more diagnostic nature of the entrance wound for making interpretations about bullet construction.

This project was supported by an award from the National Institute of Justice: 2016-DN-BX-0155.

The Use of Raman Spectroscopy to Examine Bone Composition in Infant Ribs

MIRIAM E. SOTO MARTINEZ¹, CHRISTIAN M. CROWDER² and XIAOHONG BI³

¹Forensic Anthropology Division, Harris County Institute of Forensic Sciences, ²Dallas County Medical Examiner Office, Southwest Institute of Forensic Sciences, ³School of Biomedical Informatics, University of Texas Health Science Center

During infancy, bone mineral density and bone strength increase due to alterations in bone size and composition produced by modeling. This study examines the differences in bone composition from the cutaneous and pleural cortices of the rib to assist in developing a better understanding of rib modeling and biomechanics.

Seventy-seven sternal end rib cross-sections were obtained from 38 infants (0-12 months of age). Raman spectroscopy was used to measure the molecular constituents of bone mineral and organic matrix from the cutaneous and pleural cortex at the midpoint of the rib samples. Bone composition parameters were calculated, including mineral-to-collagen ratio, mineral crystallinity, hydroxyapatite carbonation, and collagen content. Univariate statistics were used to investigate spatial and age-related differences.

Results indicate that mineral crystallinity ($p < .001$) and mineral-to-collagen ratio ($p < .001$) are significantly greater on the pleural cortex, while collagen content ($p < .001$) is significantly greater on the cutaneous cortex. Age is positively correlated with mineral crystallinity [$p = .032$ (pleural) and $.002$ (cutaneous)] and collagen content ($p < .001$) of both cortices. Age is negatively correlated with hydroxyapatite carbonation ($p < .001$) of the cutaneous cortex and mineral-to-collagen ratio ($p = .032$) of the pleural cortex.

Results indicate that bone strength and ductility of the rib cortices increase with age, although mineral-to-collagen ratio decreases with age on the pleural surface while remaining stable on the cutaneous surface. These data will assist with the development of biomechanical models for fracture prediction.

Funding was provided by the Children's Justice Act - Texas Center for the Judiciary grant program (CJA-18-05).

Further insights on Late Upper Paleolithic (Epigravettian) funerary use of Arene Candide Cave (Liguria, Italy). New AMS dates and paleopathology

VITALE S. SPARACELLO¹, IRENE DORI^{1,2}, STEFANO ROSSI³, ALESSANDRA VARALLI⁴, JACOPO MOGGI CECCHI², JULIEN RIEL-SALVATORE⁵ and VINCENZO FORMICOLA⁶

¹UMR5199 PACEA, Univ. Bordeaux, ²Dipartimento di Biologia, Lab. Antropologia, Università degli Studi di Firenze, ³Soprintendenza ABAP di Parma

ABSTRACTS

e Piacenza, Mibact, ⁴Department of Archaeology, Durham University, UK, ⁵Département d'Anthropologie, Université de Montréal, ⁶Dipartimento di Biologia, Università degli Studi di Pisa

The Pleistocene deposit of the Arene Candide Cave in Finale Ligure (northwestern Italy) was excavated beginning in the 1940s, and yielded one of the most numerous Late Upper Paleolithic skeletal series in the world. The "necropolis" consists of ten primary burials and six clusters of bones in secondary deposition, totaling 20 individuals, accumulated in two apparently distinct phases (AMS dates spanning 12,028 – 11,181 and 12,816 – 12,421 cal BP). Previous studies suggested that skeletal elements from existing burials were intentionally re-arranged around the new depositions. Two individuals bearing skeletal evidence of congenital dysplasias (possibly X-linked rickets) were put in relation through this funerary behavior, suggesting that disease and relatedness may have been factors determining mortuary gestures.

We present here the latest advancements allowed by new direct AMS dates and paleopathological differential diagnoses. Results suggest that the association between newly deposited burials and existing skeletal remains involved also individuals from different chronological phases. Furthermore, we discovered that one child burial excavated in the 1940s, and attributed to the Neolithic, belongs in fact to the terminal Pleistocene (12,098-11,827 cal BP). This child shows abundant periosteal reaction in the temporal bone, while another adolescent displays a diffused pattern of cortical bone remodeling and deposition resembling hypertrophic osteoarthropathy (HOA). Another adolescent individual presents a radio-ulnar dysplasia compatible with Madelung deformity, a dominant X-linked condition. Results further suggest that disease, including congenital disease, may have been central during the lives, and during the representation of death, in the Final Epigravettian.

Project BUR.PPH: (VSS) "Investments for the future" Program, IdEx Bordeaux, ANR-10-IDEX-03-02. Project DEN.PH.: (ID) European Union Horizon 2020 research and innovation programme under the Marie Skłodowska-Curie grant No 752626.

Using Bayes Theorem to Identify New Species in the Fossil Record

JEFFREY K. SPEAR^{1,2} and JILL SHAPIRO³

¹Center for the Study of Human Origins and Department of Anthropology, New York University, ²NYCEP, New York Consortium for Evolutionary Primatology, ³Ecology, Evolution, and Environmental Biology, Columbia University

Despite the biological importance of species, identifying species in the fossil record is difficult and debates rage about the classification of species in hominin and primate evolution. A major difficulty is that researchers bring to their

analyses different prior assumptions about the nature of species and the diversity of the fossil record. Complicating the process is the relative sparseness of the fossil record, which makes it difficult to understand diversity and limits sample sizes. We test a novel, probabilistic approach to identifying fossil species based on Bayes' Theorem. The theorem requires assumptions to be quantified and can be used with small samples, even single data points. We test the model using a sample of 167 extant female apes. Prior probabilities for the test were based on the modern species richness of catarrhine genera and the morphological diversity of extant hominoids. A random subset of seven or ten individuals was repeatedly drawn from the larger sample to represent a hypothetical fossil record. A single individual from this subset was treated as a newly discovered fossil and its status as a new species was assessed. The expected outcome of the tests based on the posterior probabilities given by the model was assessed against the actual novel species status of the test individuals using a chi-square test for goodness of fit. The expectations of the model did not differ significantly from actual species status, suggesting that the model accurately reflects the probability that a new fossil is a distinct species.

Infant condition and the timing of deciduous tooth emergence in the Brazilian Amazon

JENNIFER SPENCE¹, DEBBIE GUATELLI-STEINBERG², BARBARA A. PIPERATA², BRUCE FLOYD³ and HILTON P. SILVA⁴

¹Anthropology, Pacific Lutheran University, Tacoma, Washington, ²Anthropology, The Ohio State University, Columbus, Ohio, ³Anthropology, University of Auckland, Auckland, New Zealand, ⁴Anthropology, Federal University of Pará, Belém, Brazil.

Although highly heritable, deciduous tooth emergence timing is not impervious to environmental influence. Studies investigating the contribution of environmental factors to emergence timing are inconsistent, in part because gestation length is not always considered. Drawing on longitudinal data from 100 mother-infant dyads in a semi-urban town in the eastern Amazon Basin, and using reliable methods to consider gestational age, we tested three hypotheses: 1) there will be no sex difference in emergence timing; 2) infant size for gestational age (SGA) will be inversely correlated with first-tooth emergence age; 3) infant postnatal growth rate will be inversely correlated with first-tooth emergence age. We implemented survival analysis because the outcome variable was censored within similar but unequal intervals and the Weibull model because the conditional probability of tooth emergence increases with time. Contrary to previous studies, we found that the first tooth was 60% more likely to emerge earlier in females ($P = 0.026$). There was

a significant association between SGA and emergence timing of the first tooth ($P = 0.007$), with an increase in SGA category (small, appropriate, large) increasing the likelihood of emergence by 106%. Gains in infant length, weight, and head circumference were significant predictors of age at first-tooth emergence ($P \leq 0.004$), with the likelihood of emergence increasing from 10–170% per unit gain. Our findings confirm that environmental factors play a significant role in the variation of deciduous tooth emergence timing and demonstrate that emergence is susceptible to influence at various stages of development.

This work was supported by Fulbright and the National Science Foundation (1260745).

The Frequency and Distribution of Drug Research Across the American Journal of Physical Anthropology: Does Drug Use Affect Skeletal Biology?

MICAYLA C. SPIROS¹ and HAYDEN S. MCKEE²

¹Anthropology, Michigan State University,

²Anthropology, University of Tennessee, Knoxville

Drugs have been used by humans for thousands of years yet the focus on drug research in physical anthropology is limited. While drugs have direct effects on the human body there is a lack of anthropological scholarship examining how the skeleton reacts to these toxins. This project aims to look at the research throughout the physical anthropology discipline to determine the frequency and distribution of drug-related literature.

For this project, data were collected coding every online AJPA article that includes the word "drug" at least once throughout the publication (N=158). To determine the distribution of drug use research across the disciplines, each article was coded questioning: If drug-use was a part of the objective; the most prevalent keywords being used in these studies; if the research was human or non-human oriented; and the sub-discipline focus of the article.

After analyzing each article, the percentage whose research objective focused on drug use was approximately 6.96% (n=11). Approximately 25% of the total articles that mention drugs are in relation to human osteology (n=42) with seven related to forensic anthropology. Of these 42 articles, over half of them (n= 23) reference drugs specifically as a limitation with no articles in AJPA examining the effect of drugs on skeletal biology.

There is this belief that drugs affect skeletal morphology yet, the literature is not yet there in anthropology to support these claims. As a result, there needs to be a greater focus on how drug use affects the human skeleton.

ABSTRACTS

Environmental predictors of *Propithecus* pelage variation

AMANDA N. SPRIGGS¹, BRENDA J. BRADLEY², JASON M. KAMILAR^{3,4} and ADAM D. GORDON¹

¹Anthropology, University at Albany - SUNY, ²The Center for the Advanced Study of Human Paleobiology (CASHP), Anthropology, The George Washington University, ³Anthropology, University of Massachusetts Amherst, ⁴Graduate Program in Organismic and Evolutionary Biology, University of Massachusetts Amherst

Previous work in *Eulemur* has shown that pelage color patterns correlate with environmental variation, consistent with evolutionary hypotheses relating visibility to predator avoidance. Lemuriforms vary in pelage coloration and habitat-specific light levels, forming a natural experiment for examining selection pressures on pelage coloration. Here we explore how *Propithecus* pelage coloration co-varies with habitat variables associated with visibility. Precipitation variables served as proxies for light level and background coloration. For 28 adult male and female *Propithecus* preserved skins ($n = 6$ species), pelage variation was quantified and compared with the Eigencoats methodology. Mantel randomization tests investigated associations between pelage variation and the amount of precipitation in *Propithecus* habitats based on museum-recorded provenance. Tests were performed on distance matrices for coat variation and amount of precipitation based on number of dry months and annual amount of rainfall for a given location separately for each sex. Mantel test results showed a significant positive relationship between female and male coat coloration and precipitation variables ($\alpha = 0.05$), indicating that members of *Propithecus* have similar coats when living in areas with similar amounts of precipitation. These results imply that male and female members of *Propithecus* are under similar selection pressures related to overall pelage coloration, a relationship that could represent pressures for maintaining a specific standard of pelage coloration that is associated with a certain habitat type. If pelage coloration is important for predator avoidance, both males and females may be adhering to certain "baseline" pelage coloration based on habitat type.

Genetic discourse and public spaces: the struggle to keep DNA from becoming race

LAUREN C. SPRINGS¹, JAMES F. GARBER² and DEBORAH A. BOLNICK³

¹Anthropology, University of Texas at Austin, ²Anthropology, Texas State University, ³Anthropology, University of Connecticut

As recent technological advances have lowered the costs of direct-to-consumer genetic ancestry testing, the popularity of these tests among the general public has surged. At the same time, the rapid influx of genetic interpretations of

personal genealogical histories has led in part to the reification of races as natural and genetically bounded populations. Although this particular racial framing is not explicitly referenced by direct-to-consumer testing companies, racial concepts that have historically been linked with biological and genetic understandings of population differentiation continue to permeate public understandings of personal genetic ancestry results. Anthropological geneticists have sought to improve scientific and public understandings of the intersections of, and distinctions between, genetic ancestry and race, but because both concepts are constantly evolving, this can be a difficult task to undertake.

In this presentation, we explore how understandings of racial identity compare to genetic ancestry results within a sample of contemporary individuals ($n=43$) that elected to participate in genetic ancestry analysis. This analysis was undertaken in conjunction with an archaeological project seeking to reconstruct the population history of an 18th century British colonial settlement in Belize. We illustrate the difficulties we have encountered in communicating our results to study participants and discuss the methods we employed to improve public understandings of the incongruences between racial identifications and inferences of genetic ancestry.

Funding provided by the Wenner Gren Foundation (award 9631) and National Science Foundation (award 1826656).

Biodistance Analysis of North and South American Populations

JULIANNE R. STAMER¹ and MARK HUBBE^{2,3}

¹Center for Latin American Studies, Ohio State University, ²Anthropology, Ohio State University, ³Instituto de Arqueología y Antropología, Universidad Católica del Norte, Chile

The cranial morphology observed in South America during the Holocene has been used frequently to debate the tempo and mode of human dispersion into the Americas, given the high morphological diversity observed in the continent across time and space. However, the origin of this high morphological diversity is still poorly understood, despite its relevance for the discussion of the occupation of the Americas in general. Here, we contribute to the study of the morphological variance among Native South Americans by comparing the between-group variance of South American samples with values observed among North American, East Asian, and Australo-Melanesian samples. We analyzed 14 linear craniometrics variables data recovered from the literature, representing 49 series (2707 individuals in total), and calculated F_{st} estimates within larger regions (South America, North America and East Asia), as well as subregions within South America (Andes, Atlantic South America, and Atlantic South American without

Paleoindians). Results show that the F_{st} for whole South America (0.131) is much higher than the one observed for the comparative samples (North Americans = 0.069; East Asia = 0.077). Within South America, there is also significant differences, with Atlantic series showing the highest F_{st} estimate (0.15), and the Andes the lowest (0.068). The results show that the high cranial morphological diversity is not reflected in other regions of the planet, suggesting that local events in different regions of the continent played a major role in structuring the morphological variance among groups in South America.

The effects of femoral metaphyseal morphology on growth plate biomechanics in juvenile apes and humans

PETER A. STAMOS¹ and MICHAEL A. BERTHAUME^{2,3,4}

¹Department of Anthropology, University of California Davis, ²Department of Bioengineering, Imperial College London, ³Department of Anthropology, Durham University, ⁴Max Planck Weizmann Center, Max Planck Institute of Evolutionary Anthropology

The metaphyseal surface of the distal femur is morphologically distinct in juvenile humans and apes – in humans, it is relatively flat and planar, while in apes, it is characterized by a high degree of topographic complexity. Preuschoft and Tardieu (1996) hypothesized that these differences in metaphyseal morphology are due to differences in force transmission during locomotion: during bipedalism, the physis experiences higher compressive stresses, while during climbing and knuckle-walking, the physis experiences higher shear stresses. To counteract these shear stresses and prevent slipping and detachment of the epiphysis from the diaphysis, the distal metaphysis becomes more complex, causing the epiphysis to "lock" onto the femur.

To test this hypothesis, we created a parametric three-dimensional finite element model (FEM) of the juvenile hominoid distal femur. Based on measurements taken from surface scans, we modified the parameters of the FEM to create models which were morphologically consistent with juvenile hominoid distal femora. We then subjected these models to loading conditions simulating those experienced at the knee joint during bipedal walking, knuckle-walking, and climbing.

Our model shows that during flexed-knee loading, von Mises stresses are lower when the distal femoral metaphysis is complex, like an ape. Conversely, during straight-legged loading, von Mises stresses are lower when the distal femoral metaphysis is flat and planar, like a human. Our FEM confirms the hypothesis that the more

ABSTRACTS

topographically complex metaphyseal surface observed in juvenile apes acts to protect the growth plate from the biomechanical demands of flexed-knee locomotor behaviors.

The Wenner-Gren Foundation University of California Davis

Influence of sex, season of birth, and gestational age at delivery on growth in rural Gambian infants from birth to one year

ZOFIA STANLEY¹, JAMES DYKES², DANIEL J. NAUMENKO^{2,3}, G. KESLER O'CONNOR¹, NABEEL AFFARA⁴, DAVID B. DUNGER⁵, KEN K. ONG^{5,6}, ANDREW M. PRENTICE⁷, SOPHIE E. MOORE^{7,8} and ROBIN M. BERNSTEIN^{2,3}

¹Department of Applied Mathematics, University of Colorado Boulder, ²Institute of Behavioral Science, University of Colorado Boulder, ³Department of Anthropology, University of Colorado Boulder, ⁴Department of Pathology, University of Cambridge, ⁵Department of Paediatrics, University of Cambridge School of Clinical Medicine, ⁶MRC Epidemiology Unit, University of Cambridge School of Clinical Medicine, ⁷MRC Unit The Gambia, London School of Hygiene and Tropical Medicine, ⁸Department of Women and Children's Health, King's College London

The Superimposition, Translation And Rotation (SITAR) method for modeling growth does not assume any particular form of a growth curve, allows flexibility for modeling local variation in growth curves, and allows the calculation and extraction of growth coefficients (size, velocity, and tempo). We applied SITAR to model the growth of rural Gambian infants enrolled in the HERO-G (Hormonal and Epigenetic Regulators Of Growth) study. Measurements including weight, crown-heel length, and head circumference were collected every other day between day 9 and day 365 of postnatal life. We calculated correlations between SITAR coefficients and growth outcomes for groups split by sex, season of birth, and gestational age at birth (N=139 (F=63, M=76)). SITAR models illustrate notable differences among groups including patterns of faltering and catch-up growth associated with birth season, sex, and gestational age at birth. Across all groups, the SITAR size coefficient is significantly correlated with infant weight for age z-scores at 1 year of age ($r: 0.45-0.59$, $P < 0.05$), with nonsignificant and more variable correlations with height for age z-score ($r: 0.14-0.33$). After controlling for sex, gestational age and birth weight, season of infant birth emerges as a significant predictor of weight tempo ($R^2=0.87$, $P=0.02$) and velocity ($R^2=0.79$, $P=0.0017$). Infants born in the wet season weigh less at birth and grow more slowly than infants born in the dry

season from birth to 4 months; for the next 3-4 months, infants born in the wet season grow more rapidly. These patterns have implications for short- and long-term infant health.

Funded by the Bill and Melinda Gates Foundation (OPP1066932)

Migration into Egypt during the Second Intermediate Period

CHRIS STANTIS and HOLGER SCHUTKOWSKI
Dept of Archaeology, Anthropology, and Forensic Sciences, Bournemouth University

A foreign dynasty, known as the Hyksos, ruled Egypt between c. 1638 –1530 BCE. Their origins are thought to be rooted in the Near East, which is supported by architectural features and grave accoutrements of Tell el-Dab'a /Avaris. In this former Hyksos capital in the Eastern Nile Delta, burial culture is characterized by a blend of Egyptian and Near Eastern elements. However, investigations are still ongoing as to where the Hyksos came from and how they rose to power.

The aim of this study is to elucidate the question of possible provenience. We present the results of strontium and oxygen isotope ratios of human tooth enamel ($n = 71$) from Tell el-Dab'a. Faunal bone samples from the site ($n = 4$) as well as nearby shell and geological samples serve as the local baseline.

An influx of non-locals can be observed in the pre-Hyksos period (12th-13th Dynasties) during the establishment of Tell el-Dab'a/Avaris, while the number of local individuals is larger during the Hyksos period. This is consistent with the supposition that, while the ruling class had Near Eastern origins, the Hyksos' rise to power was not the result of an invasion, as popularly theorized, but an internal dominance and victory of a foreign elite. There is a preponderance of non-local females suggesting patrilocal residence. We discuss our findings against the current evidence of material culture and historiography, but more investigation remains in Near Eastern comparative sites to narrow our future search for the actual origins of the Hyksos.

This project receives funding from the European Research Council (ERC) under the European Union's Horizon 2020 research and innovation program (grant agreement No 668640).

A novel composite evolutionary approach reveals SPRR3 gene in the epidermal differentiation complex as a target of balancing selection in humans

IZZY STARR, THERESE WILD and OMER GOKCUMEN

Biological Sciences, University at Buffalo

Genes in the epidermal differentiation complex on human chromosome 1 shape facets of skin integrity, barrier function, and microbiome

composition impacting skin-pathogen interactions. Summary statistics describing nucleotide diversity, allele frequency spectrum, population differentiation, and linkage disequilibrium structure can be used to identify signatures of adaptive pressures across the genome. We developed a novel method utilizing principal component analysis of six such summary statistics to discover signals of selection within the epidermal differentiation complex. Our approach identified specific haplotypes that show signatures of different types of selection. One of these haplotypes corresponds to a region containing multiple members of small proline-rich protein (SPRR) family, which we found to be evolving under balancing selection. Our further analysis showed that this haplotype is linked to autoimmune and inflammatory skin disorders, and affects the expression of multiple late-cornified envelope genes. This work combined with our previous work showed that both of the genes families in the epidermal differentiation complex have evolved under balancing selection. Moreover, the variations overlapping the same genes were discussed within the context of microbiome composition and opposing mechanisms leading to psoriasis and atopic dermatitis. Based on these, we hypothesize that the genetic variation in the epidermal differentiation complex has been shaped by human interactions with the environment, microbiome, and resulting immune response.

National Science Foundation. Grant Number: 1714867

The Developmental Origins of Health and Disease: Early Life Health Conditions and Adult Age at Death in Europe

RICHARD H. STECKEL¹ and CHARLOTTE A. ROBERTS²

¹Economics and Anthropology, Ohio State University, ²Archaeology, University of Durham

Goals and Methods. This poster summarizes our analysis of evidence for early life growth disruption and its effect on mortality in the sample of 15,119 skeletons from the European History of Health Project. Linear enamel hypoplasia (LEH), cribra orbitalia (CO), porotic hyperostosis (PH) and femur length (FL) were considered in relation to age at death. The sample for this study included adult skeletons where childhood growth disruption indicators were scored. Skeletons from military sites were omitted, as were individuals who were only allocated a wide age range at death, e.g. 20 – 50 years, and skeletons with unknown sex.

Results. Only CO, and to a certain extent LEH and PO, appeared to have an effect on early mortality. FL had no systematic correlation with early death. However, the sample sizes varied according to which indicators were studied. Around 40% of individuals had LEH, 15% had CO, and 8% had PH. Results confirm overall that poorer health in

ABSTRACTS

early life leads to earlier death, except when FL was considered. This was a puzzle because other studies using height confirm the hypothesis. The effect of LEH on earlier death is statistically significant but small, which is generally consistent with other studies. The effect of CO and PH on earlier death is statistically significant and large. There were some differences between men and women, with men appearing more resilient against earlier mortality than women.

This research was funded by the National Science Foundation; by the German Science Foundation; and the Bank of Sweden Tercentenary Foundation

Species-Specific Scale Responses to Habitat Loss in a Nocturnal Lemur

TRAVIS S. STEFFENS¹, FERNANDO MERCADO MALABET² and SHAWN M. LEHMAN²

¹Conservation, Planet Madagascar, ²Anthropology, University of Toronto

Patch-level studies of habitat loss consistently show that the amount of habitat is a major determinant of species occurrence. However, patch-level research may fail to detect patterns and processes only observable at a landscape-level. A landscape-level approach that incorporates species-specific scale responses is needed to better understand what ecological parameters drive species occurrence. Our aim was to test the hypothesis that the small body size and specialized ecology (frugivorous and nocturnal) of *Cheirogaleus medius* will enable this species to persist in highly disturbed and fragmented landscapes. We surveyed line transects to determine the occurrence of *C. medius* within 42 fragments of deciduous dry forest and four portions of matrix in Northwestern Madagascar. We conducted between 11 and 21 surveys of each fragment ensuring that we conducted at least two surveys in each near the end of the study when *C. medius* is coming out of hibernation. We assessed their response to habitat loss using generalized linear mixed models in eleven different landscape scales ranging from 0.125 ha to 128 ha. We compared scale responses using Akaike's Information Criterion corrected for small sample sizes (AICc). We found that *C. medius* responded to habitat amount at scales smaller than their home range, supporting our hypothesis that small body and home range sizes in combination with nocturnality impact the scale of effect of habitat amount on *C. medius* occurrence. Our study suggests that the specialized ecology of *C. medius* provides resistance to high levels of habitat loss and fragmentation.

Sigma Xi, American Society of Primatology, Calgary and Edmonton Valley Zoos, The Explorers Club, the University of Toronto School of Graduate Studies, and the Natural Sciences and Engineering Research Council.

Occurrence of flame retardants, legacy and current use pesticides in primate habitat throughout Kibale National Park, Uganda

TESSA STEINICHE¹, SHAORUI WANG², ERIC JOHNSON³, MARTA VENIER² and MICHAEL WASSERMAN¹

¹Anthropology, Indiana University, ²School of Public and Environmental Affairs, Indiana University, ³Primate Environmental Endocrinology Laboratory, Indiana University

As interactions with human populations intensify, nonhuman primates are expected to encounter anthropogenic chemical pollutants at increasing rates. In particular, accelerated land use change and landscape fragmentation associated with the expansion of agriculture and urbanization has resulted in the widespread introduction of agrochemical and industrial pollutants throughout primate habitats. Our study was conducted in and surrounding Kibale National Park, Uganda, a protected area providing habitat to one of the world's most diverse and abundant primate communities. Passive air samplers (n= 24) were used to measure atmospheric concentrations of persistent organic pollutants (POPs), including polybrominated diphenyl ethers (PBDEs) and legacy organochlorine pesticides (OCPs), and current use pesticides (CUPs). Median levels of PBDEs, OCPs, and CUPs were 12.1 pg/m³ (1.2 - 22.8 pg/m³), 5.0 pg/m³ (0.6 - 11.2 pg/m³), and 7.4 pg/m³ (1.6 - 34.5 pg/m³), respectively. We discuss this variation in light of surrounding land use outside the park and research activity within the park. We further highlight the ecological and evolutionary implications of primate exposure to novel chemicals, chemical pollution as an overlooked threat to conservation, and future directions for the use of noninvasive biomonitoring to examine the effects of anthropogenic chemicals in wild populations.

Funding for this project was provided by Indiana University.

Trabecular patterning in the human skeleton: vertebral, humeral, femoral, and tibial variation

NICHOLAS B. STEPHENS¹, JAAP P.P. SAERS², LILY J. DOERSHUK¹, TEA JASHASHVILI^{3,4}, KRISTIAN J. CARLSON^{5,6}, ADAM D. GORDON⁷, JAY T. STOCK^{2,8} and TIM M. RYAN¹

¹Department of Anthropology, Penn State University, University Park, PA 16802, USA, ²Department of Archaeology, Cambridge University, Cambridge, CB1 3DZ, UK, ³Molecular Imaging Center, Department of Radiology, Keck School of Medicine, University of Southern California, Los Angeles, CA 90033, USA, ⁴Department of Geology and Paleontology, Georgian National Museum, 0105 Tbilisi, Georgia, ⁵Department of Integrative Anatomical Sciences, Keck School of Medicine, University of Southern California, Los Angeles, CA 90033, USA, ⁶Evolutionary Studies

Institute, University of the Witwatersrand, Wits2050 Johannesburg, South Africa, ⁷Department of Anthropology, University at Albany, SUNY, Albany, NY12222, USA, ⁸Department of Anthropology, Western University, London, ON N6A 3K7, Canada

Human skeletons are relatively gracile when compared to non-human primates. Aside from genetic differences, previous preclinical and anthropological research suggests that this skeletal phenotype may be related to reduced levels of activity and skeletal loading. While many different measures of external and internal skeletal variation have been documented in previous decades, little is known about how trabecular bone is distributed throughout the human skeleton. Here we seek to describe the structure and distribution of trabecular bone in the seventh cervical vertebral body, proximal humerus, proximal femur, and distal tibia from 15 archaeological individuals belonging to three distinct groups (Black Earth [Illinois, USA], n = 6; Kerma [Sudan], n = 6; St. John's [UK], n = 4). Using microCT scans (~30-50 µm) of each element, the entire trabecular volume was quantified using Medtool 4.2. For all the groups bone volume fraction (BV/TV) was highest in the cervical vertebra, followed by the femur > tibia > humerus, while degree of anisotropy (DA) was highest in the tibia, followed by the femur > humerus > and cervical vertebrae. Among the groups the Black Earth had the highest BV/TV and lowest DA, which agrees with their being the most active. Kruskal-Wallis statistical comparisons of BV/TV and DA between groups found significant differences among groups for the cervical vertebra (BV/TV), and tibia (BV/TV, DA). While preliminary, our results demonstrate the potential for identifying common trabecular distribution patterns among the skeletal elements, also highlighting the skeletal regions that may vary in behaviorally relevant ways.

Funding: NSF BCS-1719187, NSF BCS-1719140 RCUK/ BBSRC grant BB/R01292X/1

Biological Distance and Burial Practice: An Investigation of the Perry site (1LU25)

ASHLEY N. STEWART

Anthropology, University of Alabama

The Perry site (1LU25) is a multicomponent shell mound and village site in northern Alabama that dates to the Late Archaic (6000-3000 B.P.) and the Mississippian (A.D. 900-1500) time periods. Excavated in the 1930s and 40s by the Works Progress Administration and the Civilian Conservation Corps, this site has often been the subject of study over the past seventy years. However, population genetics and the role that biological kinship played in mortuary construction have not been explored. Further, no investigations have been made into the differences in mortuary construction between the Archaic and the Mississippian. This project seeks

ABSTRACTS

to understand the nature of biological kinship and its influence on death and burial as it is seen at the Perry site and how this changes through time. It is hypothesized that biological relationships will influence burial placement and practice in the Mississippian more than in the Archaic. Mississippian populations were more sedentary than in previous times, and the social implications of biology were more deeply felt. Biological distance analysis was conducted in order to address these questions. Using the Arizona State University Dental Anthropology System reference plaques, all individuals from the Perry site with dentition ($n = 790$) were examined to record their metric and non-metric dental traits. Using Gower's Coefficient, the genetic relationships present in the Archaic and Mississippian populations were determined. These were then compared to physical burial placement as well as burial practice, revealing Mississippian burial practice reflected genetic relationships more frequently than did those examined in the Archaic.

Identifying and Interpreting Unexpected Spatial Patterns of Bioarchaeological Data Using Geographic Information Systems

MARISSA C. STEWART^{1,2} and GIUSEPPE VERCELLOTTI³

¹Teaching & Learning Transformation Center, University of Maryland, ²Department of Anthropology, University of Maryland, ³Department of Anthropology, The Ohio State University

Geographic information systems (GIS) provide powerful tools to incorporate in bioarchaeological research that help present and organize data, but can also identify unexpected patterns that may require further exploration and analysis. This study presents results from a variety of GIS analyses that identify an unexpected pattern and discusses possible interpretations of these findings. GIS analyses, supplemented by chi-square and ANOVA tests, are used to examine the distribution of paleopathological and osteometric features of individuals buried in the medieval parish cemetery of *Pieve di Pava* (8th c.-12th c. Siena, Italy). As a parish cemetery, *Pieve di Pava* is considered to be representative of the entire medieval population inhabiting the area, including members of all socioeconomic statuses ($N=125$). Italian medieval archaeology has developed assumptions about burial placement that connect the proximity of burials to areas of perceived importance (such as the altar) to privilege. However, the site of *Pieve di Pava* does not conform to established burial expectations. Analyses contributing to the discussion include the distribution and severity of linear enamel hypoplasias, dental health indicators, and degenerative joint changes, as well as interpolation and hot spot analyses of the osteometric measurements of the upper and lower extremities. Together, these analyses identify unexpected

spatial distribution patterns of skeletal variables, suggesting areas of significance behind the apses, along the north-south intercept of the church, and in the southwestern corner of the cemetery. The results of these various spatial analyses, supplemented by statistical analyses, are discussed and various interpretations and additional questions are identified.

Embodied Cultural Identity in Late Bronze Age Central Greece

KAITLYN E. STILES

Anthropology, University of Tennessee

Although human skeletal remains represent a significant source of biocultural information, they have been largely underused in the study of Late Bronze Age (1600 – 1150 BCE) Greece. The most prominent culture, the Mycenaeans, have been characterized through mortuary contexts and material remains from elite centers. As a result, the defining attributes of Mycenaean cultural identity are based mostly on elite culture emphasizing high status, wealth, foreign trade, and a warrior ideology. The extent to which local communities outside of major centers adopted these attributes is unclear. I am testing whether the skeletal remains from the non-center, rock cut chamber tomb cemetery of Golemi Agios Georgios in central Greece exhibit biological correlates of the archaeologically defined "Mycenaean" cultural identity. Twenty-one tombs contained the remains of commingled individuals with a compiled MNI of 178. I use a contextualized bioarchaeological approach that employs embodiment theory and osteobiography to explore the skeletally manifested aspects of identity at the cemetery wide, tomb group, and individual levels. I examine demography, non-specific indicators of disease, activity markers, and cranial trauma. I found that, cemetery wide, the Golemi individuals embodied only one aspect of the perceived Mycenaean identity through relatively good health. At the group level it appears that good health does not necessarily correspond with high status or wealth. Certain groups appear to embody more "Mycenaean" attributes while others have more "local" characteristics. At the individual level, few exhibit trauma consistent with fighting styles in Mycenaean Greece, illustrating a limited physical manifestation of the "warrior" identity.

This research was funded by a U.S. Student Fulbright, the Archaeological Institute of America, the University of Tennessee, and the Wiener Laboratory in Athens, Greece.

Quantifying error in virtual data collection: the impact of MSCT scan segmentation protocol and inter-observer error in 3-D landmark placement on the human subadult pelvis

MICHALA K. STOCK¹, LOUISE K. CORRON², LAURA E. CIRILLO², HEATHER M. GARVIN³, CORTNEY N. HULSE², STEPHANIE J. COLE², KYRA E. STULL^{2,4} and ALEXANDRA R. KLALES⁵

¹Department of Exercise Science, High Point University, ²Department of Anthropology, University of Nevada, Reno, ³Department of Anatomy, Des Moines University, ⁴Department of Anatomy, University of Pretoria, ⁵Forensic Anthropology Program, Washburn University

The utility of CT scan data for creating skeletal reference databases has gained recognition, but requires protocol standardization to ensure accuracy and comparability between specimens. Here, we investigate the impact of scan processing protocols and landmark placement on error in virtual data collection.

MSCT postmortem scans of subadult individuals were obtained from the University of New Mexico Health Sciences Center, Office of the Medical Investigator. Four researchers segmented the pelvis of four randomly-sampled individuals and each performed four trials on a fifth individual. Deviation analyses in Geomagic Studio were used to visualize discrepancies and calculate pairwise comparisons of the root-mean-square error (RMSE) and the average deviation distances. Resultant RMSE values ranged from 0.13-0.78mm (mean=0.33mm), with an average deviation of 0.17mm between model vertices; although certain regions (e.g., ASIS) were prone to larger deviations. The effects of threshold value selection and smoothing protocol on overall deviation and variance at specific anatomical locations are discussed.

To examine error from landmark placement, three researchers each collected 32 pelvic landmarks on a set of 30 segmented pelvis in Amira. Error was assessed using distances from mean landmark placement and a Procrustes MANOVA. The overall average error was 2.4mm. Mean error at individual landmarks ranges from 0.9-7.4mm; landmarks associated with pelvic height exhibited the highest error. The MANOVA demonstrated significantly more variation among individuals than within landmark placement ($p=0.27$).

Altogether, results suggest that inter- and intra-observer errors associated with CT scan segmentation and landmark placement are generally acceptable, but can improve with further protocol standardization.

This work was funded by the National Institute of Justice grants 2015-DN-BX-K409 and 2017-DN-BX-K0144.

ABSTRACTS

Exploring population origins and dispersals using ancient DNA at Chelechol ra Orrak, Palau

JESSICA H. STONE¹, CAROLINE KISIELINSKI², JUSTIN TACKNEY², SCOTT M. FITZPATRICK^{1,3}, NELSON TING¹ and DENNIS O'ROURKE²

¹Department of Anthropology, University of Oregon, ²Department of Anthropology, University of Kansas, ³Museum of Natural and Cultural History, University of Oregon

Although Micronesia was one of the last geographical areas to be colonized by humans, in one of the most rapid and widespread dispersals in human history, the timing, direction, and origins of initial settlement still remain somewhat unclear. The Chelechol ra Orrak site in Palau, western Micronesia, contains the largest and oldest human skeletal assemblage in the region, and is one of only two sites that represent some of the earliest settlers in the Pacific. As such, Chelechol ra Orrak provides an excellent opportunity for direct study of population dispersals into Micronesia via osteological and genetic data. Here, we present new results from research involving the recovery of ancient DNA (aDNA) from individuals interred at the site. Targeted sequencing of the mitochondrial control region yields evidence of haplotypes consistent with Island Southeast Asian origins (e.g., M7b1a2a). However, in the case of some individuals, additional information is needed to assign haplotypes. Hybridization capture and sequencing of full mitogenomes from a subset of individuals further refined population affinities. Together, current results demonstrate genetic distinctiveness between other ancient Pacific Island and modern Palauan data, but still support archaeological and linguistic models suggestive of an Island Southeast Asian origin.

This research was supported by a Wenner Gren Foundation Dissertation Fieldwork grant (Gr. 9104), the Edna English Foundation for Archaeological Research, and the University of Oregon Global Studies Institute.

The Urban Environment of a Neighborhood in Teotihuacan, Mexico

REBECCA STOREY¹ and GINA M. BUCKLEY²

¹Comparative Cultural Studies, University of Houston, ²Anthropology, The Pennsylvania State University

The Basin of Mexico, in the central highlands of Mexico, was the location of important Precolumbian societies, including an early, large urban center, Teotihuacan. Archaeological investigation has revealed that the city was organized into neighborhoods. One of the most clearly defined was the Tlajinga district on the southern edge of the city, where excavations in three residential compounds provided a skeletal sample. Neighborhoods in Teotihuacan were composed of residences of different status, although neighborhoods had higher social status if closer to the

ritual/political center, as opposed to those on the periphery. Tlajinga was a modest neighborhood of craft specialists, but also controlled the southern entrance into the city. Two of the compounds were along the southern entrance street, while the largest skeletal sample came from a nearby lower-status compound of lapidary and ceramic specialists (Tlajinga 33). Preindustrial cities like Teotihuacan had problems with poor health and importing enough food for the residents. The hypothesis was that although there were slight status difference among the compounds, their urban environment should have been similar. Comparison of morbidity patterns from paleopathological indicators of stress and the stable isotopes of carbon and nitrogen for dietary patterns indicated that indeed there were differences. The compounds on the main southern entrance were less affected by stressors during juvenile growth and also seemed to have a greater variety of plant foods than Tlajinga 33, probably due to their slightly higher social status. The urban environment was influenced by wealth and prestige between actual close neighbors.

Funding by the National Science Foundation under Grant No. BCS-13212447 and BCS-1321232 (biogeochemical analysis), and Tlajinga 33 by the National Science Foundation (BNS 80-05825, BNS 80-05754, and BNS 82-04862).

Climate Change and Invisible Suffering: Transgenerational Impacts of Traumatic Maternal Experiences of Extreme Drought

BILINDA STRAIGHT¹, CHARLES E. HILTON², GEORGIANA ONICESCU⁶, BELINDA NEEDHAM³, AMY NAUGLE⁵, OLUNGAH C. OWUOR⁴, YUQIAN SHEN⁶, STEPHANIE M. HAFT⁵, SAMAN LESEELA¹, DANIEL L. LESEELA¹, CELINA JESKA¹ and CAROLINE SISINA KELEMPU⁴

¹Anthropology & Intercultural Studies Institute, Western Michigan University, ²Anthropology, University of North Carolina Chapel Hill, ³School of Public Health, University of Michigan, ⁴Institute of Anthropology, Gender, and African Studies, University of Nairobi, ⁵Psychology, Western Michigan University, ⁶Statistics, Western Michigan University

Evidence is accumulating that the adverse impacts of climate change are unevenly distributed, affecting the world's most vulnerable populations disproportionately. Studies that integrate examinations of culturally shaped lived experiences with their biological consequences promise to contribute important knowledge about how humans understand and recover from climate-based events across generations. In 2009, an extreme drought in northern Kenya decimated livestock, creating hunger that attracted international attention. Here we report initial findings of an ongoing, same-sex sibling epigenetic study examining the effects of maternal exposure to the 2009 drought on Samburu pastoralist children (*N* to date = 75 mothers; 75 sibling

pairs (150 children)). Mothers reported engaging in risky activities during their 2009 pregnancies compared to pregnancies of same-sex children conceived 2+ years after the drought. Additionally, mothers reported more traumas of other kinds during their 2009 pregnancies, particularly interpersonal violence, forced labor, and food withholding by male kin and even male neighbors ($p = .0276$ for combined trauma score). This resulted for many in *Iminchich*, a Samburu form of prolonged emotional distress. Children from the 2009 pregnancies differ in health outcomes from their post-drought siblings, qualitatively with respect to reported illnesses, and quantitatively with respect to BMI ($p = .0001$ for BMI z-scores based on WHO standards). We provide ethnographic "thick" description of gender-inequality and drought-induced forms of invisible suffering that are transgenerationally sedimented in children's bodies. We also consider both evolutionary and humanitarian perspectives of human-animal interactive responses to extreme climate events.

This research was funded by National Science Foundation Award #1728743, "A Bio-Cultural Investigation of Intergenerational Epigenetic Mechanisms" (Bilinda Straight, PI) and Western Michigan University FRACAA.

Placing the Denisovans in human evolution

CHRIS B. STRINGER

Centre for Human Evolution Research, The Natural History Museum, London

We have little physical evidence of the Denisovans, but rich genetic data from several individuals. Those data suggest that the Denisovans are a sister group to Neanderthals, with an estimated divergence date of ~400 ka. However, Denisovan teeth are large and seemingly lack Neanderthal derived features, in contrast to the Sima de los Huesos sample from Spain, dated at ~430 ka. This may imply that Denisovans diverged from the Neanderthal lineage prior to ~430 ka. Possible evidence of early Denisovans from China may also support this inference, since fossils such as Dali, Jinniushan and Harbin show more primitive features, and less derived Neanderthal features, than the Sima sample. However, other fossils such as Xujiayao, Maba, Penghu and Xuchang illustrate diversity and complexity in the Chinese record, tempered by the recent genetic recognition of hybridisation between the Denisovan and Neanderthal lineages.

The existence of a late Denisovan-like population in South East Asia is also inferred from the presence of related DNA in extant Oceanian peoples, but we are far from establishing which fossils in the region might represent such a population. The taxonomic status of the Denisovans also remains unclear from present data, since they

ABSTRACTS

represent a sister-group to Neanderthals (and thus belong within the Neanderthal clade), but seemingly diverged early, and are genetically as distinct from *Homo sapiens* as the Neanderthals.

Research support: The Calvea Foundation and the Human Origins Research Fund, Natural History Museum London

Comparison of eight- and four-muscle model for assessment of upper limb muscle activity during cereal grinding

MICHAL STRUŠKA, MARTIN HORA and VLADIMÍR SLÁDEK

Department of Anthropology and Human Genetics, Charles University

Our previous work has shown that the decrease in female humeral asymmetry in the early Holocene can be explained by different muscle activity during grinding on a saddle and rotary quern. However, the previous study assessed muscle activity of four muscles assuming it sufficiently reflected the humeral loading pattern. We test whether the differences in muscle activity between the querns revealed by the previous four-muscle model correspond to the differences captured by a new extended eight-muscle model. We acquired electromyographic (EMG) signal of anterior, middle, and posterior part of deltoid, infraspinatus, pectoralis major, lateral and long head of triceps brachii, and biceps brachii in 25 females during cereal grinding on the saddle and rotary quern. We compared the peak values (peakEMG) and integrals (iEMG) of EMG signal normalized to maximum voluntary contraction (MVC) between the muscles and between the querns. Sum of iEMG of the eight muscles was significantly higher for rotary quern grinding than saddle quern grinding supporting the previous results of four-muscle model. During saddle quern grinding only the lateral and long head of triceps brachii had mean peakEMG >20% MVC. This supports conclusion from the previous four-muscle model that during saddle quern grinding the upper limb is loaded mainly by elbow extensors. The newly tested eight-muscle model detected similar differences in muscle activity between grinding tools as our previous four-muscle model. We conclude that further increase of complexity of the four-muscle model is not needed to differentiate between grinding on the saddle and rotary quern.

Features of Decomposition from an Accidental Burial with a Defined Postmortem Interval in a Northern Latitude State

PHOEBE R. STUBBLEFIELD

C.A. Pound Human Identification Lab, University of Florida

This presentation contributes features of decomposition observed after a known postmortem interval for an accidental human burial that occurred in a North American northern latitude (north of 44 degrees) state. The forensic literature for postmortem interval and decomposition is sparse for northern latitude locations, and the literature that does exist features exposures rather than burials. In this circumstance two variables that normally confound association of decompositional state to postmortem interval—time since death and environmental temperature—are constrained. These features of decomposition inform the taphonomic and decompositional patterns for postmortem interval estimation in the United States Northern Plains. A clothed human body was recovered after a 36-month accidental burial in soil that was predominately silty sand, at a depth of 8 feet (2.4 m). At this geographic location the frost line extends to 70-80 inches (177-203 cm), placing this burial to well below. Soil temperature at this depth ranges from 40 to 50 degrees F (4-10 degrees C). The primary variables affecting decomposition were temperature and time, as no insect, scavenger, or plant activity was observed at that depth. Differential decomposition was observed. Soft tissue located at the upper limit of the burial (closer to the frost line) were represented by mummified remnants. Preservation increased as depth increased such that skin, skin features, muscle, and some organs were present. The skeletal preservation was consistent in bone quality with archaeological remains from the same region, but no previous reference was available for the degree of soft tissue preservation.

No funding aside from institutional salary was accepted for this research.

Do abrasion and attrition leave the same trace? A microscopic tooth wear study on chimpanzee molar wear facets

JULIA STUHLTRÄGER¹, ELLEN SCHULZ-KORNAS¹, ROMAN M. WITTIG^{2,3}, OTTMAR KULLMER^{4,5} and KORNELIUS KUPCZIK¹

¹Max Planck Weizmann Center for Integrative Archaeology and Anthropology, Max Planck Institute for Evolutionary Anthropology,

²Department of Primatology, Max Planck Institute for Evolutionary Anthropology, ³Tai Chimpanzee Project, CSRS, Abidjan, Ivory Coast, ⁴Department of Palaeoanthropology, Senckenberg Research Institute Frankfurt am Main, ⁵Department of Paleobiology and Environment, Institute of Ecology, Evolution, and Diversity, Goethe University Frankfurt

Microscopic tooth wear is caused either by tooth-substrate-tooth contact (abrasion) or by tooth-tooth contact (attrition). In particular, it has been suggested that the abrasion-dominated facet f9 may reliably be used for dietary reconstructions in recent and fossil primates. However, it largely remains unclear whether other facets within and between tooth positions represent

a comparable dietary wear signature. Here, we compared the microtexture of five wear facets (abrasion and attrition) within first (M1) and second (M2) molars as well as between upper and lower M1s and M2s in western chimpanzees (*Pan troglodytes verus*). We selected molars from two geographically close populations (Tai forest chimpanzees (Ivory Coast) N=26, north-eastern Liberia chimpanzees N=32) to test for population-specific and intra-individual variation. Abrasion-dominated (f9, f11) and attrition-dominated (f1, f3, f6) facets were analyzed with 3D surface texture (3DST) analysis, describing the complexity, height and area of wear facet features. In both populations, facets on upper and lower M1s showed no significant differentiation in their 3DST. While the same accounts for upper and lower M2s in Tai and lower M2s in Liberia chimpanzees, 3DST signatures on upper M2s in the Liberia population differ: f3 shows the highest complexity with high reliefs and areas compared to f6, while f9 is intermediate. We conclude that microwear signatures on chimpanzee M1s are not influenced by facet type, as evidenced by both chimpanzee data sets, and therefore suggest that besides the standard facet f9 the facets f1, f3, f6, and f11 can equally be used for dietary reconstructions.

Exploring the relationship between dental development, population variation, and environment

KYRA E. STULL^{1,2}, LOUISE CORRON¹, CORTNEY N. HULSE¹ and YUERAN YANG³

¹Anthropology, University of Nevada, Reno,

²Anatomy, University of Pretoria, South Africa,

³Psychology, University of Nevada, Reno

Dental development is consistently stated to be under stronger genetic control and less influenced by the environment than skeletal development. However, researchers have been recognizing population variation in dental formation for years, suggesting there is plasticity in development. The current study attempts to quantify the influence of geographic origin, socioeconomic status, and population on dental development.

Dental development was scored on modern children aged birth to 15 years of known age and sex from Colombia (n=57), France (n=240), the United States (n=880), and South Africa (n=500). Each country is characterized by the Human Development Index (HDI) and the Gini coefficient, which capture country-level differences in overall well-being, education, and economic productivity and wealth equality levels, respectively. An ANOVA was conducted to evaluate population differences in each tooth within each life history stage. The indicators, country-specific economic parameters, and social race were implemented in hierarchical linear models (HLMs) to quantify the impact of each on dental development.

ABSTRACTS

Significant population differences existed in dental development among the groups in all life history stages. In HLMs, the populations displayed the same slope but significantly different intercepts. The HDI, Gini coefficient, and social race all contributed to the models but were not significant in the models. Results suggest that greater explorations need to be made into proximate and ultimate factors influencing dental development so that anthropologists can better understand worldwide variability, as this has great impacts in society, particularly when identification is involved.

This project was funded as part of the National Institute of Justice (NIJ 2017-DN-BX-0144) and the National Science Foundation (NSF BCS-1551913)

Assessing the Prevalence and Distribution of Antimicrobial Resistance at the Human-Wildlife Interface in Rural Uganda

REBECCA M. STUMPF^{1,2,3,5}, ABIGAIL ASANGBA^{1,3}, CHRIS IRUMBA⁵, MARTIN AINEBYONA⁵, RACHEL RUSEN⁵, REBECCA L. SMITH^{3,4}, HOWARD ONYUTH⁵ and KATIE GIGGS⁵

¹Department of Anthropology, University of Illinois at Urbana Champaign, ²Department of Animal Biology, University of Illinois at Urbana Champaign, ³The Woese Institute for Genomic Biology, University of Illinois at Urbana Champaign, ⁴Department of Pathobiology, University of Illinois at Urbana Champaign, ⁵The Kanyanchu River Research Collaborative, Kibale National Park, Uganda

Antimicrobial resistance (AMR) is a growing problem across the globe. However, fundamental knowledge is lacking of global AMR presence, prevalence, and transmission dynamics. In this study, we conducted a zoonotic and anthropogenic community-wide characterization of the presence, distribution, and relative prevalence of AMR genes in rural western Uganda. We collected and extracted DNA from fecal samples of 7 species of wild primates (chimpanzee, baboon, mangabey, black and white colobus monkey, red colobus monkey, red tailed monkey, and vervet monkey), humans, domestic animals, and soil. We sequenced on Illumina HiSeq 2500 six targeted AMR genes, including macrolide (*ermB*), sulfonamide (*sul1* and *sul2*), and tetracycline (*tetC*, *tetO* and *tetW*). Results show that soil samples contained all targeted AMR genes. As expected, domestic animals had more AMR genes than wild animals. Specifically, we found the tetracyclines and sulfonamides in all domestic but not all wild samples. AMR genes *sul2* and *tetO* were present in both domestic and wild samples, while *ermB* was present in only a few, mostly domestic hosts (dog, chicken and cow) and chimpanzees. Chimpanzees had the highest number of AMR genes compared to other wild primates, potentially due to increased human exposure (tourists and field workers) and/or greater terrestrial contact. Several non-targeted

AMR genes were also identified in these diverse samples. Future work includes microbial phylogenetics to track and model AMR transmission dynamics to understand and ultimately help to mitigate AMR transmission in this region.

Funding: The Bill and Melinda Gates Foundation, NIH R01TW011182-01, NSF BCS-1441409, and The University of Illinois.

Mid-Pliocene paleoenvironment of Woranso-Mille (Ethiopia): implications for hominin diversity and *Australopithecus* paleoecology

DENISE F. SU¹ and YOHANNES HAILE-SELASSIE²

¹Department of Paleobotany and Paleoecology, Cleveland Museum of Natural History, ²Department of Physical Anthropology, Cleveland Museum of Natural History

Woranso-Mille is the only site, so far, to have reported the spatial and temporal co-existence of more than one early hominin species between 3.3 and 3.8 Ma. Significant mid-Pliocene hominin specimens that have been described from the site include a partial skeleton of *Australopithecus afarensis*, a partial foot of an as-yet-unnamed species, and mandibular and maxillary elements of *Australopithecus deyiremeda*. A fundamental question is how multiple hominin species were able to co-exist at Woranso-Mille. In order to answer this question, a thorough understanding of the paleoenvironment of these early hominins and their ecological niche is necessary. Here, we examined the paleoenvironment of Woranso-Mille through its faunal community ecological structure and taxonomic composition, based on fossil specimens recovered from hominin-bearing collection areas dated to 3.2-3.8 Ma. We examined the community structures of these collection areas using dietary and locomotor variables and compared them to each other, to those of extant modern faunal communities, and to contemporaneous fossil sites in eastern Africa. We also explored faunal similarity among the Woranso-Mille faunas and those of contemporaneous eastern African sites. The results suggest that mid-Pliocene Woranso-Mille had a high level of vegetation heterogeneity and was a mosaic of different habitat types at different geological times, with riparian woodland and floodplain grassland along a river draining into a lake, along with less mesic habitats such as woodland, grassland and shrubland. This may have promoted dietary specializations and niche differentiations among the different *Australopithecus* species at Woranso-Mille and allowed for their co-existence at the site.

Research at Woranso-Mille was funded by The Leakey Foundation, National Geographic Society, Cleveland Museum of Natural History, and National Science Foundation (BCS-0234320, BCS-0321893, BCS-0542037, BCS-1124705, BCS-1124713, BCS-1124716, BCS-1125157, and BCS-1125345)

The use of biomarkers to answer questions about the evolution of mind and behavior: Integrating human biology, human behavioral ecology, and evolutionary psychology

LAWRENCE S. SUGIYAMA and JOSHUA M. SCHROCK

Department of Anthropology, University of Oregon

Human population biologists, human behavioral ecologists, and evolutionary psychologists often differ in theoretical orientations and topics of study, but all seek to understand human adaptation and variation. Physiological, behavioral, and psychological processes interact with one another, thus the insights of these disciplines are highly relevant to one another. Research that crosses these disciplinary boundaries has the potential to open new frontiers in the study of human adaptation and variation. In this review, we show that the use of minimally invasive biomarkers is an important innovation for integrating these disciplines. Although the use of biomarkers in evolutionary studies of mind and behavior is still rare, there are a few studies that illustrate the promise of this approach. For example, minimally invasive measures of steroid hormones have been used to assess the physiological effects of competition and social status in field research. Other areas of research, such as sickness behavior and disgust psychology, have used more burdensome protocols to measure biomarkers in the laboratory (e.g., venipuncture) and would benefit from using minimally invasive methods to replicate findings in the field. We identify other areas that have not yet incorporated biomarkers but would benefit from doing so using minimally invasive methods: time allocation, foraging behavior, decision-making, welfare tradeoffs, and learning. To facilitate the adoption of minimally invasive biomarkers in evolutionary studies of mind and behavior, we outline three ways in which they can be operationalized: (1) as markers of contextual cues, (2) as markers of physiological mediators, and (3) as markers of outcomes.

The effect of the alpha-actinin 3 (ACTN3) R577X polymorphism and mtDNA on energy expenditure in modern humans

ZANE S. SWANSON^{1,2,3}, HERMAN PONTZER¹, AMY LUKE⁴, LARA R. DUGAS⁴ and MICHAEL E. STEIPER^{3,5}

¹Evolutionary Anthropology, Duke University, ²Department of Anthropology, The Graduate Center, ³New York Consortium in Evolutionary Primatology, NYCEP, ⁴Public Health Sciences, Loyola University Chicago, ⁵Department of Anthropology, Hunter College

Uncovering genetic determinants of human energy expenditure has been hampered by the limited sample sizes of most metabolic studies. ACTN3 and mitochondrial DNA (mtDNA) are two candidates for investigating effects on

ABSTRACTS

metabolic rate. Previous studies suggest that variation in mtDNA among humans relates to differences in energy expenditure, whereas the R577X polymorphism of *ACTN3*, the gene that codes for alpha-actinin-3 in type-I (fast-twitch) muscle fibers, influences athletic ability. Here we test whether *ACTN3* genotypes and mtDNA are associated with total energy expenditure (TEE, measured using doubly labeled water), resting energy expenditure (REE, measured via respirometry), and activity energy expenditure (AEE, calculated from TEE and REE), in a large sample of adult humans from five populations (n=211 genotyped for *ACTN3*, and n=117 haplotyped for mtDNA). A multivariate analysis recovered a significant relationship between *ACTN3* genotypes and REE, with homozygous RR individuals exhibiting higher REE (+117 kcal/day) compared to heterozygous RX individuals, when adjusted for body size and composition, physical activity, and manual labor status. We also found that haplogroups L1, L3, and L4 produced significantly greater slopes for the effect of fat free mass (FFM) on REE than haplogroups L0, L2, and M. These results suggest that common genetic variants have a significant influence on metabolic rate in humans.

Funding for this study was provided in part by the NYCEP IGERT grant (NSF-0966166).

A population perspective on the co-localization of trace elements in archaeological bone

TREENA M. SWANSTON¹, TAMARA L. VARNEY², IAN COULTHARD³, REG MURPHY⁴, RACHEL SIMPSON⁵ and DAVID ML. COOPER⁶

¹Anthropology and Biological Sciences, MacEwan University, ²Anthropology, Lakehead University, ³n/a, Canadian Light Source, ⁴n/a, National Parks Antigua, ⁵Archaeology and Anthropology, University of Saskatchewan, ⁶Anatomy, Physiology and Pharmacology, University of Saskatchewan

Through the identification of the spatial distribution of essential and nonessential (including toxic) trace elements in bone, we have an opportunity to determine a skeletal population's past exposure to toxic elements such as lead and reveal the presence of dietary elements such as strontium. With synchrotron X-ray fluorescence imaging (XFI), we are able to simultaneously capture spatial data for a variety of bone-seeking elements. Our current population under study, the Royal Naval Hospital cemetery (1793-1822) in Antigua, West Indies, was relocated due to the requirements of modern infrastructure. We determined the spatial distribution of a variety of elements in two millimetre by two millimetre cortical bone samples from 14 individuals, with an initial focus on identifying the distribution of lead within the bone. With a 20 micron resolution, the element spatial patterns indicated co-localization of elements lead and zinc. These patterns

are of interest because while one element, lead, is toxic, the other, zinc, is under homeostatic control. The spatial distribution of strontium suggested differential uptake during the bone remodelling process. These patterns also help to inform us as to whether the bone samples have been affected by diagenesis, because while some of the patterns are similar to bone microstructural features such as osteons, other patterns are gradients with the highest concentrations identified on the perimeter of the samples. These data provide an opportunity to learn more about not only the burial environment, but also gain insight and a temporal perspective on the population's element exposure during life.

This research was supported by a Social Sciences and Humanities Research Council (SSHRC) Insight Grant (#430-2014-1796)

Tooth be told: A preliminary investigation of dental morphological variation among medieval Polish Populations

VICTORIA M. SWENSON¹, ANNA SPINEK² and KRZYSZTOF TUNIA³

¹Anthropology, University of Nevada, Reno, ²Anthropology, Polish Academy of Sciences, ³Archaeology, Polish Institute of Archaeology and Ethnology

Medieval Poland (10th-15th c. A.D.) was characterized by long term sociopolitical transformation that drew culturally diverse immigrants across Europe and Asia. Historical, archaeological, and bioarchaeological evidence indicate an increase in craft specialization and interregional trade. This led to an increase in trade and market economy which drew people from rural into urbanized areas. Previous scholars have used cranial data to examine biological distance between medieval populations. However, the use of dental morphology to investigate geographic patterns in biological distance has been underutilized. This project investigates dental morphological variation in relation to geographic distance from various medieval skeletal samples.

To investigate population variation, we recorded the presence and absence of dental nonmetric traits using the dental morphological trait scoring system now referred to as the Turner-Scott method. Thirty-three nonmetric traits were scored on two-hundred individuals from five medieval sites. Medieval population affinities were compared using C.A.B. Smith's Mean Measure of Divergence (MMD). The MMD results demonstrate that Stręgorzyce, Gubin, and Pawłów are more similar to each other than to Płonsk and Sandomierz. Phenotypic and geographic distances were then compared using the Mantel and partial-Mantel matrix correlation test. Results of the Mantel and partial-Mantel tests indicate that dental morphological variation is significantly correlated ($r=0.787397$; $p\text{-value}=0.027$) with geographic distance. These preliminary

results highlight phenotypic similarity is associated with geographic proximity and conforms to a model of isolation by geographic distance. We conclude that the integration of dental data will provide valuable insight in medieval Poland where extensive interdisciplinary evidence is available for comparison.

This project was made possible through the support provided by the Kosciuszko Foundation, Polish Academy of Sciences, Polish Institute of Archaeology and Ethnology, and the University of Nevada, Reno.

Scapula shape and altitude in eastern gorillas (*Gorilla beringei*)

MAYA SZAFRANIEC and REBECCA S. JABBOUR
Department of Biology, Saint Mary's College of California

Eastern gorillas (*Gorilla beringei*) live at a range of altitudes associated with differences in vegetation and in locomotor behavior. At lower altitudes, trees are taller with more fruit, and gorillas climb more. As a result, eastern gorillas provide a valuable model for how hominoid postcranial morphology may vary with degree of arboreality. This study examines the relationships between altitude and several muscle attachment areas of the gorilla scapula that are predicted to reflect locomotor differences.

We collected 17 3D landmarks from the scapulae of 60 adult eastern gorillas, which were divided into three groups: low-altitude *G. b. graueri* (n=17), high-altitude *G. b. graueri* (n=20), and very-high-altitude *G. b. beringei* (n=23). We used geometric morphometrics to visualize variation between groups. We also calculated linear and area measurements from the landmarks and conducted t-tests and discriminant function analysis.

In males, the supraspinous fossa and the acromion were larger at lower altitudes, suggesting greater development of supraspinatus, deltoid, and trapezius. This altitude difference in males but not females may indicate that male locomotor behavior differs more between habitats. Alternatively, it may relate to adaptations in males for large shoulder muscles for display. In females, the infraspinous fossa was larger in low-altitude compared to high-altitude *G. b. graueri*, indicating a larger infraspinatus. The coracoid, an attachment for pectoralis minor and coracobrachialis, extended further in lower-altitude groups of both sexes. Groups did not consistently vary as predicted, but these results suggest that variation among fossil hominoid scapulae may reflect differences in arboreal behavior.

Wenner-Gren Foundation, Leakey Foundation, Sigma Xi, City University of New York, New York Consortium in Evolutionary Primatology, Saint Mary's College Faculty Research Grant and School of Science Summer Research Program

ABSTRACTS

Homeotic transformation of the human vertebral column – more global than local

ROBERT G. TAGUE

Geography and Anthropology, Louisiana State University

Individual *Hox* genes have a delimited domain of influence on the vertebral column. This study considers correlates with posterior and anterior homeotic transformation at the lumbar-sacral boundary in humans, resulting in 23 and 25 presacral vertebrae (PSV), respectively; modal PSV is 24. Skeletons of females and males between ages 20 and 49 years, listed as “black” or “white,” with seven cervical and 12 thoracic vertebrae from the Hamann-Todd, Robert Terry, and William Bass Collections are used. Individuals with 23, 24, and 25 PSV are compared for four variables: number of sacral vertebrae ($n=940$) and ratios for lengths of the posterior tubercles of 5th and 6th cervical vertebrae (C5/C6; $n=245$), 1st and 2nd ribs (rib 1/rib 2; $n=139$), and 11th and 12th ribs (rib 11/rib 12; $n=326$). Statistical tests are ANOVA, Fisher’s exact, and Student’s *t*. Results show that the sex/ethnic groups do not differ significantly for the four variables, so all groups are combined for analysis. Individuals with 23, 24, and 25 PSV differ significantly for all four variables. Partition analysis shows the following significant differences: (1) number of sacral vertebrae, all paired comparisons of 23, 24, and 25 PSV; (2) C5/C6, 23 PSV > 25 PSV; (3) rib 1/rib 2, 23 PSV < 24 and 25 PSV; and (4) rib 11/rib 12, 23 PSV > 24 PSV > 25 PSV. Results suggest that homeotic transformation at the lumbar-sacral boundary is not a local phenomenon, but is part of more global transformation from neck to sacrum.

A Case of Maternal and Perinatal Death in the Spring and Autumn Period in Jinnan region of China

TAO HAN, SEN YOU, SUNZIFENG RUAN, XINGYU MAN, XUEZHU LIAO, ANQI WANG and SHIYU YANG
Archaeology, Jinlin University

While historical documents indicate that cases of maternal and fetal death during delivery were very common in past populations, but few pregnant female burials have been reported. In this paper, a case is presented from China. The skeletal remains of the pregnant woman comes from the North Tao Si cemetery, which is located in the northeast of Xiangfen county, Shanxi Province. The cemetery was a “state tomb” of the Jin State. Large and medium-sized tomb owners should be nobles enfeoffed here by Jin State. 2016BM1 is a large stone tomb, with 6.5x5.4x10 meters in size. Many bronze and jade wares were unearthed. The material reported here comes from this tomb, and it was in the late spring and Autumn period (about 600-500 BC). The adult individual was buried in a back supine position. Most of the skeletal parts are rotten. Sex and age were

determined according to skeletal morphological traits, which suggests a female individual about 30 years old. The infant bones were in the maternal pelvic area, which was mostly destroyed due to stone extrusion, presented in an apparent head position. The infant’s gestational age is about 8 months according to long bones measurements. This paper describes and analyses arguably the first clear instance of the noble burial of a pregnant female in China. Report of this case can contribute to our knowledge of the reproductive age and challenges when pregnancy and childbirth of young females in the noble of ancient China.

Tympanic dehiscence: Its prevalence and expression in Pacific Northwest Native crania

GUY L. TASA

Department of Archaeology and Historic Preservation, Washington State Historic Preservation Office

A tympanic dehiscence (foramen tympanicum or foramen of Huschke) forms during normal post-natal development of the anterior-inferior wall of the external auditory canal. The dehiscence usually closes by 5 years of age, but the persistence of a dehiscence into adulthood is an anatomic variant commonly investigated in studies of cranial non-metric variation. The aim of the present study was to evaluate the frequency and expression of tympanic dehiscence in Native American crania from the Pacific Northwest ($n=279$) and to assess the known worldwide distribution of the trait.

The overall incidence of the trait in adult Native crania from the Pacific Northwest is 31.5%, with the occurrence in adult females (38.7%) being significantly higher ($p<0.05$, Pearson’s χ^2) than in males (25.0%). Occurrence of the trait in adults is predominantly bilateral (75.4%) and with no side predilection in unilateral occurrences. No significant differences were found between adult crania with artificial cranial modification (28/93, 30.1%) and those without (40/133, 30.1%). However, looking at modification type among adults, crania with Cowichan-style modification exhibited double the incidence (33.3%, 24/72) over those with Chinook-style (16.7%, 4/24). Incidence of the trait across age categories lends support to the position that the generally accepted timing for the normal closure of the dehiscence is erroneous.

An Archaeogenomic Investigation of Consanguinity During the Neolithic Transition

RECEP O. TASKENT¹, AREV P. SUMER³, DILEK KOPTEKIN², MUSTAFA OZKAN², FRANCISCO C.

CEBALLOS⁴, OMER GOKCUMEN¹ and MEHMET SOMEL²

¹Department of Biological Sciences, SUNY at Buffalo, ²Department of Biological Sciences, Middle East Technical University, Ankara, Turkey, ³Department of Ecology and Genetics, Uppsala University, Sweden, ⁴Sydney Brenner Institute for Molecular Bioscience, University of the Witwatersrand, Johannesburg, South Africa

The Neolithic Transition in West Eurasia led to an unprecedented increase in the human population size, greater mobility of humans as well as intense exchange of cultural practices. Sedentism and small-scale agriculture started in the Fertile Crescent by the early Holocene and spread to Anatolia in the ninth millennium BCE and eventually to Europe in the following millennia. Recent studies on ancient genomes from this era indicated that the Neolithic Transition involved major demographic shifts, with increasing population movements, admixture, and consequent rise in genetic diversity over time. However, another type of demographic shift, consanguineous mating, has yet to be extensively investigated. Modern forager societies are known to exhibit consanguineous mating practices more rarely than small-scale agricultural societies, and Paleolithic foragers may have had similarly low levels of inbreeding, leading to the question whether consanguineous mating practices could have spread after the advent of agriculture and private property. We previously showed that ancient genomes from European Mesolithic, Anatolian and European Neolithic exhibited different length distributions of runs of homozygosity indicating distinctive population histories as well as social structures within those populations. In this study, we aim to extend this work by inferring demographic traditions of early Holocene West Eurasian human populations. To this end, we are performing forward-time simulations to replicate all possible scenarios where population level processes such as bottlenecks and varying levels of consanguinity act together on human populations. Our results provide new insight into one of the major demographic shifts accompanying the Neolithic Transition in West Eurasia.

Fiber-type phenotype of the anterior superficial masseter in African apes: A preliminary test of the frequent recruitment hypothesis

ANDREA B. TAYLOR¹, MADISON WEST¹ and MEGAN HOLMES²

¹Basic Science, Touro University, ²Community and Family Medicine, Duke University

The frequent recruitment hypothesis states that vertebrates that engage in chewing with high frequency will have jaw adductors that express a high proportion of type 1 (high endurance, low tension cost) fibers at the expense of other fiber types. When fruit is scarce, *Gorilla gorilla* resort

ABSTRACTS

to herbaceous vegetation and daily time spent feeding by *G. gorilla* is greater compared with *Pan troglodytes*. These ecological differences suggest gorillas experience many more chew cycles compared with chimpanzees and thus should have jaw adductors with a higher proportion of MyHC-1/ α -cardiac fibers. As an initial test of this hypothesis in primates, we used immunohistochemistry to quantify the proportion of type 1 and type 2 MyHCs in the anterior superficial masseter (ASM) of two *G. gorilla* (n=1 male; n=1 female), four *P. troglodytes* (n=2 males; n=2 females) and two *P. paniscus* (n=1 female; n=1 unknown). Serial sections (5m) of each formalin-fixed muscle block were stained with primary antibodies against MyHC-1 (NOQ7.5.4D), MyHC α -cardiac (MYH6), MyHC-2 (MY-32) and MyHC-M (2F4). The percentage of fibers that reacted with intermediate or strong intensity to either of the type 1 (slow) antibodies (NOQ7.5.4D or MYH6) was higher in gorillas (63%) compared with either chimpanzees (24%) or bonobos (33%), providing some support for this hypothesis. Notably, 100% of African ape ASM fibers expressed MyHC α -cardiac and, similar to papionins, their ASM fibers are predominantly slow+fast hybrids, suggesting a finely graded continuum of contractile properties to facilitate more precise modulation of jaw movements and bite forces.

This work was supported by NSF BCS 1719743.

An Analysis of Modified and Processed Human Bone Artifacts from Late Prehistoric (AD 700 – 1500) Southern Texas

MATTHEW S. TAYLOR
Sociology & Anthropology, Georgia Southern University

A number of modified human bone artifacts from various Late Prehistoric (AD 700 – 1500) archaeological sites have been discovered along the coast of what is now southern Texas. A total of 29 modified bones from four archaeological sites were selected for analysis. The artifacts were classified (when possible) by age, sex, bone element, and anatomical location. They were evaluated for evidence of trauma and method of reduction. Twenty-seven of the modified bones represent adults and two represent subadults. Most of the artifacts were made from long bones, primarily of the leg, but two ribs were also noted. These artifacts were fashioned using the groove-and-snap method of reduction. The bones display cut marks associated with perimortem processing, dearticulation, and defleshing. One adult humerus had been fashioned into a *omichicahuaztli*, or musical rasp, and decorated with an incised zig-zag pattern of lines. The method of reduction, and distribution of cut marks, were compared with non-human modified bones and human bone artifacts found in other parts of North America. Explanations of these

artifacts include expressions of ancestor worship or war trophies. The similarity between these bones and similar artifacts found in contemporaneous Postclassic Mexico suggests a knowledge Mesoamerican cultural practices.

None

Dental microwear in laboratory primates: Insights into the complexity of dental microwear formation

MARK F. TEAFORD¹, MYRA F. LAIRD², CALLUM F. ROSS², ANDREA B. TAYLOR¹, PETER S. UNGAR³ and CHRISTOPHER J. VINYARD⁴

¹Basic Science, Touro University, California, ²Organismal Biology and Anatomy, University of Chicago, ³Department of Anthropology, University of Arkansas, ⁴Department of Anatomy and Neurobiology, Northeast Ohio Medical University

Dental microwear analysis has been employed in studies of a wide range of modern and fossil animals, yielding many insights into the biology/ecology of those taxa. Paleoanthropological studies have produced both expected and unexpected results (e.g., comparisons of South and East African robust australopithecines). Some critics have suggested that, because exogenous grit is harder than organic materials in food, grit should have an overwhelming impact on dental microwear patterns.

To shed light on this issue, feeding experiments were conducted on laboratory capuchin monkeys [*Sapajus apella*] with dental impressions taken before and after each feeding session. The food was a confectionary gelatin ("Jell-O") prepared with less water to make it stiffer, and it was laced with specific amounts of aluminum silicate pumice to simulate the presence of grit. Resultant casts were analyzed by SEM and confocal microscopy. We asked two main questions: (1) would new microwear features be formed in the course of single feeding bouts, and (2) would there be any changes in dental microwear texture as a result of the presence of the grit in these feeding experiments?

Initial results showed that no new features and no changes in dental microwear texture were detected. These findings suggest that the impact of exogenous grit on dental microwear is the result of dynamic, complex interactions among many factors including the material properties of both the food and the grit, grit load and amount of time spent feeding.

Funding was provided by National Science Foundation (NSF-BCS-1440542) and the American Association of Physical Anthropologists Cobb Professional Development Program.

The cost of survival: the contextual analysis of adaptive plasticity and constraint in human skeletal and dental remains

DANIEL TEMPLE
Anthropology, George Mason University

The early life environment is a crucial time for the formation of organ systems that augment survival at later points in life. Stress experienced during this time results in impairment of these systems with consequences for future growth and mortality. This study presents results from three different research projects associated with stress in the early life environment. The first study finds that linear enamel hypoplasia are frequently observed across samples, and presence alone may not predict future mortality. Instead, developmental context such as age-at-first-defect formation demonstrates that individuals who experience stress at increasingly earlier ages are at an increased risk of death ($B = -0.55$, Wald = 6.15, $p < 0.013$). The second study argues that deciduous defects of enamel (DDEs) that form in the perinatal environment may not impair growth ($p < 0.254$) or survivorship ($\chi^2 = 0.412$, $p < 0.521$; $\chi^2 = 0.796$; $p < 0.372$) at future ages within archaeological sites. Instead, when survivorship is compared between samples, DDEs result in accentuated mortality in samples where stress is substantive and experienced across the life course ($\chi^2 = 3.93$, $p < 0.048$; $\chi^2 = 8.54$; $p < 0.003$; $\chi^2 = 5.74$, $p < 0.017$). Finally, non-surviving pre-adults from hunter-gatherer samples reach full adult height. This may reflect a faster rate of growth in hunter-gatherers in association with earlier maturation. Overall, these findings suggest that impairment of future growth and survival following survival of early life stress is context dependent and may vary based on competing life history strategies.

Japan Society for the Promotion of Science (07012); National Science Foundation (BCS 1044950)

Developmental origins of health disparities: Early life adversity and DNA methylation in childhood

ZANETA M. THAYER¹, CAROLINE WALKER², KIEN LY², EMMA MARKS² and SUSAN MORTON²

¹Anthropology, Dartmouth College, ²School of Population Health, University of Auckland

Exposure to adverse experiences, especially in early life, has been associated with the development of chronic disease. These effects may be facilitated by changes in DNA methylation at genes that shape disease predisposition; however, to date little longitudinal data has been available in population representative samples to evaluate these potential associations. Here we evaluated whether early life adversity was associated with changes in salivary DNA methylation at *ABCA1*, a gene previously associated with cardiovascular disease (CVD), among an ethnically and

ABSTRACTS

socioeconomically diverse cohort of four year old children from the Growing Up in New Zealand study (N = 390). Early life adversity was measured during pregnancy and 9 months postpartum using a summary score assessing maternal anxiety, depression, household crowding, material deprivation, family stress, perceived stress, and lack of family and external support. We found a reduction in methylation at *ABCA1* after adjusting for covariates including offspring gender and ethnicity. These results suggest that early life adversity is associated with methylation at CVD related genes as early as childhood, making it a potential biomarker of later CVD risk.

Funding for Growing Up in New Zealand is provided by the New Zealand Government and managed by the Ministry of Social Development.

Genetic Astrology

MARK G. THOMAS

Research Department of Genetics, Evolution and Environment, University College London

Genetic ancestry testing is a new and growing industry that has gained widespread media coverage and public interest. Its scientific base is in the fields of population and evolutionary genetics, and it has benefitted considerably from recent advances in rapid and cost-effective DNA typing technologies, and to a lesser extent from advances in statistical inference and recent discoveries in human evolutionary genetics. There is a considerable body of scientific literature on the use of genetic data to make inferences about human population history, although publications on inferring the ancestry of specific individuals are rarer. Population geneticists have questioned the scientific validity of some population history inference approaches, particularly those of a more interpretative nature. These controversies have spilled over into commercial genetic ancestry testing, with some companies making sensational claims about their products. Here I will outline some scientific and ethical concerns about selected genetic ancestry testing claims, and discuss the issues raised, including media promotion of commercial enterprises, academic freedom of expression, science and pseudoscience.

No

Early environments and the development of the human microbiome: implications for growth and health

AMANDA L. THOMPSON and KELLY M. HOUCK
Anthropology, University of North Carolina at Chapel Hill

The human gut microbiome changes dramatically over the first years of life in response to environmental exposures. Much research has focused on the impacts of delivery mode, milk

feeding, and antibiotic use on the establishment of the gut microbiota in humans. Yet, less is known about how other aspects of the early dietary and household environment may shape the diversity of the gut microbiota and what this diversity means for child growth, health and development. Given the potential for early life conditions to influence the long-term trajectory of gut, immune and metabolic health, we use data from American infants (n=98), aged 0-18 months, and Ecuadorian infants and children (n=176), aged 0-11 years, to examine the impacts of early diet and environmental exposures on the diversity and composition of the gut microbiota. Diversity and the relative abundance of bacterial taxa differed between samples; greater diversity was seen in infants and children from the Galapagos compared to American infants and young children. In both samples, however, diet composition, exposure to a greater number of children, through siblings, daycare attendance or higher household density, and morbidity from illness symptoms were associated with phylogenetic diversity and the relative abundance of taxa, including Firmicutes, Bacteroides and Enterobacteriaceae, previously associated with child weight, gut health and cognitive development. Our analyses highlight the importance of the exposures across early life in shaping the gut microbiome and suggest that the gut microbiota plays an important role in shaping both short-term growth and development and longer term health.

A multi-method approach to evaluate the presence of non-local individuals at the prehistoric Schild site in western Illinois

ANDREW R. THOMPSON¹, KRISTIN M. HEDMAN², MATHEW A. FORT², SOPHIA C. DENT³ and DELLA C. COOK⁴

¹Department of Medical Education, University of Cincinnati, ²Illinois State Archaeological Survey, Prairie Research Institute, University of Illinois Champaign-Urbana, ³Department of Anthropology, University of North Carolina-Chapel Hill, ⁴Department of Anthropology, Indiana University, Bloomington

Identification of non-local individuals in a prehistoric context is challenging. Previous studies have utilized a variety of methods to investigate this topic, but typically only a single approach is used, which limits interpretation. This study aimed to overcome this issue by incorporating multiple sources of evidence, including dental metric, strontium isotope, and burial records, to evaluate the presence of non-local individuals at the prehistoric Schild site located in western Illinois. Isotopic data were collected from both M1 and M3 teeth and interpreted using published Sr ranges for the region. Dental metric data from Schild and one additional contemporaneous regional site (Yokem) were analyzed using discriminant function analysis. Discriminant scores were plotted with confidence ellipses and those

results were overlaid with the isotopic data. While dental metric or isotopic data were available for a large portion of the skeletal sample, a subset of 28 individuals with both isotopic and dental metric data could be directly compared. Isotopic results indicate that 14/28 individuals fall outside of the local Sr range established for the region. When the dental metric and isotopic data were integrated, 9/14 of individuals identified as non-local based on isotopic signatures also fell outside of a 75% range of the dental metric data. In contrast, only 2/14 individuals identified as local based on isotopes fell outside of this range. These results were further explored using burial records and AMS dating. This study highlights the utility and challenges of using multiple sources of data to answer complex archaeological questions.

3-D kinematics, kinetics, and EMG of knuckle-walking in chimpanzees

NATHAN E. THOMPSON¹, BIREN A. PATEL^{2,3}, JACK T. STERN JR⁴ and SUSAN G. LARSON⁴

¹Department of Anatomy, New York Institute of Technology College of Osteopathic Medicine, ²Department of Integrative Anatomical Sciences, Keck School of Medicine, University of Southern California, ³Human and Evolutionary Biology Section, Department of Biological Sciences, University of Southern California, ⁴Department of Anatomical Sciences, Stony Brook University School of Medicine

Knuckle-walking (KW) is a unique form of terrestrial locomotion utilized only by chimpanzees and gorillas among primates. Despite extensive literature on the bony correlates of KW, large gaps exist in the published 3-D forces, motions, and muscle recruitments involved in KW, making it difficult to evaluate hypotheses regarding the evolution of this unique locomotor behavior.

Here we present detailed laboratory 3-D kinematic, kinetic, and electromyographic (EMG) data on KW in two subadult chimpanzees (*Pan troglodytes*) and kinematic and kinetic data on digitigrade and palmigrade walking in two macaques (*Macaca mulatta*). We quantified 3-D ground reaction forces, digit-level metacarpophalangeal (MCP) motion, wrist motion, as well as muscle activity in eight digital and wrist flexors and extensors.

Maximum MCP extension angles for chimpanzee KW were 24–54° and in digitigrade macaques were 81–108°. In both cases maximum MCP angles decreased from digit 2 to 5. Maximum MCP angles in palmigrade macaques were similar to those of digitigrade walking. Maximum extension at the wrist was 17±10° for chimpanzee KW, 26±7° for macaque digitigrady, and 90±5° for macaque palmigrady. Chimpanzee KW also entailed noticeably more wrist adduction (~18°) compared with macaque digitigrady (~13° of abduction). In contrast to published EMG data on digitigrady, KW involved moderate levels of

ABSTRACTS

activity of the flexor carpi radialis at touchdown and toe-off, coinciding with periods of high wrist adduction. Similar to previous studies, digital muscles were largely silent during stance phase, suggesting little energy storage and/or release in the digital tendons.

This research is funded by the National Science Foundation Grants SMA 1719432, BCS 0935321, BCS 1126790.

Investigating interannual and seasonal variation in sifaka diet in Tsinjoarivo, Madagascar

EMMA THURAU¹, SAFIDY RASOLONJATOVO², FANOMEZANTSOA JEAN-LUC RAHARISON³ and MITCHELL IRWIN¹

¹Anthropology, Northern Illinois University, ²Zoology and Animal Biodiversity, University of Antananarivo, Antananarivo, Madagascar, ³Division of Research, SADABE

Studies of primate diets often estimate diet using the proportion of time spent feeding on food types over a short period of time. These studies often lack consideration for seasonal and interannual variation in diet. To address this, diet of diademed sifakas (*Propithecus diadema*) from Tsinjoarivo, Madagascar were analyzed to evaluate the temporal variability in the diet over multiple years (2003, 2006, 2007, 2009, 2014; 2-4 groups/year) within relatively undisturbed forest. For the years including both abundant and lean seasons we confirm previously-documented shifts between high frugivory and high leaf/flower consumption, respectively. For all main food types (fruit/seed, flowers, foliage), coefficient of variation of abundant season datasets ($n=8$) was consistently lower than that of lean season datasets ($n=11$); diet composition was more consistent in the high-frugivory (52-76%) abundant seasons, and lean season diet varied greatly in fruit/seed (4-45%), flowers (4-44%), and foliage (33-85%) consumption. Interestingly, the opposite pattern is seen in specific food items (particular part of a particular species): top abundant season foods were rarely repeated across datasets (6 unique top foods in 8 datasets); this likely results from supra-annual fruiting for many of these foods. Lean season datasets had more repetition (6 top foods in 11 datasets), and further, two of these top lean season foods were leaves and flowers of mistletoe (*Bakerella clavata*) (collectively accounting for 6 of 11 datasets). In summary, sifakas are more variable in the plant parts they choose in the lean season, but are restricted to fewer species, exhibiting interannual seasonal dietary flexibility.

Insulin and Energetic Regulation of Skeletal Growth

VICTORIA A. TOBOLSKY¹, JUDITH HOLLANDER², TERENCE D. CAPELLINI¹, LI ZENG² and DANIEL E. LIEBERMAN¹

¹Human Evolutionary Biology, Harvard University, ²Department of Immunology, Tufts University School of Medicine

Human growth is known to vary in response to different energetic environments but the main actors that regulate this plasticity remain unknown and understudied. Humans in industrialized nations undergo a characteristic period of insulin resistance during puberty and prior work from experimental mouse models has shown that insulin may be a central regulator of growth by facilitating the uptake of glucose to the growth plate. This suggests there may be an adaptive function for the period of insulin resistance in human puberty. This study tests the hypothesis that insulin activity in the growth plate regulates linear growth in a diet induced insulin resistant state. Our 2 x 2 design paired *db/db* experimental mice with C57BL/6J controls under two different dietary conditions introduced at four weeks: high and low glycemic matched diets ($n = 5$ males per group). Results demonstrate that the different dietary conditions at 12 weeks significantly differed in weight ($p < 0.01$) and fasting glucose ($p < 0.01$), but not tibial length, a sensitive indicator of nutritional status. Results from immunohistochemistry demonstrate differences in insulin activity in the growth plate across the conditions, suggesting insulin may play a causal role in regulating linear growth. This work has implications for disentangling the function of insulin resistance during puberty, the mechanisms by which diet regulates physical growth, and how organisms mediate the trade-off between growth and reproduction. Ultimately, this perspective can help us interpret patterns of growth among both living and archaeological populations.

Health inequality as seen in human skeletal remains in early modern period in Japan

HIROTAKA TOMITA¹, NORIKO SEGUCHI^{2,3}

¹Graduate School of Integrated Sciences for Global Society, Kyushu University, ²Faculty of Social and Cultural Studies, Kyushu University, ³Department of Anthropology, University of Montana

This study focuses on the influence of early life stress on later life experiences using human skeletal remains from the Edo Period (1603-1868) in western Japan. A total of 265 skeletal remains from the Kyushu region in Western Japan were used. Linear enamel hypoplasia on mandibular canines, which preserves a record of childhood stress events, was analyzed, paired with age at death estimation from adult skeletal remains. The Edo period society was feudal, with a rigid hierarchical social system. During this time, there

was different treatment by gender due to gender role divisions based on Confucian beliefs. This study aims to identify how early life stress might correlate with longevity: 1) are the enamel defects associated with changes in adult mortality; and 2) are there significant sex-specific differences in early life stress experiences and adult mortality? The Kaplan-Meier survival analysis was used to assess 1) the relationship between enamel growth disruption and age at death; and 2) sex differences in stress events and survivorship in later life. Results suggest sex difference in survivorship, with more stress in early life being associated with increased survivorship in males in the case in Japan. In the Kaizenji site, which contains individuals who belonged to the samurai class, results show significantly reduced survivorship in females who experienced early life stress events relative to males. These results can be interpreted to show that females showed reduced survivorship due to different treatment based on gender during the Edo Period.

This work was supported by JSPS KAKENHI Grant Number 17J04347.

The Evolution of TLR7 and TLR8 in Yellow Fever Virus Endemic Areas

NICOLE TOROSIN and LESLIE A. KNAPP
Anthropology, University of Utah

Howler monkeys are the most susceptible to Yellow Fever Virus (YFV) of all primates and die within a week after infection. In Misiones, Argentina, the howler monkey populations (*Alouatta guariba clamitans*) and (*Alouatta caraya*) were devastated by YFV in 2008-2009. To better understand the relationship between immune function and genetic variation, we used a novel comparative approach studying Toll-like receptor 7 (TLR) and TLR8 immune evolution in the howler monkey populations and sympatric humans. TLR7 and TLR8 are innate immune genes responsible for detecting single stranded RNA viruses such as YFV. Samples from *Alouatta* alive prior to the outbreak, those that died from the virus, and those that survived the outbreak were collected and the exons of TLR7 and TLR8 were sequenced. Using phylogenetic methods we tested rate of evolution in the howler monkey clade. While TLR7 is under much stronger purifying selection than other New World and Old World Primate lineages, TLR8 is not. We also found that surviving *A. guariba clamitans* had unique genetic variants compared to pre-outbreak and YFV positive individuals. Some of the genetic variants in surviving *A. guariba clamitans* were also found in more YFV resistant species, such as humans and capuchins. *A. caraya* YFV survivors did not show these trends. Additionally, using published data, we evaluated selection of TLR7 and TLR8 in human populations living in

ABSTRACTS

YFV endemic areas. Population branch statistics revealed differentiation at two loci in TLR8, with one locus in a region responsible for regulating gene expression.

Why Do We Farm? The Effect of Climate Change and Risk on the North American Foraging-Farming Transition

MELISSA G. TORQUATO and ERIK R. OTÁROLA-CASTILLO

Anthropology, Purdue University

The evolution of the genus *Homo* is characterized by the emergence of numerous biological and cultural traits including bipedalism, encephalization, and language. The expression of behavioral phenotypes responsible for increases in human fitness occurs during the transition from foraging to farming. This transition was significant because foraging was the predominant subsistence strategy for approximately 94% of human existence until evidence of plant domestication appeared roughly 11,500 years ago. Anthropologists have extensively studied the foraging-farming transition and proposed several hypotheses to explain its occurrence. One such hypothesis suggests that climate change and associated increases in foraging-risk led to the development and adoption of agriculture to mitigate the deleterious effects of increased variance in foraging returns and food insecurity. This study evaluates this hypothesis by assessing the effects of climate change and foraging-risk on the independent foraging-farming transition in Midwestern North America between 4,500–4,000 years ago. We include archaeological dietary data and paleoenvironmental proxies to analyze dietary variation and reconstruct the paleoenvironment during the transition period. Non-parametric MANOVA revealed statistically significant effects of intra-annual temperature seasonality ($F = 1.5557$; $p = 0.0296$) and intra-annual precipitation ($F=1.6082$; $p = 0.0310$) on dietary variation. Principal coordinate analyses combined with vector fitting visualized the dietary variation and the effects of dietary variables, time and paleoenvironmental proxies. These results (1) support the behavioral shift from foraging to agricultural resources approximately 4,500–4,000 years ago and (2) show that climate variables influenced subsistence behavior by increasing foraging-risk, causing humans to incorporate cultivated resources in their diet.

Contributions by MGT were supported in part by the National Science Foundation Graduate Research Fellowship Program (Grant No. 106469).

Analysis of 3D Reconstruction Methods in Computed Tomography Research

ALEJANDRO A. TORRES¹, JP BROWN² and SLOAN R. WILLIAMS¹

¹Department of Anthropology, University of Illinois at Chicago, ²Department of Anthropology, Field Museum of Natural History

Computed Tomography (CT) research continues to be praised by biological anthropologists as a non-destructive means to study human remains, although the method is not without its limitations. It can be difficult to distinguish between preservation, and taphonomic processes, which can interfere with demographic, pathological and mortuary treatment analyses. Treating CT data from mummified tissue as if it were living tissue often leads to incorrect assessments. Additionally, innovation continues to lag behind medical and forensic research. These fields have benefitted from more standardized reporting and application protocols, which facilitates comparative studies. Adopting these practices can improve CT research in bioarchaeological studies as well. This study examines innovations and methods in 3D reconstruction algorithms currently in use in forensic and medical fields and attempts to apply them to a bioarchaeological case study using CT scans of 14 mummies from the site of Ancon, Peru. These mummies date to the Middle Horizon to Late Intermediate Period (~AD 600-1476). The human remains were completely enclosed in textiles, so CT scans were used to estimate the minimum number of individuals, identify grave goods enclosed within the textile layers, estimate age, sex and stature. Several bundles contained the remains of more than one individual and artifacts were observed as well. This study compares 3D reconstruction algorithms available in VGStudio Max 3.2 and 3D Slicer, demonstrating differences in morphometric, pathological, and mortuary treatment analyses between the two programs.

Diet in the northern highlands of Ecuador during the Formative Period (3500 – 500 BC): Insights from bone collagen stable carbon and nitrogen isotope analysis

PAULA TORRES PEÑA and SANDRA GARVIE-LOK
Anthropology, University of Alberta

During Ecuador's Formative Period (3500–500 BC), its highlands are characterized by variable reliance on agriculture. Archaeobotanical studies detect maize at some sites, but do not indicate its dietary importance. Maize consumption is of interest because maize later became important to the region, sustaining population expansion and increased socio-political complexity. Here we report the results of the first isotopic study of diet in Formative Period highland Ecuador. Collagen stable carbon and nitrogen isotope analysis was performed for three sites: Rancho Bajo (1610–1450 cal. BC, $n = 13$ human); Cotocollo

(2405–361 cal. BC, $n = 1$ faunal and 26 human), and Las Orquídeas (800–400 cal. BC, $n = 13$ faunal and 8 human). Expectations were that maize would be consumed but at lower levels than in following periods. Results indicate that all groups examined had diets predominantly based on C3 resources and terrestrial animals. Maize consumption varied, showing that different subsistence practices were in place. Rancho Bajo values suggest closely similar diets for all individuals, including modest amounts of maize. The Cotocollo diet appears to have been similar to that of Rancho Bajo, though more variable. At Las Orquídeas maize consumption was higher, though still well below that seen in following periods. Comparisons to other eras indicate that maize consumption increased over time, but there were sites in all eras where maize did not play a significant role. This nuances our understanding of maize use, suggesting that local factors such as resource availability were also important to determining diets.

3D geometric morphometric analyses of the human torso morphology reveal new understandings about the torso integration in primates

NICOLE TORRES-TAMAYO¹, DANIEL GARCÍA-MARTÍNEZ¹, SHAHED NALLA², ALON BARASH³, SCOTT A. WILLIAMS⁴, ESTHER BLANCO-PÉREZ⁵, FEDERICO MATA-ESCOLANO⁶, JUAN ALBERTO SANCHIS-GIMENO⁷ and MARKUS BASTIR¹

¹Paleobiology Department, Museo Nacional de Ciencias Naturales (MNCN-CSIC), ²Department of Human Anatomy and Physiology, Faculty of Health Sciences, University of Johannesburg (South Africa), ³Faculty of Medicine, Bar-Ilan University (Israel), ⁴Center for the Study of Human Origins, Department of Anthropology, New York University, ⁵Department of Radiology, Hospital de La Ribera (Spain), ⁶CT and MRI Unit, ERESA, Department of Radiology, General University Hospital (Spain), ⁷Department of Anatomy and Human Embryology, University of Valencia (Spain)

Classic studies in Palaeoanthropology suggest that in hominins and other primates thoraces and pelves are anatomically integrated. However, this torso integration hypothesis has been only tested in isolated bones so far, but not in anatomically connected torsos. Here we aim at testing the torso integration hypothesis in two modern human populations. We considered and excluded the effect of sexual dimorphism, which is an important factor influencing the human torso shape. We segmented 50 anatomically connected torsos (CT-scans) from two different populations (25 Mediterraneans, 25 Sub-Saharan Africans). We compared the maximum medio-lateral width at 7th-9th rib levels with pelvic bi-iliac breadth in males and females within both populations. From a 3D geometric morphometrics approach, we measured 1030 (semi)landmarks on each torso model, and we quantified torso

ABSTRACTS

shape variation, mean size and shape differences, thoraco-pelvic covariation and allometric effects. Females show narrow thoraces and wide pelvis and males show the opposite trend in both populations. Indeed, we found equal thoracic and pelvic widths and curvatures only in absence of sexual dimorphism, with the lowest rib levels and the ilia showing the highest covariation. In addition, larger torsos were narrower than smaller torsos. Our study reveals therefore that sexual dimorphism leads to a complex thoraco-pelvic integration model in *H. sapiens* previously unrevealed by measuring isolated bones. These findings question some assumptions derived from the classical torso integration hypothesis and emphasize the role of sexual dimorphism when reconstructing fossil hominin body shape.

Acknowledgements: This research is funded by CGL-2015-63648-P (Ministry of Economy, Industry and Competitiveness, Spain)

The ASUDAS and fossil hominin teeth: categorical success with qualification(s)

JOEL D. IRISH

Anthropology and Archaeology Subject Group,
Liverpool John Moores University

The Arizona State University Dental Anthropology System (ASUDAS) developed by CG Turner and colleagues uses rank-scale categories to standardize recording of crown and root morphology. It is considered the gold standard for nonmetric study of modern humans. The same cannot be claimed for study of our Plio-Pleistocene ancestors. That is, despite its use in multiple publications, criticism of the ASUDAS for analyzing fossil hominins—some of it justified—is ongoing, with various researchers advocating to abandon or improve it. This presentation finds that, with appropriate screening and analytical techniques, ASUDAS data yield interspecific affinities concordant with those from other hominin morphometric data. This is not surprising, because many traits in the ASUDAS are already routinely scored by paleoanthropologists, albeit without the standardization.

First, summarizing prior results by the author and others, 78 traits are compared phenetically among samples of *Australopithecus afarensis*, *A. africanus*, *Paranthropus boisei*, *P. robustus*, *Homo habilis*, *H. erectus*, *H. naledi*, and *H. sapiens* with the mean measure of divergence statistic. Of these, 12 non-ASUDAS traits considered 'hominin-specific' by some are included to 'improve' classification among Plio-Pleistocene species. A second round of comparisons uses only the 66 ASUDAS traits. The 77- and 66-trait distance matrices are strongly correlated ($r=0.980$, $p=0.000$), so inter-sample affinities are basically identical. In both studies, as expected, the samples group by genus and otherwise evidence established interspecific variation. Thus: 1)

results from these particular traits and samples do parallel those of previous hominin studies, and 2) these same affinities are obtainable using ASUDAS traits alone.

National Science Foundation (BNS-9013942, BCS-0840674) and Liverpool John Moores University, plus workshops through National Geographic Committee for Research & Exploration (to L Berger) and Wenner-Gren (L Deleze and M Skinner).

Fragmentation as a function of cyclical work between immature and mature leaves

JORDAN N. TRAFF and DAVID J. DAEGLING

Anthropology, University of Florida

Tests on the mechanics of primate foods often examine properties such as toughness and hardness or examine rates of food breakdown during actual or simulated chewing. Here, we test foods by cyclically loading specimens between tooth analog surfaces to measure fragmentation rates and work as functions of cycle number.

Using an MTS-858 axial testing machine (Eden Prairie, MN), we subjected samples of mature and immature leaves to twenty cycles of axial loading between parallel rows of interlocking wedges under constant displacement. Force was recorded over each cycle and the degree of fragmentation was measured following each experiment. Immature leaves showed significantly more fragmentation into both small ($< 0.5 \text{ cm}^2$) and medium ($< 1.5 \text{ cm}^2$) particles than mature leaves ($P < 0.05$), but there was no significant difference in work ($P > 0.05$) or in the change of force per cycle ($P > 0.05$) between the leaf types.

These results challenge the idea that leaves can be simply described in terms of a brittle vs. tough dichotomy. Previous work on leaf material properties suggests that immature leaves are less tough, and therefore more brittle, than mature leaves. Our work supports this idea as young leaves show a higher rate of fragmentation. We expected immature leaves should also show steeper declines in force per cycle compared to mature leaves given their reduced toughness, but this was not observed. Our results suggest that the relationship between toughness and brittleness may be more complicated when applied to anisotropic, non-homogenous tissues like leaves.

Secular trends in cardiovascular and metabolic health among the Indigenous Shuar of Amazonian Ecuador

AMBER M. TREADWAY¹, MELISSA A. LIEBERT¹, FELICIA C. MADIMENOS², SAMUEL S. URLACHER³, TARA J. CEPON-ROBINS⁴, THERESA E. GILDNER⁵, JOSHUA M. SCHROCK⁶, CHRISTOPHER J. HARRINGTON⁶, DORSA AMIR⁷, AARON D.

BLACKWELL⁸, RICHARD G. BRIBIESCAS⁹, J. JOSH. SNODGRASS⁶ and LAWRENCE S. SUGIYAMA⁶

¹Department of Anthropology, Northern Arizona University, ²Department of Anthropology, Queens College (CUNY), ³Department of Evolutionary Anthropology, Duke University, ⁴Department of Anthropology, University of Colorado, Colorado Springs, ⁵Department of Anthropology, Dartmouth College, ⁶Department of Anthropology, University of Oregon, ⁷Department of Psychology, Boston College, ⁸Department of Anthropology, Washington State University, ⁹Department of Anthropology, Yale University

Market integration – the transition from a subsistence-based lifestyle to a market economy – has been linked to increased chronic disease risks (e.g., type II diabetes, obesity). Since 2005, the Shuar Health and Life History Project (SHLHP) has examined the health consequences of market integration among the Shuar, an indigenous forager-horticulturalist population from Amazonian Ecuador. In a 2013 publication, the SHLHP documented higher total and HDL cholesterol levels among adults from market-integrated communities in the Upano Valley (UV) compared to those from the remote Cross-Cutucú (CC) region. Since this study, additional cardiovascular and metabolic health measurements (body mass index [BMI], waist circumference, fasting glucose, full lipid panel [LDL, HDL, total cholesterol, triglycerides], blood pressure) were collected by the SHLHP, resulting in 10 years (2007–2017) of cross-sectional data. Using this large dataset, the present study tests for secular trends in cardiovascular and metabolic health among 492 Shuar adults (283 UV, 209 CC; 190 males, 302 females; 15–86 years). Multiple regressions were used to analyze associations between year of collection and single measures of cardiovascular and metabolic health for UV and CC Shuar (controlling for age, sex, and BMI). Results demonstrated that glucose levels increased over the 10-year period for CC Shuar ($p < 0.01$), while total and HDL cholesterol levels decreased for UV Shuar ($p < 0.001$). Triglyceride levels increased for both UV and CC Shuar over time ($p < 0.05$). This study highlights complex relationships between market integration and secular trends in cardiovascular and metabolic health among an indigenous population.

Support: Hooper Undergraduate Research Award, Northern Arizona University; National Science Foundation (#BCS-1650674, BCS-1341165, BCS-0824602, BCS-0925910, GRF-2011109300); Ryoichi Sasakawa Young Leaders Fellowship Fund; Wenner-Gren Foundation for Anthropological Research; University of Oregon.

ABSTRACTS

Female northern pig-tailed macaques (*Macaca leonina*) are more attracted to males with darker red anogenital coloration

FLORIAN A. TRÉBOUET¹, SUCHINDA MALAIVIJITNOND^{2,3} and ULRICH H. REICHARD^{1,4}
¹ANTHROPOLOGY, SOUTHERN ILLINOIS UNIVERSITY, CARBONDALE, ²BIOLOGY, CHULALONGKORN UNIVERSITY, BANGKOK, ³NATIONAL PRIMATE RESEARCH CENTER OF THAILAND, CHULALONGKORN UNIVERSITY, SARABURI, ⁴CENTER FOR ECOLOGY, SOUTHERN ILLINOIS UNIVERSITY, CARBONDALE

Primate males' conspicuous coloration has been suggested to signal social status and to have evolved primarily via male-male competition. A less commonly considered mechanism is female mate choice. We tested if the red anogenital coloration exhibited by wild male northern pig-tailed macaques (*Macaca leonina*) affected female sexual behaviors at Khao Yai National Park, Thailand. We took digital photos of the anogenital area of 5 adult males of different dominance rank against a color standard and recorded sociosexual behaviors of females over a 12-month period in 2015-16. Males' redness was quantified with color analysis software following a previously-validated method for measuring color under field conditions. Males' anogenital coloration changed over time and the intensity of redness correlated positively with the number of simultaneously receptive females. Receptive females presented more frequently to darker red colored males, cooperated more often with darker red colored males' anogenital inspections, and spent more time in proximity to darker red colored males. Male dominance rank correlated positively with coloration intensity and the group's alpha male exhibited the darkest red coloration. Interestingly, even after losing his top-rank position, the former alpha male maintained a dark red anogenital coloration and receptive females continued to direct sexual presentations to and maintained proximity with him. In conclusion, females' sociosexual responses to males are consistent with the idea that female mate choice played an important role in the evolution of male northern pig-tailed macaque anogenital coloration.

The project was funded with grants from the 2015 Graduate and Professional Student Research Awards, Southern Illinois University Carbondale, U.S.A., and Chulalongkorn University, Bangkok, Thailand.

Back-breaking poverty: Schmorl's nodes in institutionalized and impoverished populations in the late 19th and early 20th century United States

LORI A. TREMBLAY
Liberal Arts & Sciences, SUNY Delhi

The presence and prevalence of Schmorl's nodes can provide information about the trauma experienced by those who engaged in physical labor. Inmates at some mental health asylums in the late 19th –early 20th century United States were treated with labor therapy, while many of the poor also engaged in heavy physical labor to earn wages. This purpose of this study was to investigate whether differences in sex, social and socioeconomic status, and/or geographic location put individuals from these institutionalized and impoverished populations at an increased risk for developing Schmorl's nodes. Human skeletal remains from the Milwaukee County Institution Grounds Poor Farm Cemetery in Milwaukee, Wisconsin (n=115) and the Oneida State Custodial Asylum in Rome, New York (n=46) were examined for this study. Evidence of Schmorl's nodes was obtained via anthroposcopic analysis. The data collected were analyzed using Chi-Square analyses to determine whether site, status, or sex were statistically significant factors that contributed to the likelihood of developing Schmorl's nodes. The statistical analyses indicate that males were more likely to exhibit Schmorl's nodes than females (p=.0475) and that those who were impoverished (p=.009) and from the Milwaukee County Institution Grounds Poor Farm Cemetery (p=.02) were at a significantly higher risk for exhibiting Schmorl's nodes than their institutionalized counterparts from the Oneida State Custodial Asylum. This indicates that although those who were institutionalized in the Oneida Custodial Asylum performed physically demanding labor therapy tasks daily, impoverished males from Milwaukee, Wisconsin were at a much higher risk for developing Schmorl's nodes.

The Alumni Grant for Graduate Research and Scholarship and the Coca-Cola Critical Difference for Women Grant for Research on Women, Gender, and Gender Equity, both via The Ohio State University.

Collecting Biomarkers of Chronic Diseases of Ageing in Field Settings

BENJAMIN C. TRUMBLE^{1,2}, ANGELA R. GARCIA², DANIEL K. CUMMINGS³, THOMAS S. KRAFT⁴, JONATHAN STIEGLITZ⁵, MICHAEL GURVEN⁴ and HILLARD KAPLAN³

¹School of Human Evolution and Social Change, Arizona State University, ²Center for Evolution and Medicine, Arizona State University, ³Economic Science Institute, Chapman University, ⁴Integrative Anthropological Sciences, University of California Santa Barbara, ⁵Anthropology, Institute For Advanced Study in Toulouse

While collecting biomarker specimens in remote field settings without electricity or running water presents challenges, we strongly believe that nearly all methods are field friendly with the proper training, desire to gain knowledge, and funding. The Tsimane Health and Life History Project mobile medical team moves from

community to community across the Bolivian Amazon basin, utilizing a mix of point-of-care analyses and sample storage techniques to provide real-time biomedical information to Bolivian doctors, and preserve specimens for advanced analyses at later dates. A biochemist draws blood, conducts a complete blood count, and measures hemoglobin and hematocrit. Results from these point-of-care analyses, as well as a fecal smear and urinalysis, are provided to a team medical doctor, allowing them to deliver informed patient care. In addition, whole blood is aliquoted and stored in liquid nitrogen for DNA analyses, dropped onto protein saver cards for dried blood spot analyses, and the remainder centrifuged to isolate serum, which is stored in liquid nitrogen for later analyses. Over the last two decades, we have completed N=28,891 biochemical analyses from n=8,575 individuals. With greater than 95% coverage for individuals over age 60, we can assess population levels of chronic diseases of aging like cardiovascular disease and cognitive decline to assess whether these conditions are an inevitable part of aging, or novel features of urban sedentary life. This poster details our methods and data collection, in order facilitate collection of comparable data in other populations and encourage data-sharing and cross-population comparisons of the aging process.

NIH/NIA RF1AG054442

Paleoenvironmental context of early *Homo sapiens* from the Kibish Formation, southern Ethiopia: evidence from bovid ecomorphology and abundance

YEMANE G. TSIGE¹, JOHN ROWAN², SOLOMON YIRGA³ and JOHN G. FLEAGLE⁴

¹Department of Biology, Case Western Reserve University, ²Department of Anthropology, University of Massachusetts Amherst, ³Paleoanthropology and Paleoenvironment Program, Addis Ababa University, ⁴Department of Anatomical Sciences, Stony Brook University

Paleoanthropologists have long argued that environmental change played a key role in the origin and dispersal of *Homo sapiens*. Proxy evidence from lake and marine cores suggests that the late Quaternary of eastern Africa was marked by major climatic fluctuations, though corresponding environmental reconstructions from mammal faunas are scarce. The Kibish Formation of southern Ethiopia was deposited during this crucial period and has yielded an abundant mammalian fauna, including the earliest modern humans in the region, dated to ~ 196,000 years ago (ka). Here, we use fossil bovid femur ecomorphology and abundances from the three fossil-bearing units of the Kibish Formation (Member I ~ 196 ka, Member III ~ 104 ka, and Member IV ~ 8 ka) to reconstruct late Quaternary environments in southern Ethiopia.

ABSTRACTS

Ecomorphological data for fossils ($n=17$) shows that Kibish bovids have morphologies indicative of a vegetation mosaic. Forest environment morphologies dominate the distal femur sample (63.6% of the sample), whereas femoral head morphology suggests more open to light cover environments. Abundance data indicate mosaic vegetation encompassing both woodlands and edaphic grasslands. Significant numbers of tragelaphins and *Madoqua* indicate woodlands and/or thickets comprised most of the landscape during Member I times when modern humans first appear in the region, with a transition towards open and grassier environments by ~ 104 ka. Our findings suggest that early *Homo sapiens* in southern Ethiopia lived in environments not dissimilar from those today, with a woodland-thicket-grassland mosaic persisting for much of the late Quaternary along the course of the paleo-Omo River.

The Paleontological Scientific Trust (PAST, South Africa) supported this research.

Stress in Greek Mother Cities and Colonies

NYAKEH K. TUCHSCHERER

Anthropology & History, St. John's University, New York

This study uses bioarchaeological methods to reveal colonial relationships between Greek mother cities and colonies during the Archaic and Classical periods. We attempt to understand the relationships between mother cities and colonies by exploring linear enamel hypoplasia (LEH) at four Greek mother cities (Athens, Eretria, Karystos, and Corinth), and six Greek colonies (Apollonia Pontica, Apollonia in Illyria, Epidamnus, Himera, Metaponto, and Kamarina). The prevailing notion in both contemporary literature and historical narrative depicts "colonization" as causing a stressful environment, especially in the New World and in Africa. This project uses bioarchaeological tools to determine if life in colonies was more or less stressful than life in Greek mother cities within the Mediterranean. If Greek mother cities have a higher prevalence of skeletal stress markers like LEH, it is likely that relieving population pressure was a motivation for colonization. Other possible motivations for colonization might be a desire for expansion of territory or material resources. Results indicate that on average mother cities had more pathological stress than people in the colonies, with 69% ($n=204$) of individuals in Greek mother cities showing evidence of LEH and 28% ($n=1851$) of individuals in Greek colonies showing LEH ($\chi^2 p=2.2e-16$). These findings indicate that life

was stressful in Greek mother cities, and colonization may have been a vital mechanism for mother cities to relieve population pressure and alleviate scarcity of resources.

This research was funded by National Science Foundation Research Experience for Undergraduates award numbers 1560227 and 1560158, the University of Georgia, and the University of Northern Colorado.

Socioecological correlates of epigenetic variation in nonhuman primates

JENNY TUNG^{1,2}, TAURAS P. VILGALYS¹, NOAH SNYDER-MACKLER³, JOAQUIN SANZ⁴, AMANDA J. LEA⁵, SUSAN C. ALBERTS^{1,2}, LUIS B. BARREIRO⁴, CLIFFORD J. JOLLY⁶, JEFF ROGERS⁷ and MARK E. WILSON⁸

¹Evolutionary Anthropology, Duke University, ²Biology, Duke University, ³Psychology, University of Washington, ⁴Medicine, University of Chicago, ⁵Lewis-Sigler Institute for Integrative Genomics, Princeton University, ⁶Anthropology, New York University, ⁷Human Genome Sequencing Center, Baylor College of Medicine, ⁸Yerkes National Primate Research Center, Emory University

Both genetic and environmental factors shape the primate epigenome. Variation at the sequence level affects the accessibility of DNA to transcription factors and defines the potential targets of epigenetic marks. At the same time, environmental experiences can modulate these marks. Understanding both genetic and environmental sources of variance in the epigenome is therefore key to understanding its role in primate evolution. Our recent work shows that, on long evolutionary timescales, variation in DNA methylation is largely explained by genetic differences between species. Specifically, in the baboon genus *Papio*, patterns of genome-wide DNA methylation (756,262 CpG sites; $n=39$) mirror species-level genetic and geographic structure and are clearly explained by baboon phylogenetic history. On a shorter, ecological timescale, however, the environment plays an important role. For example, in a well-studied wild baboon population in Kenya ($n=69$), we find that resource quality/abundance predicts DNA methylation levels at more than 1000 CpG sites in the genome, and in captive rhesus macaques ($n=43$), experimentally manipulated social status alters chromatin accessibility at hundreds of loci. In the baboons, resource abundance-associated regions are enriched for carbohydrate metabolism, insulin signaling, and glycolysis, while in the rhesus macaques, social status-associated regions are enriched for transcription factor binding sites involved in the glucocorticoid-mediated stress response. Thus, our findings support the idea that epigenomic plasticity is important in understanding

how primates respond to key components of their environment. However, they also argue that changes at the DNA sequence level shape the backdrop against which this plasticity arises.

This research was funded by the National Institutes of Health, the National Science Foundation, and the Leakey Foundation.

Elevated activity levels do not influence extrinsic fiber attachment morphology on the surface of muscle-attachment sites

CASSANDRA M. TURCOTTE^{1,2}, DAVID J. GREEN^{3,4}, KORNELIUS KUPCZIK², SHANNON MCFARLIN¹ and ELLEN SCHULZ-KORNAS²

¹Department of Anthropology, George Washington University, ²Max Planck Weizmann Center for Integrative Archaeology and Anthropology, Max Planck Institute for Evolutionary Anthropology, ³School of Osteopathic Medicine, Campbell University, ⁴Department of Anatomy, Midwestern University

Extrinsic fibers (EFs) are a type of penetrating collagenous fiber that help anchor soft tissue into bone. The size, shape and grouping patterns of EF have previously been associated with the loading history of the muscle. They are of particular significance in anthropology as potential tools for behavioral reconstruction from skeletal remains and, specifically, from muscle attachment sites (entheses). In this study, we tested how activity level altered EF morphology on the bone surface of the fibrocartilaginous insertion of the biceps brachii, a key locomotor muscle involved in forearm flexion, using an experimental mouse model. Juvenile (J) and adult (A) female wild-type DC1 mice were subjected to three activity regimes over 78 days prior to sacrifice: control ($n=9$ J, 8A), wheel-running ($n=11$ J, 5A), and climbing ($n=10$ J, 8A). Further, we applied surface metrological techniques to perform automated, quantitative and non-destructive analysis of bone surface microanatomy. Our results show that experimentally increased activity (running and climbing) had no significant effect on the quantity ($p=0.15$) of EF insertions at the enthesis, nor on their size (e.g., EF area (μm^2): $p=0.36$), shape (e.g., % EF roundness: $p=0.13$) or other morphological parameters. We conclude that, while mechanical loading is generally considered a driving factor behind morphological variation, it does not necessarily influence enthesis morphology; the ability to reconstruct behavior from entheses is consequently limited. Our study joins a larger body of work that cautions against performing such reconstructions until an experimentally validated method can be developed.

Research performed at the Weizmann Center for Integrative Archaeology and Anthropology and the George Washington University, funded by a National Science Foundation Doctoral Dissertation Improvement Grant to Cassandra Turcotte (#1650933).

ABSTRACTS

Royal Estates and Commoner Foods: Reconstructing Diet among Servants in the Inka Imperial Heartland

BETHANY L. TURNER¹, CLAUDIA L. NUÑEZ FLORES² and BREIDY I. QUISPE VILCAHUAMAN^{1,3}

¹Department of Anthropology, Georgia State University, ²Oficina por Arqueología, Ministerio de Cultura del Perú, ³Department of Anthropology, University of California Riverside

The Inka (AD 1438-1532) have been studied intensively by ethnohistorians and archaeologists, but there is almost no bioarchaeological research on the empire and its subjects, particularly in Peru's Sacred Valley leading to the imperial capital city of Cusco. A key feature of the empire was that each emperor retained lands and assets acquired during his life, managed in perpetuity by family (*panaqa*s), and imperial servants who worked and lived on them. This study presents carbon, nitrogen, and oxygen isotope data for one such group of servants (N=81) interred at the site of Patallaqta, which was part of interconnected shrines surrounding the royal estate of Machu Picchu in the Sacred Valley. The aim is to reconstruct subsistence and diet among subjects living within an imperial seat of power, and test hypotheses that Machu Picchu's servants consumed more high-status foods than Patallaqta's. Carbonate and collagen isotope data from dentin, enamel, and bone indicate (1) diets centered on a mix of C₃ vegetables and maize, terrestrial meat and riverine fish, (2) almost no change in diets and water sources over individuals' lifespans, and (3) modest variation in diet among the inhabitants. Results at Patallaqta also vary somewhat from published values from Machu Picchu; the latter exhibit markedly higher standards of deviation, but lower mean $\delta^{13}\text{C}$ and slightly lower mean $\delta^{15}\text{N}$ values. These results suggest that, despite marked differences in Sr and Pb isotope values—which are presented elsewhere and which indicate different social statuses—the residents of these two sites consumed "commoner" diets.

This study is funded by the National Science Foundation (BCS-1359595, PI: Turner). Samples were exported and analyzed with permission from the Ministerio de Cultura del Perú (Expedientes N° 9216-2016 & 0000015618-2017)

Comparative Analysis of the Health of Free Blacks in the Northeast, South and Southwest

EVONNE D. TURNER-BYFIELD
Anthropology, Ohio State University

Many studies have researched the health of free blacks in the context of slavery, ignoring unique lived experiences of free people of color. Skeletal remains from free black cemeteries provide a window into the biohistory of free Africans in the U.S. This study provides a bioarchaeological comparison of health indicators of three 19th century populations of free blacks.

Data for this comparison is derived from the First African Baptist Church Cemetery (FAB) in Philadelphia (n=90), the Cedar Grove (CG) Church free black cemetery in Arkansas (n=80) and the Freedman (FC) free black cemetery in Dallas Texas (n=1,157), available in the Western Hemisphere Global History of Health database. The prevalence of periosteal infection, degenerative joint disease (DJD), cribra orbitalia, porotic hypertosis and trauma were compared between sites to gain insight into health disparities of 19th century blacks in industrial north or rural south/southwest. Results show similarly low prevalence of skeletal trauma in all sites (FAB = 3.27%; CG = 2.54%; FC = 2.48%; (p>0.05 for all comparisons). The remaining markers show significant differences between sites: Cribra Orbitalia and Hyperostosis Porotica are more prevalent in CG (28.57% and 20.51%) than on the other two sites (FAB: 1.92% and 3.28%; FC (13.75% and 6.24%). DJD is less prevalent in CG (9.54%) than on the other sites (FAB: 33.23%; FC (38.68%). Finally, infectious disease is more prevalent in CG (62.42%) than on FAB (20.26%) or FC (67.79%). These results indicate very different life experiences among the individuals who were buried in the three cemeteries.

Impact of socioeconomic status on breastfeeding initiation and duration

ERICA E. TYLER and LAWRENCE M. SCHELL
Anthropology, SUNY Albany

The nutritional, immunological, and developmental benefits of breastfeeding are well documented. However, there are societal and economic barriers in the U.S. that often interfere with a mother's ability to breastfeed the six months recommended by the American Pediatrics Association. These barriers often lead to a smaller likelihood of breastfeeding initiation, lower breastfeeding duration, and reliance on formula feeding. This presentation discusses the impact of socioeconomic status on breastfeeding initiation and duration rates and whether this is buffered by mother's educational level and support system. The Albany Pregnancy Infancy Lead Study assessed the impact of numerous environmental variables on infant growth and development. Data were collected from 1992-1998 from pregnant women who were residents of Albany County and eligible for the Women, Infants and Children Program (n=246). The variables under study were maternal age, education level, and current employment. The median age of mothers was 22 years (min=14, max=38). There was a significant difference in breastfeeding duration (in minutes) based on maternal age (p=0.001) at the 3-month visit. The percentage of employed mothers who breastfed decreased from 21% at the 3-month visit to 2% at the 12-month visit. A statistically significant association was found between years of

maternal education and breastfeeding initiation at the 3-month visit (p=0.004); helpers did not have a statistically significant impact on breastfeeding initiation or duration. These findings show that maternal education positively impacts breastfeeding initiation but not continuation to 6 months.

Incomplete (or completely missing) skeletal collections as the result of excavation and curation practices

JAIIME M. ULLINGER
Sociology, Criminal Justice, and Anthropology,
Quinnipiac University

Historically, excavation and curation may have contributed to groups of people being under-represented in the bioarchaeological record. Four factors will be discussed: (1) Burials were not always seen as useful in understanding social processes, and were discarded; alternatively, certain bones were seen as more useful than others, resulting in differential curation; (2) Specific questions related to prehistory have resulted in the removal (and disposal) of more recent burials that were of less interest; (3) Skeletons from the same site were sent to numerous institutions around the globe for study and/or display; and (4) Post-excavation storage may consolidate burials from targeted time periods or areas, which can be catastrophic if the facility is damaged or destroyed. Each factor will be discussed with specific examples from the Near East, including the sites of Tell ed-Duweir, Tell el-Hesi, Bab edh-Dhra', and Jericho. For example, Iron Age peoples in Israel are under-represented both because of current restrictions on the excavation of Iron Age burials and historical excavation practices. In the 1930s, over 500 crania (but only 80 femora and 7 clavicles) from Tell ed-Duweir were transported to the Natural History Museum in London for study. Therefore, while studies involving the crania may accurately reflect a sample of people from the site, and have been used by bioarchaeologists to examine biological relatedness, no other skeletal element is well-represented, leaving many questions unanswered. Moving forward, we must continue to advocate for not only thorough excavation of human burials, but for funding to curate skeletons in perpetuity.

Comparison of Musculoskeletal Disorders Associated with Diabetes in Three North American Historical Human Skeletal Collections

CHARITY F. UPSON-TABOAS
Anthropology, Indiana University

The effects of diabetes mellitus on bone are indirect. Musculoskeletal disorders (MSDs) associated with diabetes are due to the duration of the disease and are a consequence of chronic

ABSTRACTS

hyperglycemia. The purpose of this research is to examine the differences in severity of thirteen diabetes-related MSDs and to determine which are best indicative of diabetes.

Materials were examined from three well known North American historical human skeletal collections with documented causes of death – the Hamann-Todd Osteological Collection (Cleveland Museum of Natural History), the Robert J. Terry Anatomical Collection (Smithsonian National Museum of Natural History), and the William M. Bass Donated Skeletal Collection (University of Tennessee Knoxville). Individuals with diabetes as their cause of death (n=63) were matched to controls whose deaths were not associated with diabetes (n=63).

Periodontal disease (PD), hand related disorders (HRD), diffuse idiopathic skeletal hyperostosis (DISH), peripheral neuropathy (PN), lower extremity amputation (LEA), and osteoarthritis (OA) were more severe in diabetics than in controls ($p=0.0459$, $p=0.0192$, $p=0.0022$, $p=0.0011$, $p=0.0339$, $p=0.0440$, respectively). PN and DISH together were considered to be best indicative of diabetes ($p<0.0000$, $R^2=0.2055$).

This research contributes to anthropology by developing a model for identifying patterns of skeletal involvement suggestive of diabetes in the past. The ability to identify possible cases of diabetes in other historical and archaeological human skeletal collections may allow future research to investigate the questions of heritability and/or the effects of the environment on the susceptibility of developing diabetes, further adding to the understanding of the origins of diabetes.

This project was funded in part by Indiana University David C. Skomp Summer Research Feasibility Fellowships.

A deformation-based geometric morphometric analysis of the vestibular apparatus in the Miocene apes *Hispanopithecus laietanus* and *Rudapithecus hungaricus*

ALESSANDRO URCIUOLI¹, CLÉMENT ZANOLLI², DAVID BEGUN³, SERGIO ALMÉCIGA^{1,4,5}, JEAN DUMONCEL⁶, SALVADOR MOYÀ-SOLÀ^{1,7,8} and DAVID M. ALBA¹

¹Institut Català de Paleontologia Miquel Crusafont-Paleoprimatology and Human Paleontology, Universitat Autònoma de Barcelona, ²Laboratoire PACEA, UMR 5199 CNRS, Université de Bordeaux, ³Department of Anthropology, University of Toronto, ⁴Division of Anthropology, American Museum of Natural History, ⁵New York Consortium of Evolutionary Primatology, (NYCEP), ⁶Laboratoire AMIS, UMR 5288 CNRS, Université de Toulouse, ⁷Institució Catalana de Recerca i Estudis Avançats, (ICREA), ⁸Unitat d'Antropologia (Departament de Biologia Animal, Biologia Vegetal i Ecologia), Universitat Autònoma de Barcelona

The late Miocene hominoids *Hispanopithecus* from Spain and *Rudapithecus* from Hungary are considered to be closely related great apes (Hominidae), but uncertainties persist regarding their taxonomic distinction and exact phylogenetic placement (stem hominids vs. stem hominines). Previous studies have detected a strong phylogenetic signal in the vestibular apparatus morphology among primates. Here we use deformation-based geometric morphometrics to assess the morphological affinities of the vestibular apparatus in *Hispanopithecus laietanus* (IPS18000) and *Rudapithecus hungaricus* (RUD77 and RUD200) among a large sample of extant catarrhines. We use between-group principal components analyses (bgPCA) to explore the position of the fossils in the vestibular 3D morphospace and phylogenetic comparative methods to reconstruct its evolution. Our results indicate that hylobatids display a rather monkey-like morphology, whereas great apes clearly occupy a distinct portion of the morphospace. Our bgPCA results reflect a strong phylogenetic signal and confirm that *Hispanopithecus* and *Rudapithecus* exhibit a hominid-like morphology (thick semicircular canals, small anterior and lateral ones), their differences being compatible with the distinction of two genera. Along the first two axes of variation, and under different phylogenetic assumptions, *Rudapithecus* more closely approaches the reconstructed ancestral states for hominines and hominids as a whole, whereas *Hispanopithecus* appears more similar to orangutans (due to the possession of rather stout semicircular canals and a cranio-caudally compressed anterior canal). Although formal cladistic analyses would be required to test whether these similarities are pongine synapomorphies or hominid symplesiomorphies, our study confirms the potential of vestibular morphology for phylogenetic reconstruction between fossil and extant apes.

Funded by the Generalitat de Catalunya (CERCA Programme) and the Agencia Estatal de Investigación (BES-2015-071318, CGL2016-76431-P and CGL2017-82654-P; AEI/FEDER EU), French CNRS, and performed using HPC resources from CALMIP (2018-P1440)

Minimally invasive biomarkers in evolutionary anthropology: Tools for understanding human variation, adaptation, and developmental plasticity

SAMUEL S. URLACHER
Evolutionary Anthropology, Duke University

Minimally invasive biomarkers (MIBs) of physiological processes provide a participant-friendly means to quantitatively, and often sensitively, operationalize hypotheses in evolutionary anthropology. At the most fundamental level, MIBs have been employed to document global variation in key aspects of human biology (e.g., reproduction, immune function, stress, aging). The gradual

progression of the field has seen increasingly sophisticated use of MIBs to investigate human adaptation, particularly via mechanisms of phenotypic and developmental plasticity. This poster reviews these efforts. In doing so, it highlights the application of MIBs to test evolutionary life history theory and energetic tradeoff models of human biological variation. Data collected from Shuar forager-horticulturalist children of Amazonian Ecuador ($N = 339$) and Garisakang forager-horticulturalist children of lowland Papua New Guinea ($N = 79$) are presented to illustrate the use of MIBs (finger-prick blood spot measures of immune activity and salivary measures of diurnal cortisol rhythms) to investigate the adaptive nature of plasticity in human linear growth. Such studies have great potential for improving understanding of the ability of humans to adapt to local socio-environmental conditions as well as to illuminate the biocultural mechanisms underlying the developmental origins of health and disease. A review of the field underscores the importance of repeat-measures, longitudinal data collection and multi-method approaches for inferring causality in MIB association studies. A key challenge remains convincingly demonstrating the adaptive nature of observed physiological relationships. Future research must better focus on documenting long-term fitness advantages (e.g., reproductive success) and physiologically redundant, functional interactions of examined traits.

National Science Foundation (SMA-1606852; BCS-1340958; DGE-1144152); Czech Science Foundation (13-25602P)

The chemical signature of weaning: comparing the trace element concentration of captive lowland gorilla breast milk (*Gorilla gorilla*) and wild mountain gorilla (*Gorilla beringei beringei*) plant foods

MEAGAN M. VAKIENER¹, WINNIE ECKARDT², VERONICA VECELLIO², TARA S. STOINSKI², ANTOINE MUDAKIKWA³, SHANNON C. MCFARLIN¹ and MICHAEL L. POWER⁴

¹Center for the Advanced Study of Human Paleobiology, The George Washington University, ²Research and Conservation, Dian Fossey Gorilla Fund International, ³Department of Tourism and Conservation, Rwanda Development Board, ⁴Nutrition Laboratory, Smithsonian National Zoological Park

Weaning is a critical life history milestone, but is often difficult to determine in wild primates from behavioral observations alone. Prior work has indicated that profiles of the trace elements barium (Ba) and strontium (Sr) preserved in hard tissues can offer high-resolution information for reconstructing weaning in both extant and extinct populations. However, examining the trace element concentrations of infant and juvenile diets is necessary to provide a context for interpreting variation in hard tissue signatures.

ABSTRACTS

This study analyzes wild Virgona mountain gorilla (*Gorilla beringei beringei*) plant foods (N = 48), and longitudinal breast milk samples from captive western lowland gorillas (*Gorilla gorilla*; N = 5), to understand trace element variability in solid foods and milk across lactation stages. Plant and breast milk samples were analyzed using inductively coupled plasma mass spectrometry to measure Ba, Sr, and calcium (Ca). Plants were significantly lower in Ba (t (47) = 3.65, p < 0.001), Sr (t (47) = 4.28, p < 0.0001), and Ca (t (47) = 4.60, p < 0.0001) concentrations compared to milk, but calcium normalized Ba (Ba/Ca; t (47.04) = 8.24, p < 0.00001) and Sr ratios (Sr/Ca; t (49.76) = 19.66, p < 0.00001) were significantly higher in plants, contrary to some suggested explanations about the chemical patterns in enamel. These results suggest that biopurification (the differential movement of elements through "biological filters"), bioavailability, and trace element concentrations may all play a role in the observed signature in hard tissues, having important implications for retrospective studies of weaning.

The Leakey Foundation; The Wenner-Gren Foundation; The George Washington University; National Science Foundation (BCS 1751608, 1520221), Nacey Maggioncalda Foundation

The Blood Microbiome of Human and Non-Human Primates

NEGIN VALIZADEGAN^{1,2}, REBECCA M. STUMPF^{1,2} and JESSICA F. BRINKWORTH^{1,2}

¹Anthropology, University of Illinois at Urbana-Champaign, ²Carl Woese Institute for Genomic Biology, University of Illinois at Urbana-Champaign

There are interspecies differences in immune responses in human and non-human primates. Although often presumed to be sterile, blood samples from healthy individuals contain thousands of commensal bacteria. We have increasing evidence of a mutual relationship between the gut microbiome and immune system regulations and development, but our knowledge is limited on whether a similar interaction between the blood microbiome and immune system exists. For example, lipopolysaccharide (LPS), a major component of cell-walls of Gram-negative bacteria, can both strongly stimulate innate immunity and induce host immune tolerance to Gram-negative bacteria. Blood microbiome, therefore, may impact immune responses to infection and contribute to immune divergence between species. In this study, we collected blood samples from human, rhesus macaque, common marmoset and ring-tailed lemur, and assessed their microbial contents. We measured blood endotoxin concentrations using the PyroGene™ Recombinant Factor C and detected blood microbiome composition using 16s rRNA sequencing. We conducted alpha and beta diversity analysis and measured relative abundances of microbial taxa using the information acquired from 16s

rRNA. We observed strong variations in circulating LPS quantities and host blood microbial communities across primate species, and these differences adhere to host phylogenetic relationships, suggesting that the blood microbiome has evolved and diverged in primates. The results of this study shed light on microbe-primate co-evolution as an important immune compartment, and contribute to a better understanding of primate infectious disease responses.

Funding Citation: University of Illinois at Urbana-Champaign, Department of Anthropology; Franklin Mosher Baldwin Memorial Fellowships, Leakey Foundation (Award # 0888118, ID # 214236).

Childhood growth, cessation, and recovery: Links between lines of growth arrest and bone quantity

TESSA R. VALLEROY¹ and LIBBY W. COWGILL²

¹Department of Anthropology, University of Missouri, ²Department of Anthropology, University of Missouri

While it is generally believed that lines of growth arrest ("Harris Lines") appear on bone diaphysis due to episodes of stress, there has been difficulty linking lines to specific metabolic insults, and there is evidence that Harris lines could be the product of regular hormonal fluctuation during growth. In this analysis, we explore the relationship between tibial Harris lines and bone growth in length and cross-sectional properties. Harris Lines were assessed on mediolateral radiographs of tibiae from six geographically diverse samples of immature individuals under the age of 18 (n=265), and number of lines and distance from the distal metaphyseal surface was recorded. Midshaft tibial cross-sectional geometry was calculated from the same radiographs and midshaft molds.

The results of the analysis yielded mixed results. Harris Line count (and Harris Line count standardized by age) is positively correlated with tibia cross-sectional properties (p<0.001). In addition, bone quantity is affected by how recently the line of growth arrest formed; individuals with more recent insults have weaker diaphysis. The positive correlation between Harris Line count and bone strength may be in part a product of increased survivorship in individuals with higher Harris Line numbers, and provides a cautionary warning about overly simplistic interpretations of indicators of non-specific stress.

This project was supported by the University of Missouri-Columbia College of Arts and Science Undergraduate Research Mentorship Program.

Virtual Reality Evolutionary Anatomy Lab (VREAL): Virtual lab spaces for instruction and collaboration

ADAM P. VAN ARSDALE¹, JORDAN TYNES², KAMILE LUKOSIUTE², AUBREY SIMONSON² and SHANE COX²

¹Anthropology, Wellesley College, ²Knapp Center, Wellesley College

Increasing quality and decreasing costs have made virtual reality (VR) and augmented reality (AR) technologies more accessible for teaching and research. Coupled with an increasing investment in open-access, primary-data resources, these advances have created an opportunity to systematically examine the efficacy of VR and AR learning applications in the classroom. Largely supported by undergraduate work, we developed a VR application intended to supplement in-class instruction with a fully-immersive, VR evolutionary anatomy lab (VREAL). During the 2017-2018 academic year, this application was piloted in classes aimed at instruction in human osteology and human evolution with the goal of examining the qualitative and quantitative effectiveness of the VR intervention. In both of these classes, student access to primary materials (human skeletal teaching collections, fossil cast collections) is limited by in-class time and/or material accessibility. VREAL enhanced access to materials through the use of high-resolution scans of digital material, in addition to offering them augmented abilities to manipulate these materials in an immersive environment (e.g. size modification, superimposition). Qualitative assessment suggested students found VR-applications to be highly-engaging and enhancing to their overall enthusiasm for fossil-based work. Quantitative assessments, while limited in our pilot, also suggest to a positive learning effect. These results are encouraging and point toward future areas of development and testing for VR-based educational resources in evolutionary anthropological contexts. This work also brings out some of the challenges of such applications and suggestions for best practices, including emphasizing user experience and shared or collaborative learning goals.

Grit in unexpected places: The prevalence of grit in the diets of robust capuchin species

ADAM VAN CASTEREN¹, MARIANA D. FOGAÇA^{2,3}, DOROTHY M. FRAGASZY⁴, PATRÍCIA IZAR⁵, CALLUM F. ROSS⁶, ROB S. SCOTT⁷, BARTH W. WRIGHT⁸, KRISTIN A. WRIGHT⁹ and DAVID S. STRAIT¹

¹Department of Anthropology, Washington University in Saint Louis, ²Neotropical Primates Research Group, ³Biodiversity and Conservation, Federal University of Maranhão, ⁴Department of Psychology, University of Georgia, ⁵Department of Experimental Psychology, University of São Paulo, ⁶Organismal Biology and Anatomy, University of

ABSTRACTS

Chicago,⁷Department of Anthropology, Rutgers University,⁸Department of Anatomy, Kansas City University of Medicine & Biosciences,⁹Department of Biomedical Sciences, University of Missouri-Kansas City

Robust capuchin monkeys inhabit a diverse array of habitats across the south American continent. Their reliance on mechanically challenging foods and their robust craniodental features have led to their classification as fallback hard object feeders. Their membership in this category is supported by complex microwear textures on their molar teeth, yet research into the mechanics of microwear formation has suggested that such surface complexity may reflect not just food mechanical properties, but also the presence of hard external particles, such as quartz, adhering to foods. This raises the question of whether complex textures are exclusively the product of diet or could also be affected by the presence of external abrasives. For this to be true for robust capuchins, there would have to be a persistent source of such abrasives across seemingly disparate environments. We collected samples of grit from non-fruit food resources of two robust capuchin species (*Sapajus libidinosus* and *Sapajus nigritus*) that forage in contrasting environs: the savannah cerrado and montane rainforest of Brazil. We found that despite large environmental variations, some non-fruit food resources appear to be grit reservoirs in both environments. Fourier-transform infrared spectroscopy confirmed the presence of quartz in our samples and preliminary morphological analysis has demonstrated a particle size range spanning three orders of magnitude. Our results indicate that despite varying environmental conditions, robust capuchins are regularly exposed to moderately high levels of dietary grit that are potentially responsible for the removal of substantial amounts of dental enamel.

This research was supported by grants from the National Science Foundation (NSF-BCS-1440541, NSF-BCS-1440542, NSF-BCS-1440545, NSF-BCS-1627206).

Micro-sampling tooth dentine for stable carbon and nitrogen isotope analysis: early life dietary analysis of prehistoric hunter-gatherers around Lake Baikal, Siberia

VICTORIA M. VAN DER HAAS¹, OLGA I. GORIUNOVA^{2,3}, VLADIMIR I. BAZALIISKII^{2,3} and ANDRZEJ W. WEBER^{1,2,4}

¹Anthropology, University of Alberta, ²History, Irkutsk State University, ³Institute of Archaeology and Ethnography, Siberian Branch of the Russian Academy of Sciences, ⁴LAMPEA, Aix-Marseille University

This paper presents an investigation into the early life dietary history of middle Holocene hunter-gatherers from the Cis-Baikal region, Siberia, using the method of micro-sampling dentine of permanent molars. Dentine has been sectioned into 1-millimeter thick slices. Each was analyzed

for carbon and nitrogen stable isotope ratios. Each section represents roughly 9 months of developmental life. This sampling method allows for a more complete and informative record of early life dietary history with a greatly improved temporal resolution of the biochemical signatures of the developmental period. Bone bulk sampling methods do not allow such insights as a result of a bone turnover rate. Previous ⁸⁷Sr/⁸⁶Sr, ¹⁴C, ¹³C/¹²C, ¹⁵N/¹⁴N tests on bone of the same individuals examined in this study demonstrated that during the Early Bronze Age (EBA) hunter-gatherer groups migrated from the north of the Cis-Baikal, the Upper Lena area, towards the coast of Lake Baikal, the Little Sea micro-region. Some hunter-gatherers appear to have retained diets typical of their homeland while in other cases local diets were relatively quickly adopted. Dentine micro-sampling has provided new data on the weaning duration and early childhood diet of the EBA Cis-Baikal hunter-gatherers. Prior to the method, this was unknown in individuals that survived well into adulthood. This research contributes to our overall understanding of human development on Lake Baikal during the EBA, as well as to methodological advancements.

This research was made possible by the Baikal Archaeology Project, University of Alberta; SSHRC (MCRI grants Nos. 410-2000-1000, 412-2005-1004 and 412-2011-1001); and AMIDEX, Aix-Marseille University.

Effect of sampling bias in endocast volume comparisons between Neandertals and recent modern humans

CAROLINE VANSICKLE^{1,2} and ZACHARY COFRAN³

¹Department of Anatomy, A.T. Still University of Health Sciences, ²Evolutionary Studies Institute, University of the Witwatersrand, ³Anthropology Department, Vassar College

Popular literature on human evolution frequently references how Neandertals had larger brains than modern humans. Yet, paleoanthropologists recognize that Late Pleistocene humans in general had large brains, and that brain size has decreased in humans over the last 30,000 years. Here, we investigate how sample biases complicate the interpretation of this evolutionary trend. We consider both the effects of sample size bias (i.e., comparing a small number of Neandertals to a larger and potentially more diverse sample of recent humans) and of sample selection (i.e., which recent human sample is best for drawing conclusions about evolutionary changes since the Late Pleistocene). We use bootstrap resampling to test the former and multiple human samples to test hypotheses about the latter. Among the recent human samples, we examine the importance of cold-adaptation (Ipiutak and Tigara, Point Hope), European ancestry (Terry Collection), and having a larger range of variation (Morton Collection, recalculated) when making comparisons with Neandertal crania.

When possible, we compare same-sex and similar-body-size individuals to the Neandertal sample. Our results suggest that the null hypothesis of no difference in cranial capacity between Neandertals and more recent modern humans is supported in some comparisons, but rejected in others. These findings indicate that it is not always true that humans today do not have cranial capacities seen in Neandertals, and that researchers need to thoughtfully consider their comparative sample when studying such topics.

Should I stay or should I go? Assessing residential mobility in Bronze Age Switzerland through the isotopic evidence

ALESSANDRA VARALLI^{1,2}, JOCELYNE DESIDERI², MIREILLE DAVID-ELBIALI², GWENAËLLE GOUDE³, MATTHIEU HONEGGER⁴ and MARIE BESSE²

¹Department of Archaeology, University of Durham,

²Department F-A. Forel for Environmental and aquatic sciences, University of Geneva, ³Aix Marseille Univ, CNRS, Minist Culture & Com, LAMPEA, ⁴Institut d'Archéologie, Espace Paul Vouga, Hauterive, University of Neuchâtel

It is still debated whether the major cultural changes that occurred in Europe during the Bronze Age (BA) were related to a circulation of knowledge or human migrations. Researches through multidisciplinary approaches (isotopes, archaeology) strongly contribute towards untangling these complex dynamics for pre-protolithic communities. Since prehistoric times, Switzerland has played a major role in European exchanges for its strategic position between the Danube area and the Mediterranean, offering pivotal information towards reconstructing human mobility during BA period. Jointly analyzing anthropological, archaeological and isotopic data from three sites in western Switzerland (2200-800 cal. BCE), our aim is to shed light on residential mobility and social practices of BA European populations. We explored intersite/intrasite mobility throughout the BA via multi-element and multi-tissue isotope analysis (S on bone and dentine collagen; Sr on apatite enamel), by analysing sixty-three human and fauna samples.

Results suggest that the majority of individuals were locals, in agreement with the archaeological evidence (kind of grave goods and funerary practices). Sulphur data indicates low residential mobility of most of the individuals across their lifespan. Nevertheless, the early BA sample shows a greater S and Sr variability than later times. The presence of some non-local individuals, mainly women, is detected for both the early and final BA. Therefore, in a scenario of relative S and Sr signature homogeneity, which may

ABSTRACTS

suggest a continuity with communities installed previously in this area, we detected evidence of a greater female mobility, as demonstrated for BA sites in Central Europe.

This research was funded by the Fyssen Foundation, the Schmidheiny Foundation, the Boninchi Foundation and the University of Geneva.

I see, you smell: interspecific variation in sensory use for fruit evaluation among sympatric New World monkeys

CARRIE C. VEILLEUX¹, CHIHIRO HIRAMATSU², SHASTA WEBB³, FILIPPO AURELI⁴, COLLEEN M. SCHAFFNER^{4,5}, SHOJI KAWAMURA⁶ and AMANDA D. MELIN^{3,7}

¹Anthropology, University of Texas at Austin, ²Human Science, Kyushu University, ³Anthropology & Archaeology, University of Calgary, ⁴Instituto de Neuroetología, Universidad Veracruzana, ⁵Psychology, Adams State University, ⁶Integrative Biosciences, University of Tokyo, ⁷Medical Genetics, University of Calgary

Because sensory adaptations are often associated with foraging, variation in sensory function between sympatric species can influence niche partitioning. However, little work has explored sensory variation in wild sympatric primates foraging on the same foods. Here, we used behavioral data from three sympatric platyrrhines (*Ateles geoffroyi*, *Alouatta palliata*, *Cebus capucinus*) in the dry forest of Sector Santa Rosa, Costa Rica, that differ in diet, locomotion, and sensory function. We calculated how often visual inspection, smell, and touch were used during feeding bouts to evaluate fruits from six shared plant species (1283 bouts). Using generalized linear mixed models, we found differences among platyrrhines in the use of all three senses. Platyrrhine species significantly influenced variation in visual inspection (LRT, $p=0.017$), smell ($p=0.007$), and touch ($p<0.0001$). When evaluating the same fruits, *Cebus* and *Alouatta* used vision more than *Ateles*, *Ateles* used smell more than *Cebus* and *Alouatta*, and all three differed in the use of touch (*Cebus*>*Ateles*>*Alouatta*). We also found an effect of color vision phenotype on the use of smell when combining all three species ($p=0.002$), suggesting that dichromats use olfaction more often than trichromats. Intraspecific analyses of the polymorphic species revealed that color vision phenotype influenced smell use in *Cebus* but not *Ateles*. Our results suggest that even when feeding on the same fruit species, sympatric primates differ in how they use their senses for fruit selection. Olfaction may be particularly important for *Ateles* when evaluating fruits to compensate for reduced manual dexterity due to derived adaptations for suspensory locomotion.

The Effects of Soundscape on the Prairie Madness Phenomenon

ALEX D. VELEZ¹, MERCEDES CONDE-VALVERDE², JULIO MARCHAMALO-AMADO² and ASHLEY E. AHONEN¹

¹Anthropology, Binghamton University, ²Ciencias de la Vida, Universidad de Alcalá

"Prairie madness" is an historical phenomenon wherein migrant populations who settled the Great Plains region of the United States during the late 19th and early 20th centuries experienced episodic bouts of depression and violence. The cause is commonly attributed to the isolation between the households and settlements. However, contemporary historical accounts also specify the sound of meteorological phenomena such as the winds on the plain as a catalyst. In order to assess whether acoustic environment could play a role in the development of symptoms and behaviors associated with Prairie Madness, this study conducted spectral analysis of several rural locations in the Great Plains region, and recordings of different environments, including urban centers. Results indicate that environments featuring wind and rain tend to have much less diversity in the bandwidth of frequencies present. The sound of the wind and rain appears to scatter most frequencies, leaving only a band from 1-1000 Hz, and some sounds at 5000 Hz unaffected. The strongest frequencies found in the windy and rainy environments of the plains also coincide with human hearing sensitivities, specifically a spike in sensitivity which occurs between 500 and 1000 Hz. A number of conditions, such as misophonia and acute hyperacusis, are known to cause increased sensitivity to environmental sounds. Both conditions can result from high stress environments and are known to cause behavior consistent with descriptions of prairie madness such as depression, and aggressive behavior. Thus, this study maintains an environmental factor for the development of the Prairie madness phenomenon.

The behavioral ecology of grit avoidance in gelada monkeys

VIVEK V. VENKATARAMAN¹, PETER J. FASHING² and NGA NGUYEN²

¹Institute for Advanced Study in Toulouse, Toulouse School of Economics, ²Department of Anthropology, California State University Fullerton

Exogenous grit has recently been implicated as a critically important factor in the evolution of mammalian molar crown height and the formation of dental microwear textures. Because grit has no nutritive value, interrupts feeding, and causes tooth wear, foraging behavior should minimize the consumption of exogenous grit via altered food selection and/or food-cleaning. Yet little is known about how primates avoid grit during foraging, and how grit avoidance itself may be constrained by other demands. We conducted

a preliminary study on the behavioral ecology of grit avoidance with gelada monkeys, grassland primates with high-crowned molars, dexterous hands for food-cleaning, and a diet based on graminoids and forbs, including underground storage organs (USOs) (i.e. a diet with substantial exogenous grit). Specifically, we studied gelada feeding behavior at Guassa Plateau in northern Ethiopia during the dry season, when the vegetation is coated in dust and geladas increasingly incorporate USOs into their diet. During 10-minute focal follows on 20 individuals, we measured food-cleaning behaviors of USOs and replicated the amount of grit removed from food objects. We also assessed the tradeoffs between intake rate and cleaning behavior, and measured possible social influences on the ability to thoroughly clean food items. Geladas remove and avoid grit on USOs via digital manipulation and spitting. More generally, consuming monopolizable foods under time constraints and in the presence of other individuals appears to magnify the tradeoff between intake rate and cleaning behavior.

Shoulder morphology and substrate use in extant cercopithecoid monkeys

MARIE VERGAMINI¹, LISA M. DAY², ERNESTO GAGARIN^{2,3}, HANNAH FURCHAK² and AMY L. RECTOR²

¹Integrative Life Sciences, Virginia Commonwealth University, ²Anthropology, School of World Studies, Virginia Commonwealth University, ³Department of Biology, Virginia Commonwealth University

Substrate use in Old World monkeys is reflected in morphological variation in forelimb bones. Studies of the elbow region suggest that Old World Monkey locomotor repertoires, including degree of arboreality and terrestriality, can be distinguished using variation of the distal humerus and proximal ulna. Given that the shoulder may not be as directly involved in weight bearing during monkey locomotion compared to the elbow joint, the relationship between morphological variation and arboreality in the shoulder joint may not be the same.

Here, we use 3D geometric morphometrics to determine if differential substrate use can be identified through analysis of shape variation in the Old World Monkey proximal humerus. 32 points capturing the shape of the proximal humerus were collected using a Microscribe from a sample of more than 50 extant cercopithecoids from 15+ species. Monkey species were placed in locomotor categories including arboreal, terrestrial, semi-terrestrial, and leaping based on their primary locomotor strategy during traveling. Variation was analyzed using PCA, PGLs, and phylogenetic ANOVAs.

Results suggest that shoulder joint morphology, specifically that of the proximal humerus, can successfully differentiate arboreal, terrestrial,

ABSTRACTS

semi-terrestrial, and leaping substrate use in modern cercopithecoids. This study indicates that primates that use a mixed locomotor approach have morphological adaptations for traveling in both arboreal and terrestrial environments, and that leaping and phylogeny also variably influence the morphology of the proximal humerus. As a valuable factor of these primates' ecology, this locomotor information sheds light on niche differentiation, resource competition, and community organization.

Through introgressed DNA, a single genome contains the story of many populations

BENJAMIN VERNOT

Department of Evolutionary Genetics, Max Planck Institute for Evolutionary Anthropology

Genetic evidence has emerged that Denisovans and Neandertals have interbred both with the ancestors of modern non-Africans, and with each other. As a consequence, the genomes of many modern and ancient individuals harbor long fragments of DNA inherited from widely diverged populations. The presence of this "introgressed" DNA can be inferred through genome-wide signatures such as *f₄* statistics, but identifying specific fragments of introgressed DNA presents additional challenges.

We developed methods for identifying such fragments in modern humans, and identified Denisovan and Neandertal DNA in 1523 geographically diverse individuals. From this introgressed DNA we and others have discovered signatures of both positive and negative selection, and learned about the history of interactions between modern humans and our archaic cousins. However, despite evidence of similar interactions between Neandertals and Denisovans, it has not been possible to identify specific introgressed DNA fragments in either population.

Here, I will review these results, and discuss the genome of an individual from Denisova Cave ("Denisova 11"), with a Neandertal mother and a Denisovan father. The unique nature of this individual's genome allows us to identify introgressed fragments present in either parent, which would appear as homozygous tracts of Neandertal or Denisovan DNA. Strikingly, we identify only Neandertal homozygous regions, indicating that the Denisovan father inherited DNA from a distant Neandertal ancestor. From these regions, we infer that this Neandertal ancestor came from a different population than the Neandertal mother of Denisova 11.

Max Planck Society, the Max Planck Foundation (31-12LMP Pääbo to S.Pä.); the European Research Council (694707, 324139, 715069); Russian Science Foundation (14-50-00036 to M.B.K., M.V.S. and A.P.D.).

A bioarchaeology of care case study: Possible Juvenile Rheumatoid Arthritis from 14th-15th century Transylvania

KIRSTEN A. VEROSTICK¹, KATHERINE M. PADULA¹, DEVIN N. WILLIAMS¹, ZSOLT NYARADI², ANDRE GONCIAR³ and JONATHAN D. BETHARD¹

¹Department of Anthropology, University of South Florida, ²Department of Archaeology, Haáz Rezső Múzeum, ³Department of Archaeology, Archaeo Tek-Canada

Recently bioarchaeologists have started exploring questions related to impairment, disability, and care provisioning in the past. These analyses require that biological data from the skeleton are coupled with mortuary data and in some instances, documentary sources. Ultimately, this approach enables researchers to better understand disability in the past and explore how people would have cared for their community members.

This presentation presents a case study from the under-studied region of Eastern Europe. In the medieval village of Bögöz, located in the Transylvanian region of the Kingdom of Hungary, a set of human remains, identified as GR-13, were recovered from a medieval church cemetery during rescue excavations. Radiocarbon dating places GR-13 at approximately AD 1300 to 1415. GR-13 was a young adult female, between 18-25 years old at time of death. Sometime after burial, GR-13 was bisected by a pillar during church renovations. Due to the placement of the pillar, only a partially complete skeleton was recovered. GR-13 displays multiple pathological changes, including erosive porosity, and cystic and subchondral erosive lesions of major joint complexes, including the elbow and ankle. The pathologies present in GR-13 are highly consistent with a diagnosis of juvenile rheumatoid arthritis (JRA). Our analysis suggests GR-13's everyday life would have been affected following the onset of JRA. Following Tilly's Index of Care model, she would have needed assistance in procurement of food and water, and support in long-distance transportation for survival. The Index of Care provides a unique way to better understand disability in medieval Europe.

The Late Middle Pleistocene fossils from Montmaurin (Haute-Garonne, France). A contribution to the question of the emergence of the Neandertal lineage

AMELIE VIALET¹, MARINA MARTINEZ DE PINILLOS², JOSÉ-MARIA BERMUDEZ DE CASTRO², MARIA MARTINON-TORRES², BENOIT BERTRAND³ and THOMAS COLLARD⁴

¹Homme&environnement, National Museum of Natural History, ²Anthropology, Centro nacional de Investigacion sobre la Evolucion Humana, ³EA7367 - IML, Lille university, ⁴EA4490 - PMOI, Lille university

Hominin fossils were discovered in the Montmaurin caves (S-W of France) in 1950's. Among them, the mandible from La Niche was attributed to a preneandertal (i.e. *H. heidelbergensis*). Until now, except this specimen, the others discovered in the same site (two thoracic vertebrae, one right tibia) are quite unpublished while the fossils from a very close cavity called Coupe-Gorge (a right maxillary bone bearing C-P4, 3 isolated teeth and a fragmentary juvenile mandible) were forgotten.

This is the purpose of this study to highlight such "unknown" fossils. Attributed to the Late Middle Pleistocene, they belong to the current debate on the origins of the Neandertal lineage. That's why a new examination was done. Results show a mixture of archaic and Neandertal features not only on the La Niche mandible but also on the Coupe-Gorge maxillary bone. The former shows a derived teeth pattern and a primitive mandibular corpus (well-marked planum alveolare on the inner part of the symphysis, foramen mentale at the level of P₄). The latter is not as inflexed as in Neandertals (the nasal bones are oblique, not horizontal) but is similar to them by its sloped or bilevel nasal floor.

The Montmaurin fossils evidence a not fully Neandertal form during the Late Middle Pleistocene although this species is supposed to emerge at that time. It suggests two possibilities: 1- this event occurred later or 2- an archaic group co-existed in parallel with the first Neandertals.

Spectrum of Neandertal introgression across modern-day humans indicates multiple episodes of human-Neandertal interbreeding

FERNANDO A. VILLANEA and JOSHUA G. SCHRAIBER

Institute for Genomics and Evolutionary Medicine, Temple University

Neandertals and anatomically modern humans overlapped geographically for a period of over 30,000 years following human migration out of Africa. During this period, Neandertals and humans interbred, as evidenced by Neandertal portions of the genome carried by non-African individuals today. A key observation is that the proportion of Neandertal ancestry is 12-20% higher in East Asian individuals relative to European individuals. Here, we explore various demographic models that could explain this observation. These include distinguishing between a single admixture event and multiple Neandertal contributions to either population, and the hypothesis that reduced Neandertal ancestry in modern Europeans resulted from more recent admixture with a ghost population that lacked a Neandertal ancestry component (the 'dilution' hypothesis). In order to summarize the asymmetric pattern of Neandertal allele

ABSTRACTS

frequencies, we compile the joint fragment frequency spectrum (FFS) of European and East Asian Neandertal fragments and compare it to both analytical theory and data simulated under various models of admixture. Using maximum likelihood and machine learning, we found that a simple model of a single admixture does not fit the empirical data and instead favor a model of multiple episodes of gene flow into both European and East Asian populations. These findings indicate more long-term, complex interaction between humans and Neandertals than previously appreciated.

This work was supported by NIH grant R35 GM124745

An evolutionary model for the origins of temporal discounting in humans and non-human animals

BRIAN A. VILLMOARE¹, DAVID KLEIN², PIERRE LIENARD¹ and TIMOTHY MCHALE³

¹Anthropology, University of Nevada Las Vegas, ²., University of California, ³Department of Anthropology and Museum Studies, Central Washington University

The propensity of humans and non-human animals to discount future returns for short-term benefits is well known in disciplines that focus on decision-making, such as economics and behavioral sciences. In economics, this phenomenon is known as 'temporal discounting', and research has focused on various descriptive and predictive parameters, conditions that might affect the length of the long-term decision window, and differences among social and political human groups. However, the underlying causes of temporal discounting have only occasionally been alluded to. Here we propose an evolutionary model that describes how and why the tendency toward discounting future returns would have evolved, even in circumstances in which discounting is irrational.

We use the model of a fitness landscape to examine the implications of decision-making, using time as an axis. We generated a simulated population of organisms ('agents') at one behavioral adaptive peak, faced with the disappearance of that peak, and the appearance of two other peaks, one more temporally distant than the other. The organisms use a random-walk behavioral pattern, with 'decisions' to move based on proximity to a peak.

Our results demonstrate how unlikely it would be for natural selection to favor delayed gratification. In most circumstances, the allure of the short-term reward is simply too strong, even when the distant reward is mathematically greater (typically many times greater). Our interpretation of these results is natural selection will generally not favor delayed gratification if it requires passing over a lesser reward (i.e. 'waiting').

The empirical evidence of a relationship between enthesal changes and past human behaviors: Some examples and counterexamples, focusing on the upper limb

SÉBASTIEN VILLOTTE
UMR PACEA, CNRS

The side dominance and asymmetry of upper limb enthesal changes (ECs) are analyzed in 1439 adult human skeletons to assess the reliability of ECs as indicators of past behaviors. ECs are expected to be at least in part acquired through adult life due to biomechanical factors, and should thus reflect the right-hand dominance seen in our species. ECs were qualitatively recorded for four fibrocartilaginous entheses on the humerus (lesser and greater tubercles, medial and lateral epicondyles) and one on the radius (radial tuberosity).

ECs frequencies are very low in young adults and increase with age. Frequencies are similar for the left and right radii and significantly higher for the right humeral entheses. Where there is asymmetry, the right side clearly tends to have higher scores for the humerus, but this pattern is not seen in the radius. When an individual displays two or more asymmetries, they more frequently occur on the same side, especially when the radial tuberosity is excluded from the analysis.

It seems clear that, for the entheses considered here, most if not all ECs are acquired through adult life. ECs at the radial tuberosity seem randomly distributed whereas ECs at the humerus are predominantly found on the right side and often unilaterally, following an expected pattern. It is thus likely that biomechanical factors play a significant role in the occurrence of humeral ECs (and thus that past behaviors can be discussed), whereas it is less probable for the radius.

A parietal fragment from Denisova cave

BENCE T. VIOLA¹, PHILIPP GUNZ², SIMON NEUBAUER², VIVIANE SLON³, MAXIM B. KOZLIKIN⁴, MICHAEL V. SHUNKOV^{4,5}, MATTHIAS MEYER³, SVANTE PÄÄBO³ and ANATOLY P. DEREVIANKO^{4,6}

¹Department of Anthropology, University of Toronto, ²Department of Human Evolution, Max-Planck-Institute for Evolutionary Anthropology, ³Department of Evolutionary Genetics, Max-Planck-Institute for Evolutionary Anthropology, ⁴Institute of Archaeology and Ethnography, Russian Academy of Sciences, Siberian Branch, ⁵Department of Archaeology, Novosibirsk State University, ⁶Department of Archaeology, Altai State University

The Denisovans are an Asian sister group of Neanderthals, originally described based on ancient DNA from a phalanx fragment from Denisova Cave (Altai Mountains, Russian Federation). Since then, three teeth found in the cave have been identified from this group. Genetic data indicates that this population

contributed genes to modern humans across large parts of Asia and in Melanesia, but currently, no fossils from outside Denisova Cave have been clearly attributed to Denisovans. One reason for this is that the extremely limited morphological evidence hampers comparisons. A newly discovered parietal fragment, *Denisova 13*, attributed to the Denisovans based on its mtDNA, gives us a first glimpse at the Denisovan cranial morphology.

Denisova 13 derives from the South Gallery of Denisova cave, although due to a collapse of the section, its stratigraphic position is not secure. Based on its preservation and the accompanying sediments we tentatively attribute it to Layer 22. The specimen consists of two adjoining fragments of the posterior half of the left parietal, extending about 78 mm laterally of *lambda*, and about 51 mm anteriorly, preserving portions of both the sagittal and lambdoid sutures.

We compare *Denisova 13* to a large sample of recent and fossil modern humans, Neanderthals and Middle Pleistocene *Homo*, using geometric morphometrics based on three-dimensional landmarks and sliding semilandmarks collected on computed-tomographic scans and surface scans.

We will discuss the implications of these comparisons to our understanding of Middle and Late Pleistocene hominins in Asia.

Funding: Social Sciences and Humanities Research Council (Insight 430-2016-00590 to BV), European Research Council (694707 to SP), the Max-Planck-Society, and the Russian Science Foundation (14-50-00036 to MVS, APD and MBK).

The muddle in the middle: Dental morphological assessment of population diversity on the Peruvian Central Coast during the Prehispanic Period

TATIANA VLEMINCQ-MENDIETA¹, SIMON HILLSON², LAWRENCE S. OWENS^{3,4}, PETER A. EECKHOUT⁵ and KRZYSZTOF MAKOWSKI⁶

¹Department of Anthropology, University of Nevada, Reno, ²Institute of Bioarchaeology, University College London, ³Department of History, Classics and Archaeology, Birkbeck College, University of London, ⁴Department of Archaeology, University of South Africa (UNISA), ⁵Faculté de Philosophie et Sciences Sociales, Université Libre de Bruxelles, ⁶Departamento de Humanidades, Pontificia Universidad Católica del Perú

Archaeological and ethnographic evidence has been used to support claims of population movements throughout the Prehispanic Andean area, including the Central Coast of Peru. These take the form of migrations, invasions, and even pilgrimages; the oracular site of Pachacámac is believed to have attracted pilgrims from all over the Andes, seeking guidance and healing. However, mobility has not been demonstrated using population biology. To assess this issue bioarchaeologically, 173 individuals from five collections pertaining

ABSTRACTS

to four different groups were analyzed using 20 dental non-metric traits defined by the ASUDAS (Arizona State University Dental Anthropology System). The four groups were selected to represent 1600 years of Central Coast occupation: a Pre-Lima group (Tablada de Lurín, n=25), a Lima group (Huaca Pucllana, n=10; Huaca 20, n= 50), an Ychsma group (Pachacámac, n=51) and an Inca group (Pueblo Viejo-Pucará, n=37). Biological affinities were assessed using descriptive (frequencies) and multivariate statistics (PCA, multidimensional scaling and cluster analysis). The results showed the Inca sample to be distant from the other three, suggesting continuity in all pre-Inca groups, followed by a notable discontinuity. All the pre-Inca cultural variability is solely that – cultural – so the Pre-Lima/Lima transition, the Lima collapse, and the rise of the Ychsma were caused by internal social dynamics and not population migration or replacement. The arrival of the Inca marks the first incursion of non-locals into the area, also confirming the historically-attested Inca habit of using *mitmaq* settlements in their colonization practice.

The benefits of negative energy balance? Oxidative stress and inflammation in wild Bornean orangutans (*Pongo pygmaeus wurmbii*)

ERIN R. VOGEL^{1,2}, DANIEL J. NAUMENKO^{1,2,3}, TIMOTHY D. BRANSFORD^{1,2} and SRI SUCI UTAMI ATMOKO⁴

¹Anthropology, Rutgers, The State University of New Jersey, ²The Center for Human Evolutionary Studies, Rutgers, The State University of New Jersey, ³Anthropology, University of Colorado Boulder, ⁴Biological Sciences, Universitas Nasional Jakarta

The extreme and unpredictable fruiting pattern of Southeast Asian rainforests has led to a number of energy-conserving strategies in Bornean orangutans. Recent studies have demonstrated that during episodes of fruit scarcity, orangutans decrease caloric intake and enter negative energy balance, as evidenced by ketosis. Yet, we lack a basic understanding of how negative energy balance impacts overall health in wild primates. Studies on several model organisms have shown that nutritional intake, energetic stress, inflammation, and protective host immunity are inextricably linked, and when an animal is malnourished, the immune response is significantly impaired. Alternatively, caloric restriction has been associated with reduced oxidative stress in both humans and mice. We tested the hypothesis that negative energy balance is associated with reduced oxidative stress and immune activation in wild Bornean orangutans at the Tuanan Research Station in Central Kalimantan, Indonesia. We used ELISA to determine concentrations of 8-hydroxy-2'-deoxyguanosine (8-OHdG) and neopterin (n=232), and RIA for C-peptide of insulin (UCP) in urine (n=153). We found that orangutans experiencing negative

energy balance had reduced oxidative damage (8-OHdG; p<0.0001) and inflammation (neopterin; p=0.02). Neopterin and oxidative stress were positively correlated ($r^2_{adj}=0.73$, p<0.0001). Our preliminary results suggest that during periods of caloric restriction and resulting negative energy balance, reduced oxidative damage may confer benefits to orangutan physiology and health. This finding is supported by several studies that have found that lower levels of oxidative stress are associated with decreased inflammation in humans. Future studies will examine the role of antioxidants in mediating these complex relationships.

This work was supported by a Bigel Grant, Aresty Fellowship, and CHES Undergraduate Research Award to D.J.N.; and NSF, Leakey, USAID and CHES research grants to E.R.V. D.J.N., S.U.A., and T.D.B.

Cortical Defects of the Distal Femur in Pacific Northwest Natives

JULIETTE VOGEL

Department of Archaeology and Historic Preservation, Washington State

In addition to the well-known squatting facets identified in the distal tibia, a number of nonmetric traits at the proximal and distal ends of the femur have also been linked to habitual squatting postures. One of these traits, located on the posterior aspect of the distal femur and most commonly above the medial condyle, has been identified by researchers under various names, including "tibial imprint," "tendon lesion," and "distal femoral cortical excavation." In a sample of 40 precontact Natives recovered from sites across the state of Washington, nine adults (23%) presented with this trait. The sample included subadults as well as adult males and females who had observable distal femora. This study examines possible etiologies for the trait, its association with tibial squatting facets (when observable), and its frequency among squatting populations. Furthermore, this research aims to contribute to the growing body of literature that addresses the significance of this relatively under-reported trait.

NCSE's Scientist in A Classroom Program: Using Primatology to Teach Middle Schoolers about Climate Change and Evolution

LAUREN J. VOLKERS¹, MARIE VERGAMINI² and AMY L. RECTOR¹

¹Anthropology, School of World Studies, Virginia Commonwealth University, ²Integrative Life Sciences, Virginia Commonwealth University

The National Center for Science Education (NCSE) provides K-12 classrooms resources to teach "controversial" science materials. NCSE's *Scientist in a Classroom* is a two day program facilitating professional scientists using various fields

of expertise to teach climate change and evolution. In Spring 2017, Marie Vergamini, a Virginia Commonwealth University graduate student, used primatology as a lens for communicating these materials with mostly underrepresented students at Richmond Public School Lucille M. Brown Middle.

The first day "Get-To-Know-You" visit centered on learning what primatology is, what primatologists study, and how to become a primatologist. Prior to this visit, most students were completely unfamiliar with the field. The second day "Do Science" visit followed by using orangutan behavior and ecology to explore evolution and how climate change is drastically affecting wild orangutan populations. Students first participated in behavioral activities, learning how to groom, eat, forage, and nest-build like an orangutan. These activities also explored the similarities and differences in primates, especially between humans and orangutans. Students subsequently discussed how an unsustainable palm oil industry causes deforestation, uncontrollable changes in fire seasons, and extreme loss of orangutan habitat.

NCSE's *Scientist in a Classroom* program is an excellent outreach opportunity for scientists from all fields, including biological anthropology, to assist K-12 teachers in exploring climate change, evolution, and science careers in their classrooms. Biological anthropologists are uniquely positioned for such programs as they are trained to talk about human evolution and can provide fun, safe, and interactive environments for students to engage in these topics.

Decolonizing science communication by telling regional stories

LIZZIE WADE

News department, Science

The emergence of ancient DNA and anthropological genetics has led to not only new ways of studying the human past, but new ways of writing about it. These studies and stories can be rich in never-before-imagined detail, often at the level of individual lives. But they are inevitably based on meaning derived from differences in individuals' and populations' genomes. Stories and studies that emphasize the differences between people from different continents, and how those groups have moved and interacted over millennia, are often deemed the most "newsworthy" in a media landscape of limited time, resources, and attention spans. In this talk I will discuss how that bias toward continental-scale stories can unconsciously recapitulate and reinforce racist colonial categories and hierarchies, including those of biological race. I propose that telling regional stories can expand the general public's

ABSTRACTS

perception of the human past and why it matters, and may be a more accurate representation of the way individuals in the past experienced their lives and communities.

Bioarchaeology of non-binary genders: perspectives from the Adena tradition of the Ohio Valley region

ROBYN WAKEFIELD

Basic Sciences, Anatomy, New York Chiropractic College, Division of Anthropology, Carnegie Museum of Natural History

Ethnohistorical and bioarchaeological research noted the presence of non-binary genders among indigenous groups in North America (Hollimon 2001, 2011). Gender fluidity was often associated with religious practitioners or shamans (Carr and Case 2006; Hollimon 2001). The Adena tradition was an Early Woodland (3000-2200BP) cultural horizon that spanned from the American midwest through the northeast, characterized by conical burial mounds. Skeletal remains (n=105) from two Adena sites, Cresap Mound and McKees Rocks Mound, in the Ohio Valley region were investigated via bioarchaeological methods: age, sex, stature, trauma, infectious disease, stress indicators, and musculoskeletal stress markers (MSMs). Funerary data was also collected including burial location, burial type, head orientation, body position, and grave good inventories. Data was analyzed via multivariate statistical procedures such as PCA/MCA and Ward's (1964) method of cluster analysis. The results of biosocial cluster analyses revealed a distinct cluster of elite burials characterized by the presence of artifact caches that are similar to those found in Hopewell shamanistic burials (Carr and Case 2006), defined by the presence of copper beads and effigy items, antler head-dresses, hemispheres of semi-precious stones, and elaborate lithic points. In the Adena burials, members of this distinct cluster included an old adult male, a young adult female, and adults of undetermined sex with similar MSM patterning to the rest of the sample. It is concluded that this distinct cluster of burials represents a "third gender" class of shamanistic practitioners.

Goethe, Darwin, and Wolff: Does Wolff's "Law" Mean Anything?

ROBERT A. WALKER

Anatomy, New York Chiropractic College

Wolff's Law is the postulate that bone reacts and remodels in response to the external forces applied to it. This is sometimes restated as: the body will produce bone where it is needed, and remove bone where it is not needed, and will do so with greatest economy of tissue. Goethe, as quoted by Darwin (Origin, 1st ed.: 147), stated that "in order to spend on one side, nature is forced to economize on the other side." This is the way

that bone growth and remodeling is often represented, particularly in clinical settings. However, there are many problems associated with a straightforward application of Wolff's "Law." First, as formulated it applies only to the application of compressive forces to bone. Second, bones behave differently in different locations within the skeleton, and is complicated by differential responses to hormonal and other physiological effects. Further, different locations respond differently to imposed mechanical forces, particularly in response osteoporosis and other bone metabolic diseases. As has been demonstrated in our laboratory, remodeling patterns in the long bones among diverse vertebrate taxa follow similar patterns, regardless of locomotor patterns or loading regimes. Each bone is itself an organ with a long phylogenetic history. Muscle origins and insertions do not change significantly due to strain but are highly conserved developmental processes. This all suggests strong underlying developmental control of skeletal growth and modeling. Wolff's "Law" is best seen as a general description than a hard and fast rule for skeletal remodeling.

This research is supported in part by a grant from the New York Chiropractic College Research Department.

Physical (in)activity and the etiology of osteoarthritis

IAN J. WALLACE¹, GRANT RIEW¹, REBECCA LANDAU¹, NICHOLAS B. HOLOWKA¹, ALISON M. BENDELE², ALAN J. GRODZINSKY³, ELIOT H. FRANK³ and DANIEL E. LIEBERMAN¹

¹Human Evolutionary Biology, Harvard University, ²Bolder BioPATH, Inc., ³Center for Biomedical Engineering, Massachusetts Institute of Technology

Osteoarthritis (OA) is a common joint disease whose causes are poorly understood, but a long-standing hypothesis is that OA stems primarily from the cumulative effects of joint mechanical loading throughout life. Based on this "wear and tear" hypothesis, many anthropologists assume that the presence of OA in the skeletal remains of ancient humans can be interpreted as evidence of a highly physically active lifestyle. Here, we use guinea pigs to experimentally test the hypothesis that greater physical activity results in greater joint deterioration. Guinea pigs are an appropriate model for OA research because unlike most laboratory animals, they spontaneously develop the disease as humans do. Animals were either treated daily with a treadmill-running regimen for 22 weeks or served as controls (n=18/group). After the experiment, histological and biochemical analyses were conducted of articular cartilage in the proximal tibia to assess tissue composition and degradation. The results indicate that rather than causing greater joint wear and tear, elevated physical activity actually resulted in reduced cartilage deterioration. Specifically, exercised

animals had cartilage with significantly ($p < 0.05$) higher aggrecan and collagen content (based on biochemistry), as well as smaller OA lesions (based on histology). These results are inconsistent with any hypothesis predicting that high physical activity is a main driver in the etiology of OA and call into question typical interpretations of OA in studies of ancient human skeletons. Ultimately, our findings raise the intriguing possibility that physical inactivity, rather than physical activity, may be a more potent risk factor for OA.

Supported by the Hintze Family Charitable Foundation and the American School of Prehistoric Research.

No dilemma: A broad pelvis explains some of the advantages of women's gait

CARA M. WALL-SCHEFFLER^{1,2} and MARCIE J. MYERS³

¹Biology, Seattle Pacific University, ²Anthropology, University of Washington, ³Biology, St Catherine University

There is currently flux in terms of the tradition of assuming human female's locomotion is disadvantaged due to specific aspects of 'female' morphology, namely mediolaterally broad pelvis, particularly in the bi-iliac breadth, but also in the bi-trochanteric breadth. A flurry of studies have quantified the energetics and kinematics of walking among women and men, and have shown either no differences, or, in fact, certain advantages for women during walking, and particularly during load carrying. Here we investigate how a mediolaterally broad pelvis could lead to morphologically-specific kinematics and thus the energetic advantages identified in these other studies. Women (N=17) and men (N=17) were asked to walk on a treadmill while the muscle activity in seven lower limb muscles was recorded using surface EMG. Using independent t-tests, we compared the muscle activation patterns of participants with broader pelvis for their mass (BPM) with those with more narrow pelvis (NPM), during the quartiles of swing phase and the quartiles of stance phase (Collision, Rebound, Pre-Load, Push-Off). People with BPM have more hamstring activation at the end of swing phase ($p=0.05$) and less at the collision ($p=0.1$) whereas the opposite pattern is seen in NPM. Similarly, BPM have more hip adductor activity at push-off but less at pre-collision than people with NPM ($p=0.1$). Given the reduction of muscle activity at the costly collision quartile, these differing activation patterns based on different pelvic morphology could be the reason that women show energetic savings, particularly when loaded.

The Role of Microbiota in Human Reproductive Tract Cancers

DANA M. WALSH^{1,5}, ISMAIL MERT², JUN CHEN³, XIAONAN HOU⁴, SARAVUT J. WEROHA⁴, NICHOLAS

ABSTRACTS

CHIA^{1,5}, HEIDI NELSON⁵, ANDREA MARIANI⁶ and MARINA R.S. WALTHER-ANTONIO^{1,5,7}

¹Center for Individualized Medicine, ²Gynecologic Oncology, ³Biomedical Statistics & Informatics, ⁴Medical Oncology, ⁵Surgery, ⁶Gynecologic Surgery, ⁷Obstetrics & Gynecology, Mayo Clinic, Rochester, MN

Recent research has demonstrated the various roles our microbial partners, or microbiota, play in human health. In cancer, the role of the microbiota is complex; it may prevent disease or trigger it, and it may determine whether treatment is effective or not. While the role of microbiota has been established in colorectal cancer, its involvement in gynecological cancers has not. We examined the role of gut and reproductive tract (RT) microbiota in ovarian (OC) and endometrial cancer (EC), respectively. We used a patient-derived xenograft (PDX) OC mouse model to study the role of gut microbiota in response of treatment-resistant OC tumors to chemotherapy. Here, we found that the anti-diabetes drug metformin can enhance resistant tumor response while enriching gut microbiota that produce bile acids. Our tissue culture work suggests that these microbially-produced bile acids may be able to induce apoptosis in resistant cancer cells. In EC, we've shown that the cervical and vaginal microbiota in cancer patients is distinct from that of patients with benign disease and that *Porphyromonas somerae* is significantly enriched among cancer patients. We have established an invasion assay with *P. somerae* and an EC cell line to explore the bacteria's role in EC. Our data implies that *P. somerae* is capable of adherence and invasion of the cells, particularly in low oxygen environments that are similar to the tumor microenvironment. Together, our work shows that gut and RT microbiota can influence OC and EC, providing new opportunities for development of novel therapeutics that benefit patient outcomes.

Dietary variation in an urbanizing city: A temporal analysis of diet in Late Medieval London using stable isotopes

BRITTANY S. WALTER^{1,2}, SHARON N. DEWITTE³, TOSHA DUPRAS⁴ and JULIA BEAUMONT⁵

¹Defense POW/MIA Accounting Agency Laboratory, Department of Defense, ²Department of Anthropology, University of Nebraska, ³Department of Anthropology, University of South Carolina, ⁴Department of Anthropology, University of Central Florida, ⁵School of Archaeological and Forensic Sciences, University of Bradford

The process of urbanization is often characterized by high levels of migration, elevated food insecurity, and risks of disease epidemics. Stable isotope analysis of human skeletal remains can be used to identify dietary trends associated with urbanization that may not be evident using osteological analyses alone. Here we evaluate patterns of $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ isotope values from individuals from a Late Medieval London

cemetery (c. 1120-1539 CE) to assess how diet changed through time in an urbanizing environment with increasing population density and periods of famine, including separate analyses for age cohorts and the sexes. Analyses reveal that isotope values varied both through time and by age cohort, but not by sex. Post-hoc regression analysis indicates that $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values increased steadily from 1120-1400 CE, which could reflect a decrease in the variation of food sources as a result of changing import strategies prior to the Black Death. Post-hoc pairwise comparisons show that adults exhibit elevated $\delta^{15}\text{N}$ values compared to non-adults, which may be a result of physiological changes affecting isotope values of growing individuals, migration, and differential access to certain protein sources. Analyses between and within the sexes indicate a lack of difference between the sexes through time, contrary to previous studies of less-urbanized English towns that have found a significant difference in stable isotope values between the sexes. This indicates a lack of sex-related consumption practices in large cities like London, and suggests that females may have played a more equal role in these large, urbanized areas.

Funding for this research was provided by the National Science Foundation (BCS-1540208 and BCS-1261682), and the University of South Carolina SPARC Grant.

Determining sex in forensic anthropology: A review of proposed methodologies

STEPHANIE A. WALTMAN

¹Sociology, Anthropology, and Gerontology, Youngstown State University

Methodologies of sex estimation in forensic anthropology are constantly being developed and retested to ensure the highest levels of accuracy. The two most utilized areas of the skeleton for sex estimation are the pelvis and the skull. Most argue that the skull is the second-best method for sex estimation if the pelvis is not available. However, others have proposed utilizing post-cranial elements as the second-best indicator of sex. This study examined 201 individuals (99 male, 102 female) from the Hamann-Todd Osteological Collection, testing two methods of sex estimation. The first method utilizes 10 weighted non-metric cranial traits, and the second utilizes five single metric sectioning points. The authors of the postcranial method assert that a single postcranial measurement is more desirable than the skull in sex determination. This method is applicable to ancestry specific groups, and was tested on 104 individuals of European descent and 97 of African descent. This study compared the accuracy of the methods and the accuracy of the methods against the known sex of the specimens. Results indicated the nonmetric method had an error rate of 0.25 in comparison to the metric sectioning points of which the highest

error rate was 0.17. Ultimately it was concluded that the metric method had higher accuracy than the nonmetric method in determining the sex of an individual.

Tainted love: Why do female olive baboons dart after copulations?

JESSICA T. WALZ¹ and DAWN M. KITCHEN²

¹Sociology, Criminology, and Anthropology, University of Wisconsin-Whitewater, ²Anthropology, The Ohio State University

Frequently, female savanna baboons "dart" following copulation, running up to several meters from their male partners. We hypothesized that this behavior is a function of postcopulatory sexual selection. We tested whether behavior patterns followed predictions based on female choice, paternity confusion, or male competition in olive baboons (*Papio anubis*) at Gombe Stream National Park. We recorded all interactions between focal females ($n = 13$) and adult males ($n = 30$) in three groups over two study periods, and used non-parametric statistics and generalized linear mixed models to test for effects of copulation success, female partner preferences, and male and female characteristics on darting behavior. Females did not dart different distances when copulating with preferred versus non-preferred partners (Wilcoxon signed-rank test: $T = -0.52$, $p = 0.60$, $n = 13$), contrary to female choice predictions. However, females darted shorter distances following incomplete than complete (i.e., with ejaculation) copulations (Wilcoxon signed-rank test: $T = -2.28$, $p = 0.02$, $n = 12$) and females had shorter dart distances during copulations that occurred within the ovulatory window (GLMM: $\beta \pm \text{SE} = 0.21 \pm 0.08$, $t = 2.50$, $p = 0.01$), supporting contradictory predictions. We also consider important differences in darting behavior among olive baboons and chacma baboons that correspond with their different social structures. Taken together, our results suggest that darting behavior in olive baboons may not strictly function as either a mechanism of female choice or paternity confusion, but rather serves a dual function.

Thanks to the following institutions for contributing to the funding of this project: The Leakey Foundation, International Primatological Society, American Society of Primatologists, Sigma Xi, Animal Behavior Society.

The Global History of Health Project - Asia Module

QIAN WANG¹ and QUANCHAO ZHANG²

¹Biomedical Sciences, Texas A&M University College of Dentistry, ²School of Archaeology, Jilin University

The 'Global History of Health Project' (GHHP), started by Richard Steckel and colleagues, is a platform to systematically document a series of selected health and disease parameters of

ABSTRACTS

human skeletal remains of recent millennia in the context of environmental and socioeconomic changes. This unique project provides an unprecedented look of recent human history to gauge the quality of life and human adaptability in challenging living conditions. Inspired by the GHHP saga staged in the Americas and Europe, we have initiated the GHHP - Asia Module in 2018 to extend this project to Asia, an important theater for the rise of many first civilizations. Human burials have been found throughout the Asian continent from the Neolithic Age to Bronze and Iron Ages and onwards. Most importantly, the majority of burials are associated with archaeological evidence of environmental settings and socioeconomic modes. The project will unlock rich yet mostly untapped information from large skeletal collections in China, Mongolia, Japan, South Korea, East Russia, India, and Southeast Asia and beyond, and establish a contextualized database recording the history of human pathology, focusing on oral pathology and joint diseases, in Asia during the past 10,000 years. The inclusion of the Asia story in GHHP will not only enrich the first hand skeletal and oral health status over generations in recent human history in an evolutionary sense, but also expand existing databases for global and local health agency authorities on policy making for contemporary populations with different economic-social status, ranging from pre-agriculture to modernization.

A Study of Remains of Human Beings Excavated in the Graveyard of Xiabandi

YONGDI WANG

School of Archaeology, Jilin University

The subject material is centered around the remains of mankind unearthed in the burial ground of Xiabandi, Kashgar Prefecture in Xinjiang. This graveyard is located in both Xindi countryside and Xiabandi countryside. The oral health of residents in the burial area is in bad condition. The wear rate of teeth prong is inversely proportional to age as a result of using dental tools instead of resulting from nutrition and development. Some other observable oral diseases are as follows: apical abscess, aplasia of enamel, dental calculus and periodontitis. Apical abscess will appear as people's age increases, so it tends to turn into apical ulcers. Some dental fistulous tracts are even connected with maxillary sinus. At this moment, invisible bony traumas are primarily found on the cranio-face. Infectious diseases such as osteoma and periostitis are also found out. And the older these persons are, the more likely are they to suffer the hyperplasia of joints. The analysis of pathological phenomena suggests that violent clashes among this group as well as between this group

with the other groups are least likely to occur. It is estimated that some persons of this group may travel by riding a horse through the investigation of leg bones.

A newly generated whole genome of *Treponema pallidum* subsp. *endemicum* strain Iraq B: implications for reconstructing the evolutionary history of treponematoses

ZIYU WANG¹, BARBARA J. MOLINI², GEORGE R. MILNER¹ and SHEILA A. LUKEHART^{2,3}

¹Anthropology, Penn State, ²Medicine, University of Washington, ³Global Health, University of Washington

Bejel (*Treponema pallidum* subsp. *endemicum*) is an endemic treponematoses closely related to syphilis (*T. pallidum* subsp. *pallidum*). Although bejel was prevalent throughout Europe prior to the early 20th century, its genetic diversity is not well understood as only one reference genome is currently available. Because bejel coexisted with syphilis in Europe in the 16th century, an expanded genomic dataset can contribute to longstanding questions on the evolutionary history of the *T. pallidum* complex and ultimately, the origin of syphilis.

We focused on sequencing and reconstructing the genome of the *T. pallidum* subsp. *endemicum* Iraq B strain (isolated in Iraq in 1951). We extracted and prepared DNA libraries using two tissue samples from Iraq B-infected laboratory rabbits. A targeted DNA capture was applied to exclude host genome DNA. Quantitative PCR with primers unique to *T. pallidum* TP0574 were used to estimate the proportion of *T. pallidum* DNA in the pre- and post-capture DNA libraries, and primers unique to the rabbit "cystic fibrosis conductance transmembrane regulator" gene were used to estimate the proportion of host DNA. As expected, the copy number of the TP0574 gene increased by 600-fold. With a high quality genome (average coverage of 15x for at least 80% of the genome), genetic characteristics of the Iraq B strain and its phylogenetic position within the *T. pallidum* complex has the potential to further our understanding of genetic variations and disease manifestation of treponemal infections.

National Science Foundation Graduate Research Fellowships Programs (Fellow ID: 2015183290); Department of Anthropology, Pennsylvania State University; National Institutes of Health (R01AI42143).

Bony labyrinth shape variation as a marker of prenatal stress and the maternal environment

DEVIN L. WARD¹, EMMA POMEROY², JOCELYN E. ROY¹, LAURA T. BUCK^{3,4}, JAY T. STOCK^{4,5}, MARY T. SILCOX⁶ and T. BENICE VIOLA¹

¹Department of Anthropology, University of Toronto, ²School of Natural Sciences and Psychology,

Liverpool John Moores University, ³Department of Anthropology, University of California, Davis, ⁴Department of Archaeology, University of Cambridge, ⁵Department of Anthropology, Western University, ⁶Department of Anthropology, University of Toronto, Scarborough

The bony labyrinth surrounds the organs and fluid of the inner ear, which are responsible for detecting sound and motion during life. It reaches adult morphology before birth and experiences limited subsequent remodeling. Labyrinthine shape variation may, however, reflect developmental instability related to the maternal gestational environment. While advances in computed tomographic (CT) technology provide the opportunity to visualize the labyrinth in three dimensions, its complex shape makes quantifying its form challenging. We apply Geometric Morphometrics (GMM) to assess within-group shape variability in the bony labyrinth of a model organism, the rat. We hypothesize that labyrinthine shape will differ between offspring of mothers fed a low protein and control diet during gestation. To test this, we collect shape data from cranial μ CT scans and process the resulting landmark data using GMM and principal component analysis. Plots of several principal components illustrate some separation between low-protein and control group rats, with significant overlap. Separation seems to be focused on the lateral semicircular canal, suggesting that the slowest-growing areas of the labyrinth are more susceptible to environmental perturbations during development. The preliminary results of this study indicate that maternal malnutrition may have a lasting morphological impact on the form of the bony labyrinth. This effect should be investigated further in human samples, where the extended period of in utero development and maternal gestational conditions are associated with the potential for many long-term health problems.

UoFT Pilot Grant to DLW; NSERC Discovery Grant to MTS; SSHRC Insight and Connaught New Researcher Grants to BV; Henry Sidgwick Research Fellowship to EP; ERC Grant 617627 to JTS.

Using R stats to teach about hominins and adorable primates

KERRY A. WARREN¹ and MARC KISSEL²

¹Human Evolution Research Institute, University of Cape Town, ²Anthropology Department, Appalachian State University

The R programming language, and associated packages, are used by many researchers in the fields of palaeoanthropology and primatology. Frequently, researchers use these tools to evaluate patterns in the natural world, which can, themselves, be taught to willing learners at some point in the future, when these patterns are more accepted or established. Here we propose creating tools, using a combination of

ABSTRACTS

machine learning, statistical, photographic and Shiny libraries, to both learn about the patterns visible in extant and fossil primates and hominins, as well as generate data on how humans perceive these patterns. We highlight one case study where students are both participating in the generation of data, while additionally learning about themes relevant to anthropology. The study program (titled "Aye know Aye'm pretty") allows for students to choose between photos of the faces of various primates, voting for the cutest photo (during which they learn about the relative primates through adorable facts) which are then ranked according to user selection. Using computer vision techniques, the programme "learns" which primate photos are more likely to be ranked as cuter than others. These techniques support previously held assumptions about relative "cuteness" for humans being concentrated in the orbital areas of the face. Here, not only is statistical data and analytics being generated about the perceived cuteness ranked by humans, but it is also a tool for education and environmental awareness for primates. We argue that similar programs may be designed with similar education and data generating outcomes.

This research is funded by the Centre of Excellence in Palaeosciences and the National Research Foundation of South Africa.

Breastfeeding and complementary feeding patterns in a rural Gambian population

JENNIFER WASHABAUGH^{1,2}, SOPHIE E. MOORE^{3,4}, NABEEL AFFARA⁵, DAVID B. DUNGER⁶, KEN K. ONG^{6,7}, ANDREW M. PRENTICE³ and ROBIN M. BERNSTEIN^{1,2}

¹Department of Anthropology, University of Colorado Boulder, ²Institute of Behavioral Science, University of Colorado Boulder, ³MRC Unit The Gambia, London School of Hygiene and Tropical Medicine, ⁴Department of Women and Children's Health, King's College London, ⁵Department of Pathology, University of Cambridge, ⁶Department of Paediatrics, University of Cambridge School of Clinical Medicine, ⁷MRC Epidemiology Unit, University of Cambridge School of Clinical Medicine

Sub-optimal feeding practices in infancy can contribute to growth faltering, through a complex cycle of infection and malnutrition. Here, we describe breastfeeding patterns and introduction of non-breast milk foods (NBMFs) during the first year of life in 203 rural Gambian mother-infant pairs, as part of the HERO-G (Hormonal and Epigenetic Regulators of Growth) study. We assess the predictive power of the age of introduction of NBMFs on infant growth outcomes, indexed by height-for-age (HAZ), weight-for-age (WAZ), and weight-for-height (WHZ) Z-scores at 1 and 2 years of age. All infant feeding data were collected from mothers every ten days using a dietary questionnaire. We calculated the average age of cessation of exclusive breastfeeding (EBF)

using 1) the first reported age of introduction of NBMF (5.4 months) and 2) after two consecutive NBMF reports (6.4 months). Over 99% of infants were still receiving breast milk by one year of age. Our models, which included season of infant birth, infant sex, maternal age, and maternal parity, did not identify any significant predictors of age of NBMF introduction. The earlier calculated age at NBMF introduction (5.4 months) was not significantly associated with any indices of infant growth. The later calculated age at NBMF introduction (6.4 months) was significantly positively correlated with HAZ ($P < 0.01$) and WAZ ($P < 0.01$) at one year of age. However, no associations were found with infant growth at 2 years of age. Further analyses are needed incorporating other potential effect modifiers, such as infant morbidity, before these findings can be fully interpreted.

Funded by the Bill and Melinda Gates Foundation (OPP1066932)

Presence of Xenoestrogens in the Hunter-Gatherer Diet of Mbendjele BaYaka from Republic of Congo

MICHAEL D. WASSERMAN^{1,2}, IRIS THOMPSON¹, EMILY CHESTER¹ and KARLINE JANMAAT^{3,4}

¹Department of Anthropology, Indiana University, ²Human Biology Program, Indiana University, ³Department of Primatology, Max Planck Institute for Evolutionary Anthropology, ⁴Institute for Biodiversity and Ecosystem Dynamics, University of Amsterdam

Xenoestrogens and other xenosteroids are understudied chemical components of non-human primate and human diets that have the putative capability to alter physiology and behavior via direct effects on rates of transcription and translation through binding with steroid hormone receptors and then steroid hormone response elements. As a result of these cellular mechanisms, xenoestrogens may influence non-human primate and human ecological interactions and evolutionary changes now and in the past. Therefore, we analyzed plant, fungi, and insect foods of Mbendjele BaYaka hunter-gatherers living in a forested environment in the Republic of Congo for estrogenic activity using estrogen receptor β transfection assays. Due to the increased effects of xenoestrogens on children compared to adults, we also investigated the foraging effort of Mbendjele BaYaka children on these foods. Based on an analysis of 21 dietary items making up 59.8% of children's dietary interactions, we found 14 items had no estrogenic activity detected, five items had low levels of estrogenic activity detected equivalent to 0-32 pmol estradiol, and two items had high levels of estrogenic activity equivalent to 32-800 pmol estradiol. The high activity items *Gnetum buchozianum* from the Gnetaceae plant family and the caterpillar *Gonimbrasia melanops* from the moth family Saturniidae accounted for 4.3% of the

dietary interactions of Mbendjele BaYaka children. Thus, our study provides evidence for the consumption of dietary xenoestrogens, including phytoestrogens, in a traditional hunter-gatherer society, indicating that humans likely began consuming estrogenic plants before the domestication of soy or other crops that contain estrogen mimics.

Use of Special Stains to Narrow Etiology in the Histopaleopathology of Anemia

LELIA WATAMANIUK

Anthropology, McMaster University

Lelia Watamaniuk

Department of Anthropology, McMaster University

Understanding anemia in the paleopathological record is complicated by its nature: a complex symptom of several pathological conditions, each with its own set of biological and cultural characteristics. Regardless of etiology, anemia causes skeletal changes via one pathophysiological process: marrow hypertrophy causing bone restructuring (e.g. the 'crew cut' anemic skull). Several classes of disease cause anemia: nutritional deficiency, chronic infection, hemoglobinopathy, hemolysis. Previously, it was not possible to identify its etiology without the presence of the cellular marrow. This pilot study demonstrates that the application of Prussian Blue Stain (aka Gomori Trichrome) and Turnbull's Blue Stain to histological samples allows the differentiation of those anemias that result in iron overload and those that do not. Variants of Thalassemia produce anemia and secondary iron overload, not present when iron is deficient. Excess iron can be incorporated into osteoid and deposited into mineralized bone at mineralization fronts. Histological samples ($n=45$) of ribs of individuals from the Greek site of Apollonia (5th-3rd Centuries BC), where macroscopic signs of anemia of unknown etiology were present, were examined via light microscopy with both Prussian and Turnbull's Blue stains ($n=90$ specimens total) to characterize the presence or absence of iron deposits within the hard tissue. These were compared to biopsy samples of known diagnosis from Hôpital St Luc, Montreal, QC ($n=15$). The results are presented here. The ability to eliminate a nutritional deficiency as the cause of anemic change has strong implications for understanding food related behaviours of past peoples.

This research was self funded.

ABSTRACTS

Finding Biological Markers of Mobility in Late Prehistoric Portugal and Spain: A Stable and Radiogenic Isotope Approach

ANNA J. WATERMAN¹, ROBERT H. TYKOT² and DAVID W. PEATE³

¹Department of Natural and Applied Sciences, Mount Mercy University, ²Department of Anthropology, University of South Florida, ³Department of Earth and Environmental Sciences, University of Iowa

The archaeological record provides evidence of large population centers forming, flourishing, and suddenly declining in many parts of the Iberian Peninsula during late Prehistory. Although scholars assume that population migration and long-distance trade played an important role in these regional developments, little is known about specific patterns of people moving from rural agricultural communities to large-scale aggregation centers and how these movements played into the transition to intensive agriculture and year-round sedentism. In this study, we outline results of research we have completed over the last decade that identifies migrants via radiogenic isotope ratios (⁸⁷Sr/⁸⁶Sr) in burials near major late prehistoric Iberian Peninsula aggregation centers, and then use stable isotope data ($\delta^{15}\text{N}$, $\delta^{13}\text{Cap}$, $\delta^{13}\text{Cco}$ and $\delta^{18}\text{O}$) to compare dietary patterns between migrants and the local populations. The results of this analysis demonstrate that the number of migrant individuals at the surveyed sites is quite variable (between 5 and 30%). When isotopic markers of diet are examined, most migrants do not show marked differences from local populations. However, in several cases individuals do exhibit distinct dietary patterns that may relate to migrant status. The results of this study are compared with other published data focused on human populations in late prehistoric Portugal and Spain to assess interregional dietary and mobility trends. Directions for future research are discussed.

Absent to Limited Breastfeeding in 19th Century Dairy Farmers from the Netherlands

ANDREA L. WATERS-RIST^{1,2} and MENNO L.P. HOOGLAND²

¹Anthropology, University of Western Ontario, ²Faculty of Archaeology, Leiden University

Most stable isotope studies of breastfeeding and weaning in past populations find infants consumed breastmilk well past their first year of life. Stable nitrogen ($\delta^{15}\text{N}$) and carbon ($\delta^{13}\text{C}$) analysis of a large sample (n=277) of rural dairy farmers from the 19th century Dutch village, Middenbeemster, offer insight into their infant feeding practices. Archival identification permits analyses of nonadult diet according to sex and year-of-death. Fetal (n=27) and reproductively-aged female (n=47) baseline isotope means are used in combination with an intra-long-bone

sampling strategy (recent metaphyseal collagen vs. older diaphyseal collagen) to assign feeding status to 55 nonadults from one month to six years of age. In the youngest infants (1-11 months), only 10 out of 20 have evidence for breastfeeding, with weaning commencing as early as one to two months of age. In older infants (12-35 months), 3 out of 13 have high $\delta^{15}\text{N}$ values that could reflect a past period of breastfeeding or could be due to non-dietary factors (tissue catabolism). In the few 3-6-year-olds with high $\delta^{15}\text{N}$ (n=5/22) the likely cause is non-dietary. There are no statistically significant differences in isotopic ratios or feeding patterns between girls and boys in any age group nor are there temporal trends in nonadult isotopic data. We argue that infants were fed cow's milk at a very young age, sometimes from birth, with nursing episodes infrequent and the weaning process rapid. This is a rare finding for a pre-modern population that calls for future research on health and demography.

A portion of this research was funded by a Marie Curie International Incoming Fellowship (#302801) held by AWR.

The Role of Black Feminist Theory in Critiquing Scientific Practices and Concepts of Race

RACHEL J. WATKINS

Anthropology, American University

Bioanthropological studies of anatomical collections are foundational to scientific conceptualizations of race that remain at the center of discussions about human genetics, health and identity. However, they rarely factor into these discussions as a historical or contemporary point of reference. Examining the current status of research on anatomical collections offers insight into how race persists as a lens through which to understand human biological variation in academic and public spheres. Specifically, research on anatomical collections reflects biological anthropology's continued investment in the production of scientific knowledge without a critical examination of the social relations in which knowledge is produced.

This paper uses Black feminist theory to shed light on how these investments and social relations work to: 1) naturalize the epistemological underpinnings of the discipline built upon notions of racial hierarchy; 2) naturalize the position of people of color (POC) in the field as research subjects versus knowledge producers; and thus, 3) naturalize the underrepresentation of POC in the field. Sylvia Wynter's notion of biocentricity is used to illustrate the racially determined scientific and social order maintained through our discipline's critique of scientific racism without attending to structural inequalities within the field. Hortense Spillers' body/flesh distinction is used

to deconstruct the ways that we attend to the agency of the people whose remains we study - while space for racialized minorities to participate in the research process remains inadequate.

Changes in Male Grooming Networks Associated With Permanent Fission of a Chimpanzee Community at Ngogo

DAVID P. WATTS

Anthropology, Yale University

New chimpanzee (*Pan troglodytes*) communities result from permanent fissions, which involve dissolution of strong male social bonds and are rare. The extremely large Ngogo community has recently undergone a permanent fission, providing a unique opportunity to analyze underlying social and demographic causal factors. Because theoretical models invoke constraints on grooming networks as one such factor, I examined changes in male grooming cliques, determined when the grooming network was partitioned non-randomly, and tested the hypothesis that grooming networks predicted future community membership.

I applied UCINET v6.629 to annual data sets (1995-2008) on male grooming to generate multiple network measures, including co-participation in cliques. I used the E-I permutation test in UCINET to determine when the grooming network was non-randomly partitioned into subgroups comprising males of the two new communities and the LRQAP procedure to determine whether and when positions in grooming networks predicted community membership.

A single grooming network existed until 2017, but co-participation in cliques by western males dropped sharply by 2015, when hostilities between the nascent daughter groups started, and the grooming network showed significantly non-random partitioning then ($p < 0.01$). Grooming ties were independent of subsequent community membership as late as 2008, but significantly predicted membership from 2009 on ($p < 0.01$).

These results support the argument that chimpanzee community stability depends partly on the cohesion of male grooming networks, although demographic and other social changes have contributed importantly to the Ngogo fission.

NSF SBR-9253590, BCS-0215622; L.S.B. Leakey Foundation; National Geographic Society; Yale University

Variation in Sexual Dimorphism Due to Climatic Stress

MARIA E. FEILER and ERIN B. WAXENBAUM

Anthropology, Northwestern University

Skeletal sexual dimorphism presents itself in humans through the anatomical shape of the cranium and pelvis. Some physical

ABSTRACTS

anthropologists maintain that climate could have a significant effect on sexual dimorphism. Despite ongoing research pertaining to climatic effects on soft tissue or size dimorphism, little to no research has looked at how climate affects nonmetric skeletal indicators of sex.

To further understand the plasticity of the human skeleton, we performed a cross-population comparative study of standard nonmetric sex indicators of the cranium and pelvis. The populations examined - a Native Alaskan archaeological sample (n=104) and a component of the Terry Black collection (n=99) - represent different degrees of climatic stress. These sex-balanced groups were compared for statistical significance through the Tukey-Kramer method and Greene's t-test to determine whether they differed in degree of sexual dimorphism within and between samples. The results of this study indicate that the relationship between climate and sexual dimorphism is more complicated than initially understood. There appears to be a shift to a hyperfemale morphotype in the mastoid process and nuchal crest, as well as less dimorphism in the mental eminence and orbital ridge in populations experiencing more climatic stress. However, potential confounding factors suggest that more research is required to untangle the complex relationship between climate and the human skeleton.

This research opens discussions of how life history factors, including climate, nutrition, stress, and disease, could affect standard forensic and archaeological procedures and potentially contribute to the production of more accurate skeletal assessment in the future.

Noninvasive genomics of Gombe chimpanzees: evaluating methods for wild primate population genomics

TIMOTHY H. WEBSTER^{1,2}, ANDREW T. OZGA³, IAN C. GILBY^{4,5}, MELISSA A. WILSON SAYRES^{2,3}, YINGYING LI⁶, BEATRICE H. HAHN⁶, REBECCA S. NOCKERTS⁷, MICHAEL A. WILSON^{7,8,9}, ANNE E. PUSEY¹⁰ and ANNE C. STONE^{3,4,5}

¹Department of Anthropology, University of Utah, ²School of Life Sciences, Arizona State University, ³Center for Evolution and Medicine, Arizona State University, ⁴Institute of Human Origins, Arizona State University, ⁵School of Human Evolution and Social Change, Arizona State University, ⁶Departments of Medicine and Microbiology, University of Pennsylvania, ⁷Department of Anthropology, University of Minnesota, ⁸Department of Ecology, Evolution, and Behavior, University of Minnesota, ⁹Institute on the Environment, University of Minnesota, ¹⁰Department of Evolutionary Anthropology, Duke University

While studies of individual DNA markers have improved our understanding of behavior, ecology, and evolution, recent advances in sequencing make it possible to incorporate information from

across the entire genome, giving unprecedented insight into the population history of non-model species. However, for many species, it is impossible to legally, ethically, or logistically to obtain high quality tissue samples required for genomic analyses. In this study, we evaluate the success of several sources of host DNA and capture methods in generating genome-scale data in wild chimpanzees (*Pan troglodytes schweinfurthii*) from Gombe National Park, Tanzania. We extracted and captured endogenous DNA in feces, dental calculus, dentin, and urine using both whole-genome capture and targeted exome capture. We found that urine harbors significantly more endogenous DNA (mean = 96.5%) than other sources (feces mean = 44.9%; calculus mean = 38.3%; ANOVA: $F(3,22) = 146.7$; $p = 1.08 \times 10^{-14}$). Further, we found that while whole-genome capture is possible, it is not cost effective in feces and calculus because of the high abundance of microbial DNA. Exome sequencing, on the other hand, led to 20-fold enrichment of coding targets compared to whole-genome capture in feces. However, compared to feces, exome capture from urine was far more successful and provided more complete coverage of the coding region of the chimpanzee genome (urine: 94.3% of coding sites were callable; feces: 14.9% of coding sites were callable). We discuss the utility of targeted capture and the promise of urine for wild primate genomics.

Effect of Reproduction on Javan Slow Loris Mother's Activity Budget and Ranging Behavior

ARIANA WELDON^{1,2}, STEPHANIE POINDEXTER^{1,2,4}, MARCO CAMPERA^{1,2}, MUHAMMAD A. IMRON^{2,3} and K.A.I. NEKARIS^{1,2}

¹Department of Anthropology, Oxford Brookes University, ²Little Fireface Project, Java, Indonesia, ³Faculty of Forestry, Universitas Gadjah Mada (UGM), Yogyakarta, Indonesia, ⁴Anthropology Department, Boston University

Reproduction is an energetically taxing yet crucial process for all species survival. Prior research measuring behavioral changes throughout primate reproductive stages have focused on species with distinct reproductive states or seasonal reproduction. Slow lorises (*Nycticebus* spp.) demonstrate slow reproduction cycles relative to their body size and show little evidence of birth seasonality in the wild or captivity. Due to their unusual reproductive cycle, little is known about the effect each reproductive stage may have on the behavior of slow loris mothers.

Using a six-year data set focused on the Javan slow loris (*N. javanicus*) comprised of nine females and 41 live births between 2012 and 2018, we sought to identify any potential behavioral and ranging changes females may exhibit at varying reproductive stages. We defined four reproductive stages, (1) pregnant, (2) lactating,

(3) overlapping, where mothers were lactating and pregnant, and (4) absent, where females did not fit into the previous categories. Our results suggest that social activity are influenced by reproductive stage ($p = 0.020$) and significantly decrease when pregnant compared to absent periods ($p = 0.025$). Home ranges also significantly differed ($p = 0.03$) in the period prior to birth (mean: 5.0 ha, min-max: 1.7-9.9 ha) and non-reproductive periods (mean: 8.5 ha, min-max: 5.2-19.2 ha). Similar to other primates with clear reproductive periods or seasonality, slow loris behavior and home range size are affected and likely mitigating the demands placed on mothers during their reproductive cycle.

PTES, Disney Worldwide Conservation Fund, Margot Marsh Biodiversity Foundation, MbZ Species Conservation Fund, National Geographic, and Cleveland, Phoenix, Omaha, Columbus and Augsburg Zoo.

Palaeoproteomic analysis of Early Pleistocene *Gigantopithecus blacki*

FRIDO WELKER^{1,2}, JAZMIN RAMOS-MADRIGAL¹, WEI WANG³, MARTIN KUHLWILM⁴, MARC DE MANUEL MONTERO⁴, FABRICE DEMETER^{1,5}, CARLES LALUEZA-FOX⁴, TOMAS MARQUES-BONET^{4,6,7}, JESPER V. OLSEN⁸ and ENRICO CAPPELLINI¹

¹Natural History Museum of Denmark, University of Copenhagen, ²Department of Human Evolution, Max-Planck-Institute for Evolutionary Anthropology, ³Anthropology Museum of Guangxi, ⁴Institute of Evolutionary Biology, UPF-CSIC, ⁵National Natural History Museum, UMR7206 Anthropologie Évolutive, ⁶Catalan Institution of Research and Advanced Studies, ICREA, ⁷Centre for Genomic Regulation, Barcelona Institute of Science and Technology, ⁸Novo Nordisk Foundation Center for Protein Research, University of Copenhagen

Gigantopithecus blacki is a giant hominid known from a few subtropical and tropical localities dated to between 2.0 and 0.3 Ma in southern China and northern Vietnam. The first remains of the species were discovered and identified by von Koenigswald in a Hong Kong drugstore where they were sold as "dragon teeth". Knowledge on the species remains limited to relatively large amounts of teeth and four mandibles. Nevertheless, it is one of the few, if not the only, extinct non-hominin hominid for which Pleistocene fossil specimens are available. Its relationships to or within Hominidae remains tentative due to the paucity of postcranial *Gigantopithecus* remains, and the primitive status of most shared dental characteristics between *Gigantopithecus* and other extinct (early) hominids.

To clarify the phylogenetic status of *Gigantopithecus blacki*, we sampled a *Gigantopithecus* molar from Chuifeng Cave, China, for palaeoproteomic analysis. The site is dated by ESR, U-series and paleomagnetic methods to approximately 1.38-1.92 Ma. We

ABSTRACTS

attempted proteomic analysis of both dentine and enamel samples. The endogenous enamel proteome component shows the preservation of heavily degraded proteins, with a degree of fragmentation and modification not observed in ancient proteomes before. Phylogenetic analysis of these protein sequences allows us to determine conclusively that *Gigantopithecus* represents an early diverging sister lineage of extant pongids. Our analysis provides the first molecular sequence data for an extinct hominid outside the genus *Homo*. We thereby simultaneously demonstrate that ancient proteins deriving from skeletal tissues survive deep into the Pleistocene at subtropical sites.

The authors acknowledge the financial support of the VILLUM Fonden (#17649) and MSCA Fellowship (#795569).

Ancestral climatic histories and their influence on interindividual variation in cold-induced vasodilation responses

KALI A. WEST¹ and BRUCE FLOYD²

¹Anthropology, Binghamton University,

²Anthropology, University of Auckland

Cold-induced vasodilation is argued to be a protective response designed to prevent cold injury and preserve limb function in the presence of freezing temperatures. Variation among individuals in response to cold stress are likely influenced by population genetics reflecting ancestral climatic histories, developmental environments and acclimatization. Previous literature acknowledges but has yet to explain the presence of high levels of variation in CIVD responses. This study evaluates variation in CIVD response using the average difference in the skin and water temperatures recorded every two second for 30 minutes in 8° C water. Individual responses are judged relative to their rank-order diversity in ancestral climatic backgrounds. Using self-reported data of geographic origins of grandparents and great-grandparents, participants (n = 176) were grouped into three climate categories based upon average temperature of the coldest month during 1931-1960 gathered from World Bank Climate Change Knowledge Portal records. The 18 participants in the "Diverse" category represented individuals whose ancestors came from both relatively cool and warm environments (<5° C or >12° C). Those 66 participants in the "Cool" category and the 93 participants from the "Mild" category report ancestors from locations below 5° C or above 12° C, respectively. Although the "Diverse" group was hypothesized to exhibit more variation, this group was the least variable (CV = 0.41) with the highest average response (x = 2.66) as compared to the "Cool" (CV = 0.46; x = 2.50) and the "Mild" (CV = 0.54; x = 1.99) groups, respectively.

Team-based learning in an introductory bio anth course (or, why I will never go back to just lecturing!)

JESSICA L. WESTIN

Math/Science Department, Kirkwood Community College

Traditional lecture, wherein the professor stands at a podium and exposit on the subject of the day, not pausing for questions or to involve students, is (hopefully) becoming an artifact of the past. Evidence suggests that greater student engagement and information retention result from a more active-learning classroom setting. Many styles of active learning exist, including team-based learning (TBL), a method of "flipped classroom" teaching in which students prepare for class by completing assigned readings and watching prepared videos before arriving in the classroom. Class time is then spent clarifying course concepts and completing hands-on activities to further aid learning. To incentivize students to complete the preparatory work, a quiz is given at the start of the class period. A hallmark of the TBL method is that students are placed into teams for the duration of the semester. Students complete assigned quizzes both individually and with their team, and they submit classroom assignments as a group. This poster will describe the method as implemented in an introductory biological anthropology course (Human Evolution) at Kirkwood Community College in Cedar Rapids, Iowa. A discussion of student success before and after the transition from a lecture-heavy version of the course to TBL will be presented, as well as survey data from students regarding their experiences with the teaching method. Additionally, the instructor's perspective on the benefits of TBL for classroom and time management will be discussed.

This research was supported by the Office of Institutional Research and the Math/Science Department at Kirkwood Community College.

Male-Female Friendships in Kinda Baboons

ANNA H. WEYHER and JASON M. KAMILAR

Anthropology, University of Massachusetts Amherst

Male-female relationships are associated with several benefits in social species, such as baboons. In addition to reproduction, previous studies have found that these "friendships" can reduce predation risk, harassment from other individuals, and increase longevity. Importantly, these benefits can vary across species and even among populations. Here, we quantified several aspects of male-female relationships in a group of habituated Kinda baboons at Kasanka National Park, Zambia. We collected data over a 36 month period to measure the amount of grooming between male-female dyads, time

spent in proximity, roles of each partner in initiation and maintenance of friendships, and the length and strength of relationships. We used proximity and grooming data to create a sociality index that measured the strength of relationships between males and females. We found that males groomed female friends twice as often as females groomed the male. In addition, males usually initiate grooming and the grooming dyad is typically terminated by the female. These dyadic relationships remained consistent across all female reproductive states. The average duration for a friendship was about 2.5 years and females remained with the same male throughout the study period unless the male died or emigrated out of the group. Our results show that males play a more active role in initiating and maintaining social bonds than females and illustrate the unique male-female relationships in Kinda baboons compared to other baboon populations.

The MZ SNP: A Xq27.2 region associated with prostate cancer is also associated with monozygotic twinning

KILIAN KELLY¹, SONYA BASHAR², KATHRYN B.H. CLANCY³, HONG HUANG⁴ and LORENA MADRIGAL¹

¹Anthropology, University of South Florida,

²College of Medicine, University of South Florida,

³Anthropology, University of Illinois, Urbana-

Champaign, ⁴School of Communication, University of South Florida

Biological anthropologists are interested in the genetic bases of twinning because differential fertility may be a way by which natural selection acts. Work on population-twinning differences assumes that the twinning type that differs among populations is dizygotic twinning (DZ). This idea stems from the view that monozygotic twinning (MZ) is a teratogenic event whose frequency is equal across human populations. However, there are reports of human genealogies with large concentrations of MZ twins, inherited via the father's side (Harvey, Huntley, & Smith, 1977). We (Huang, Clancy, Kelly, & Madrigal, 2018) have shown that a region in the Xq27.2 region is significantly associated with MZ twinning and have obtained 100s of human genealogies with the purpose of testing a hypothetical form of inheritance of MZ twinning. As of the writing of this abstract, we have finished cataloguing one of two folders, which included 118 pedigrees of families of twins including unlike-sex pairs and same-sex pair twins (SST). Of the 118 pedigrees, we obtained 36 SST pedigrees, to which we added 10 MZ pedigrees from (Harvey et al., 1977), and one MZ pedigree from (Hamamy, Ajlouni, & Ajlouni, 2004) for a sample size of n=47. Our pedigrees range from 2 to 9 generations. We did not detect a significant difference in male-female SST (Fisher's exact test $X^2 = 0.0829$). As of the

ABSTRACTS

time of this writing, we have been able to explain 100% of these 47 SST pedigrees as following a novel type of inheritance, in several families inherited via the father's side.

A sample of HbAS African American football players differs significantly from a control African American football team in its mean weight and BMI. Is HbAS a benign condition in football?

DEANDRE WHITE¹, CHRISTINA M. BALENTINE², CARROLL FLANSBURG³, RYAN W. GRIEGER⁵, JUSTIN LUND⁴, MICHELLE CIAMBELLA⁵, EDUARDO GONZALEZ⁶, ERIC CORIS^{1,7}, ANNE C. STONE⁸ and LORENA MADRIGAL⁹

¹Anthropology, University of South Florida, ²School of Human Evolution and Social Change, Arizona State University, ³Human Genetics, Geisinger Health System, ⁴School of Human Evolution and Social Change, Arizona State University, ⁵School of Life Sciences, Arizona State University, ⁶College of Medicine, University of South Florida, ⁷College of Medicine, University of South Florida, ⁸School of Human Evolution and Social Change Center for Evolution and Medicine, Arizona State University, ⁹Anthropology, University of South Florida

There have been multiple deaths and more injuries of mostly African American (AA) football players with sickle cell trait (SCT), the heterozygous state of sickle cell anemia. To explain what factors contribute to their risk levels when playing, a college SCT sample of 29 players (all of whom self-identified as African-American) was compared to a control group of 88 players (from FAMU, a Historically Black University) by weight, height and football-team position types. The control players were significantly heavier than the SCT player ($p=0.0144$). The majority of SCT players occupied non-linemen positions whereas the control players mainly occupied the opposite (Fisher's exact test = 0.0245). Linemen positions require a larger BMI than do non-linemen positions. Within the SCT sample, all linemen carried the BCL11A SNP, which has been associated with higher levels of fetal hemoglobin (HbF) in previous studies. Players with BCL11A had a significantly higher BMI compared to those without it ($p=0.04$). These results may suggest that SCT linemen players were able to play in these positions because they had higher levels of HbF. Although SCT is due to a single Mendelian mutation, its severity and clinical manifestations are the result of polygenic interactions, including those that impact HbF, which contradict a simple Mendelian view. Our team incorporates complex genetic analyses and critical bio-cultural approaches, where we ask why the deaths of these healthy, mostly AA young men remain unexplained. Results oppose former conclusions that the condition and elevated risk are benign and inexplicable (O'Connor et al, 2012).

Funded by a Graduate Student Grant of the NCAA given to Carroll Flansburg while attending USF.

From flesh to mesh: Bodies as maps in 3D GIS

J. ALYSSA WHITE, JOHN POUNCETT and RICK SCHULTING

School of Archaeology, University of Oxford

Spatial patterning is an integral part of palaeopathological analysis of skeletal tissue, and, yet, lesions are typically 'mapped' onto a 2D model of the body on an *ad hoc* basis. This mapping is not done in a way that facilitates data accumulation and comparison between studies.

A freely available and licensed model of the human body, composed of a triangular mesh with a 3D coordinate system, was used in GIS to record, query, and analytically investigate spatial data on human skeletal tissue. Data were incorporated into the model in a variety of ways. The skeletal elements of the model were subdivided, allowing for more precise recording of the preservation of fragmentary remains. Associated 3D features were created to represent and investigate patterns of skeletal pathology, particularly traumatic injuries. Skeletons and associated features were attributed with relevant information, such as sex, age, cemetery location, and time period. Once the data were put into a geospatial format, they could be rapidly visualised and queried in order to explore patterns by categories of interest. This method allows for the compilation and exploration of data more quickly and more systematically than is currently possible.

Data on traumatic injuries and skeletal preservation from prehistoric hunter-gatherers and early agriculturalist from the Japanese archipelago were used to demonstrate the utility of treating the body as a 3D map. Of particular interest outside of archaeology, this method has potential for demonstrating patterns of traumatic injuries in a forensic context to a non-expert audience.

Supporting Agencies: Clarendon Fund; Great Britain Sasakawa Foundation; Merton College; Meyerstein Fund; School of Archaeology, Oxford; Sasakawa Fund, Oriental Institute, Oxford

Meta-analysis identifies 48 SNPs with multiple independent effects on human facial features

JULIE D. WHITE¹, JASMIEN ROOSENBOOM², KARLIJNE INDENCLIEF^{3,4}, JAAVED MOHAMMED⁵, JIARUI LI^{3,4}, ALEJANDRA ORTEGA-CASTRILLON^{3,4}, TOMEK SWIGUT⁵, MYOUNG KEUN LEE², TOMAS GONZALEZ-ZARZAR¹, ARSLAN A. ZAIDI⁶, JOHN R. SHAFFER⁷, ELEANOR FEINGOLD^{7,8}, STEPHEN RICHMOND⁹, RYAN J. ELLER¹⁰, SUSAN WALSH¹⁰, MARY L. MARAZITA^{2,8}, JOANNA WYSOCKA^{11,5}, SETH M. WEINBERG^{12,7}, PETER CLAES^{3,4} and MARK D. SHRIVER¹

¹Department of Anthropology, Pennsylvania State University, ²Center for Craniofacial and Dental Genetics, Department of Oral Biology, University of Pittsburgh, ³Department of Electrical Engineering,

ESAT/PSI, KU Leuven, ⁴Medical Imaging Research Center, MIRC, UZ Leuven, ⁵Department of Chemical and Systems Biology, Stanford University School of Medicine, ⁶Department of Biology, Pennsylvania State University, ⁷Department of Human Genetics, University of Pittsburgh, ⁸Department of Biostatistics, University of Pittsburgh, ⁹Dental Health and Biological Sciences, College of Medicine, University of Wales, ¹⁰Department of Biology, Indiana University-Purdue University Indianapolis, ¹¹Department of Developmental Biology, Stanford University School of Medicine, ¹²Department of Anthropology, University of Pittsburgh

The genetic factors that have shaped contemporary facial features are unknown and likely complex. As with all complex traits, it is probable that the genetic mechanisms involved have both singular and concerted effects. We performed a meta-analysis GWAS with the imputed genetic data and 3D facial photographs of two large cohorts of European ancestry ($N_{US} = 4,066$; $N_{UK} = 3,566$). We identified 213 genomic regions significantly associated with facial shape with symmetric effects in the US and UK datasets. Of these regions, 48 significantly affect multiple parts of the face (e.g. both the forehead and chin), suggesting that some of the SNPs identified have pleiotropic impacts on facial phenotypes. Gene Ontology of the 161 genes within 500 kb of these SNPs highlights functions in embryo development, skeletal development, and morphogenesis. 36 (22.36%) of the nearby genes are also transcription factors, including *PAX3* and *TBX15*. In comparison, the 165 SNPs without multiple facial effects are collectively within 500 kb of 835 genes, of which 100 (11.97%) are identified as being transcription factors. A comparison of these two proportions has a z-score of 3.5 and a p-value of 0.0002, supporting the hypothesis of an enrichment in the association of transcription factors with pleiotropic facial SNPs compared to single-effect SNPs. This work assists us in understanding the complex effects of single SNPs on different parts of the face, an essential step forward in understanding the evolutionary processes and current genetic mechanisms regulating human facial variation.

Classifying the Middle Pleistocene hominins: Testing taxonomic hypotheses using supraorbital morphology

SUZANNA WHITE¹, CHRISTOPHE SOLIGO¹, MATT POPE² and SIMON HILLSON²

¹Department of Anthropology, University College London, ²Institute of Archaeology, University College London

The taxonomy of Middle Pleistocene hominins (MPH; sometimes classified as *Homo heidelbergensis*) is highly debated. This study tested four taxonomic hypotheses taken from the literature: that MPH do not represent a valid species and members should be classified

ABSTRACTS

within *Homo sapiens*, *Homo neanderthalensis*, and *Homo erectus*; that MPH represent a single, monotypic species; that MPH represent a single, polytypic species; and that MPH represent separate, geographically-defined species (i.e. *Homo heidelbergensis sensu stricto* and *Homo rhodesiensis*).

Geometric morphometric methods were used to record the morphology of the supraorbital region using 230 3D landmarks and semilandmarks. These were placed on a sample of 710 specimens of different species and subspecies within *Gorilla*, *Pan*, *Papio*, *Macaca*, *Homo*, *Australopithecus*, and *Paranthropus*, including 13 MPH (Bodo, Kabwe, Saldanha, Florisbad, Zuttiyeh, Narmada, Maba, Dali, Petralona, Ceprano, Arago 21, Sima de los Huesos 5, and Steinheim). The four hypotheses were tested by comparing variation using Procrustes distances, and by assessing morphological distinctiveness through the application of discriminant analysis to principal components.

Results indicated that none of the four hypotheses were fully substantiated by the recorded pattern of supraorbital morphological variation in MPH. While the results support the conclusion that the 13 MPH include representatives of different species, it also suggests that these species do not map on to simple geographic boundaries. Instead, it is suggested that the MPH group studied here incorporates a distinct Middle Pleistocene species along with specimens that may be best included within *Homo sapiens* or *Homo neanderthalensis*, and potentially another hominin group.

This research was supported by the London Arts and Humanities Partnership

An examination of musculoskeletal markers to analyze activity levels of a documented modern population using the Coimbra method

EMILIE L. WIEDENMEYER, M. KATE SPRADLEY and NICHOLAS P. HERRMANN

Anthropology, Texas State University

Knowledge of a deceased individual's previous activity patterns can provide vital information for a biological profile. Activity levels can be investigated through the examination of activity-induced musculoskeletal markers in enthesal sites. Although studies have analyzed activity and occupation in bioarchaeological populations, few have evaluated them in modern populations.

This study examines a documented modern skeletal population at the Forensic Anthropology Center at Texas State University (N=54, male=36, female=18) and uses the bioarchaeological Coimbra method (2013) to analyze the enthesal sites to identify variables affecting activity levels. The study scored the enthesal changes on both upper arms of each individual based on the robusticity and prevalence of the changes to

their enthesal sites. After analyzing the scores and correlating them to frequencies of outside variables (sex, age, ancestry, occupation, and socio-economic status), the results showed patterns suggesting age had a considerable effect on the scores. The results also showed that certain enthesal sites such as the subscapularis attachment site, and features such as bone formation or erosion, exhibited a higher frequency of enthesal changes potentially relating to activity and age.

These findings suggest that modern skeletal populations can potentially be analyzed with a bioarchaeological method, but the results have several confounding variables that must be addressed, including possible unreliable self-reported data and secular trends in activity levels that can affect occupational activity markers. By testing the Coimbra method on a modern population, the results also showed steps necessary to improve its accuracy for future applications in bioarchaeology and potentially forensic anthropology.

Conditional dispersal and its effects on kin cooperation in female *Colobus vellerosus*

EVA C. WIKBERG¹, NELSON TING^{2,3} and PASCALE SICOTTE⁴

¹Department of Anthropology, University of Texas at San Antonio, ²Department of Anthropology, University of Oregon, ³Institute of Ecology and Evolution, University of Oregon, ⁴Department of Anthropology and Archaeology, University of Calgary

Despite a growing number of studies reporting conditional dispersal, it is not clear how this dispersal pattern affects the distribution of kin and the occurrence of cooperation. To further our understanding of this topic, we focused on the Boabeng-Fiema black-and-white colobus, in which some females and all males disperse from their natal group. We collected demographic and behavioral data during one year from eight groups. We genotyped animals at 17 short tandem repeat loci to be able to calculate dyadic estimated relatedness values. As predicted in a population with male-biased dispersal, females but not males were more closely related within than between groups (permutation test, F: N=62, $\bar{X}R=0.16$, 95%CI: 0.07–0.14; M: N=10, $\bar{X}R=0.24$, 95%CI: 0.04–0.32). However, it was only in one of three multi-male groups that females were more closely related than males residing in the same group. The strength of female grooming relationships was affected by kinship (GLMM N=466 dyads, coefficient estimate=0.48, 95%CI: 0.25–0.70) and time spent co-resident (coefficient estimate=0.32, 95%CI: 0.07–0.57). In groups with recent female immigrants, time spent co-resident was more important than kinship in structuring relationships. Strong grooming relationships, regardless of kinship, predicted cooperative home

range defense (GLMM, N=446 dyads, grooming coefficient estimate=0.10, 95%CI:0.03–0.17). Thus, the links between dispersal patterns, access to kin, and cooperation should be reconsidered in future models of the evolution of social structure.

Funding: Alberta Innovates, American Society of Primatologists, International Primatological Society, Leakey Foundation, Natural Sciences and Engineering Research Council of Canada, Sweden-America Foundation, Wenner-Gren Foundation, and the University of Calgary

The Aetiology of Enthesal Changes - Insights from the Biomedical Literature

CYNTHIA A. WILCZAK¹, CHARLOTTE Y. HENDERSON², VALENTINA MARIOTTI^{3,4} and SÉBASTIEN VILLOTTE⁵

¹Anthropology, San Francisco State University, San Francisco, USA, ²CIAS – Research Centre for Anthropology and Health, Department of Life Sciences, University of Coimbra, Coimbra, Portugal, ³Laboratorio di Bioarcheologia ed Osteologia Forense – Antropologia, Dipartimento di Scienze Biologiche, Geologiche e Ambientali- Alma Mater Studiorum Università di Bologna, Bologna, Italy, ⁴CNRS, EFS, ADES, Aix Marseille Université, Marseille, France, ⁵CNRS, UMR 5199 PACEA, Université de Bordeaux, Pessac cedex, France

Advances in enthesal-related tissue imaging using ultrasonography (US), power doppler (PD), magnetic resonance imaging; and quantitative CT scanning have led to an effusion of studies describing features associated with enthesitis/enthesopathies. Many of the findings are relevant to bioarchaeological studies of enthesal changes (ECs). The "Delphi process" provides international consensus definitions for US visualized components of enthesitis that largely correspond to the feature definitions of the Coimbra method. Clinical studies confirm many of the results from skeletal analysis including the higher prevalence of enthesiophytes versus erosions; the increase in EC prevalence with age and BMI; and differences in specific EC features by enthesitis, e.g., the high frequency of cysts and erosions at the rotator cuff. PD findings suggest inflammation proceeds or even triggers structural changes whether the aetiology is traumatic, degenerative or disease-related. While the pattern and types of changes at the entheses do not, for the most part, discriminate among the various aetiologies, in enthesitis of psorotic arthritis and spondyloarthropathies the inflammation persists for longer and is more likely at the bony enthesitis instead of within the tendon and the osseous structural changes are more severe on average. Given these observations, the degree of fine and macro-porosity as measures of vascular infiltration have some potential for discriminating disease-related from mechanical or degenerative aetiologies in the skeleton. Among other relevant findings are the frequency of subclinical ECs;

ABSTRACTS

increased support for ECs induced by physical activity; stronger associations between rotator cuff tears and cortical irregularities; and evidence of concomitant bone marrow changes.

Nasofacial skeletal differentiation among Equatorial Africans, Europeans and African-Americans

ALEXIS S. WILLIAMS¹, ADAM D. FOSTER² and ROBERT G. FRANCISCUS¹

¹Department of Anthropology, University of Iowa, ²Department of Anatomy, School of Osteopathic Medicine, Campbell University

Biological anthropologists have long highlighted nasofacial differences between African and African-derived populations, compared to European populations – an interest driven by U.S. centered forensic applications, and research focused on nasal climatic adaptation. A tendency in these endeavors has been to explicitly, or implicitly, regard African-American skeletal samples as proxies for Equatorial Africans. There is, however, abundant historical and genetic evidence to document that African-Americans reflect varying levels of European admixture over the past 400 years. Here, we evaluate the extent to which European admixture (and possible genetic drift) in African-Americans has resulted in nasofacial divergence from the ancestral Equatorial African phenotype. We used 18 linear nasofacial measurements collected on Equatorial Western African crania (n=120), and on Western Europeans (n=112) and Central Europeans (n=108) with approximately equal sex composition to create validated discriminant function (DF) predictive equations that yielded correct classification into African vs. European groups ranging from 91.4% - 100% (Mean=98.08%). We collected identical measurements on Terry Collection (n=122) and Hamann-Todd (n=131) African-American crania (also with approximately equal sex composition) and then used the Equatorial African vs. European DF equations to predict into which group individuals in the African-American samples were assigned. The number of African-Americans classified as European ranged from 19.4% in Terry Collection males when using Central Europeans, to 47.8% in Hamann-Todd males when using Central Europeans, and averaged between 26.2% - 29.92% across all possible DF inputs including sex – values that are similar to the average European admixture estimates in African-Americans derived from recent genetic analyses.

This work was supported by a Leakey Foundation Grant and NSF SBR-9312567 to Franciscus, and ICRU funding from the University of Iowa to Williams.

Late Neolithic children of Belgium: A comparison of deciduous molar morphology from four caves burials

FRANK L. WILLIAMS¹ and REBECCA L. GEORGE²

¹Anthropology, Georgia State University, ²Anthropology, University of Nevada Reno

The karstic caves of the Belgian Meuse River Basin have yielded nearly 200 collective burials. Children are well represented among the cave burials allowing for a regional overview of deciduous molar trait frequencies per site with respect to temporal variation. Radiocarbon dated caves with subadult gnathic remains include Hastière Caverne M (n = 5) from the Early/Late Neolithic, Sclaigneaux (n = 9) and Bois Madame (n = 6) which are dated to the Final/Late Neolithic and Maurenne Caverne de la Cave (n = 7) associated with four dates ranging from prior to the Early/Late to the terminus of the Final/Late Neolithic period, from 4,635 to 3,830 years BP. Dental molds of the original material were cast in epoxy resin, and the resulting dental casts were scored using Hanihara's standards for deciduous molars and supplemented with traits from the ASUDAS. The hypoconulid is present at all sites, although the largest is found at Hastière Caverne M. A metaconulid is small if expressed at all. Carabelli's trait ranges from a small pit to a large cusp. Hastière Caverne M exhibits the most pronounced expression of Carabelli's cusp and presents the only protostylid observed. Although the results are contingent on the idiosyncrasies of preservation and small sample size, it appears that Early/Late Hastière Caverne M differs from the Final/Late Neolithic cave burials of Sclaigneaux and Bois Madame. Hastière Caverne M may have been partially distinct, occurring several centuries prior to the population restructuring associated with the onset of the Bronze Age.

Funding for this project was received by Fulbright-Belgium and the Commission for Educational Exchange between the USA, Belgium and Luxembourg.

Dental Health At the Cusp of the Third Epidemiological Transition

LASHANDA R. WILLIAMS¹, AJA LANS² and SIOBAIN DUFFY³

¹Graduate Program in Ecology & Evolution, and Department of Ecology, Evolution, & Natural Resources, Rutgers University, ²Department of Anthropology, Syracuse University, ³Department of Ecology, Evolution, & Natural Resources, Rutgers University

Often times contemporary disease patterns can be better understood with a thorough investigation of the disease's historical trajectory. The epidemiological transition model provides researchers a framework to examine how and why diseases evolve and spread throughout human populations. Our goal is to consider how this model might be used to understand the oral health of past populations from the United States.

The prevalence of oral disease in US residents was not measured systemically until the 1950s and 60s. In this study, we seek to assess the preservation of dentition across museum collections and reconnect measures of oral and systemic health. We examined 938 dental sockets of 44 geographically and ethnically diverse Americans who died between 1890-1920 in effort to assess the prevalence of dental caries, calculus, root exposure, antemortem tooth loss, and attrition. We observed gross caries in 30 teeth, with a majority located on the occlusal surface. We also observed 111 cases of antemortem tooth loss and 304 teeth with ≥ 3 mm of the root exposed. Additionally, we measured the abundance of calculus across all surfaces of teeth and devised an additive score to use to investigate relationships between calculus and other dental pathologies. Preliminary findings reveal a relationship between overall calculus abundance and both attrition and root exposure, but not caries. Future work will expand our sample size and incorporate cranial and postcranial elements for a more holistic assessment of health and disease at the turn of the 20th century.

This study was funded by a National Science Foundation Dissertation Improvement Grant (BCS-1826220) and Rutgers University's Center for Human Evolutionary Studies.

A nearly complete lower back of *Australopithecus sediba*

SCOTT A. WILLIAMS^{1,2}, THOMAS C. PRANG¹, MARC R. MEYER³, KELLY R. OSTROFSKY⁴, THIERRA K. NALLEY⁵, DANIEL GARCÍA-MARTINEZ^{2,6,7,8}, MARKUS BASTIR^{2,6,7}, PETER SCHMID^{2,9}, STEVEN E. CHURCHILL^{10,2} and LEE R. BERGER²

¹Center for the Study of Human Origins, Department of Anthropology, New York University, ²Evolutionary Studies Institute and Centre for Excellence in Palaeosciences, University of the Witwatersrand, ³Department of Anthropology, Chaffey College, ⁴Center for the Advanced Study of Human Paleobiology, Department of Anthropology, The George Washington University, ⁵Department of Medical Anatomical Sciences, Western University of Health Sciences, College of Osteopathic Medicine of the Pacific, ⁶Paleoanthropology Group, Museo Nacional de Ciencias Naturales (MNCN-CSIC), ⁷Faculty of Sciences, Biology Department, Universidad Autónoma de Madrid, ⁸Laboratoire PACEA – De la Préhistoire à l'Actuel: Culture, Environnement et Anthropologie, CNRS, Université de Bordeaux, ⁹Anthropological Institute and Museum, University of Zurich, ¹⁰Department of Evolutionary Anthropology, Duke University

The lower back is adapted to mobility and stability across mammals and reflects posture and locomotion in the framework of a species' evolutionary history. Upright bipedalism is one such positional behavior, and due to limited fossil evidence, disagreements exist as to when, how, and in what evolutionary context bipedalism evolved. Here, we describe and comparatively

ABSTRACTS

analyze new lumbar vertebrae from Malapa that contribute to a nearly complete lower back of adult female *Australopithecus sediba* (MH2). Vertebral remains from a newly discovered breccia block refit with previously known lower lumbar vertebrae at multiple contacts, affirming their association. These new fossils confirm that the *A. sediba* vertebral column was numerically configured like that of other known early hominins (e.g., *A. africanus* and *Homo erectus*), with five lumbar vertebrae and a cranially positioned transitional vertebra. We quantify vertebral wedging and find that MH2 demonstrates the most dorsally wedged lower back of known adult early hominins, with a sum wedging angle falling between male and female modern humans. Additionally, we carry out a 3D GM study of middle lumbar vertebra morphology and find that *A. sediba* is derived in the direction of humans among extant taxa but shares some features (e.g., spinous process shape) with African apes and others (e.g., transverse process orientation) with fossil members of the genus *Homo* (e.g., Kebara 2). More work on the axial skeleton of *A. sediba* and other taxa will contribute to our understanding of the phylogenetic relationships and functional morphology of the locomotor skeleton of early hominins.

SAW thanks the Leakey Foundation for support

A Photogrammetric Method for Quantifying Enteseal Shape and Rugosity

ERIN MARIE S. WILLIAMS-HATALA^{1,2}, KEVIN G. HATALA^{1,2}, MICHAEL L. COLLYER¹, SABREEN MEGHERHI¹, KAY L. FISKE¹, OLIVIA CIROLI¹ and KARYNE N. RABEY³

¹Biology, Chatham University, ²Center for the Advanced Study of Human Paleobiology, The George Washington University, ³Division of Anatomy, Department of Surgery, University of Alberta

Enteses (muscle, tendon, and/or ligament attachment sites) can appear as raised and/or rugose areas on bone surfaces, that are visible without magnification. This presentation, combined with their presumed direct connections to soft-tissue structures, has led to their use among biological anthropologists in attempts to reconstruct muscle anatomy and, in turn, the behaviors of extinct hominins. Despite the commonality of this practice, the nature of muscle-entesis relationships have seldom been investigated in detail. Further, most surface enteseal analyses have relied upon qualitative descriptions rather than quantitative measurements, making it difficult to conduct meaningful statistical analyses.

Here we present methods to quantitatively measure aspects of surface enteseal morphology that are widely used in qualitative descriptions—length, width, area, and rugosity. We also use these measures to evaluate

relationships between entesis morphology and the anatomy of the associated muscles. All measurements were taken from photogrammetric models, enabling three-dimensional quantification of enteseal area and rugosity. The opponens pollicis and the deep pollical flexor (n = 46 and 51, respectively) enteses of modern humans and non-human primates (n = 9) were quantified, and results were compared with associated muscle architectural variables (physiological cross-section area, muscle mass, fiber length, muscle-tendon unit length). All correlations were weak and statistically insignificant. Our results demonstrate that though these characteristics of gross enteseal morphology do not reliably predict aspects of the associated muscle, the method enables repeatable quantification of variables frequently limited to qualitative descriptions, which can be used to statistically access relationships between muscle and enteseal anatomies.

This research was supported by Chatham University and the University of Alberta.

Paleobiology and Taphonomy of the Middle Paleolithic Neandertal Remains from Ciemna Cave, Southern Poland

JOHN C. WILLMAN^{1,2}, BOLESŁAW GINTER³, RAQUEL HERNANDO^{1,2}, MARINA LOZANO^{1,2}, KRZYSZTOF SOBCZYK³, DAMIAN STEFAŃSKI⁴, ANITA SZCZEPANEK⁵, KRZYSZTOF WERTZ⁶, PIOTR WOJTAŁ⁶, MIROŚLAW ZAJĄC⁴, KATARZYNA ZARZECKA-SZUBIŃSKA⁷, ERIK TRINKAUS⁸ and PAWEŁ VALDE-NOWAK³

¹Paleoanthropology, IPHES, Institut Català de Paleoeologia Humana i Evolució Social, ²Àrea de Prehistòria, Universitat Rovira i Virgili (URV), ³Institute of Archeology, Jagiellonian University, ⁴Archeological Museum of Kraków, ⁵Institute of Archeology and Ethnology, Polish Academy of Sciences, ⁶Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, ⁷Department of Paleozoology, Wrocław University, ⁸Department of Anthropology, Washington University in Saint Louis

Middle Paleolithic human remains from the uplands and the Carpathian zones of Central Europe are rare and fragmentary despite a relative abundance of archeological remains in the region from this period. The dearth of human remains raises questions regarding the roles of humans in site formation processes in the region. Fragmentary human remains from Ciemna Cave in southern Poland, a pair of isolated manual phalanges (Ciemna 1a and 1b) from layers dated to the Eemian interglacial (MIS 5) and a partial mandibular incisor (Ciemna 2) from layers dated to more than 50 ka BP, provide additional data relevant to these questions. The human remains occur, as with many Central European sites, in the context of a cave that was principally a carnivore (especially ursid) den with only occasional human occupation. A morphological and

taphonomic assessment of these remains was undertaken. Results suggest that Ciemna 1 was ≤ 4 years of age-at-death based on comparisons of intermetaphyseal length to age in recent and Late Pleistocene humans. Both phalanges exhibit postmortem modification that exposed a considerable amount of trabecular bone. The Ciemna 2 fragmentary mandibular incisor is small for a Neandertal. It exhibits a well-developed groove on the distal interproximal root surface and rounded edges on several areas of the fractured root surface. A differential diagnosis of the taphonomic modifications of the phalanges (e.g., underground water washing, soil acidity, or digestive corrosion) and incisor (e.g., *in vivo* tooth-picking behaviors, postmortem manipulation, or post-depositional processes) is provided.

Support from Marie Skłodowska-Curie Actions (H2020-MSCA-IF-2016 No. 749188); AGAUR (Ref. 2017SGR1040 and 2017PFR-URV-B2-91); MINECO/FEDER (Ref. CGL2015-65387-C3-1-P); and Polish National Science Centre (No. UMO-2014/15/B/HS3/02219 – “The Last Neanderthals in the Ciemna Cave”).

Development of a Radiological Checklist for Differential Diagnosis of Cancer and Neoplastic Disease in Mummified Human Remains

JENNIFER WILLOUGHBY and ANDREW NELSON
Anthropology, University of Western Ontario

Diagnosis of cancer in archaeological remains is complicated by factors of preservation, myriad diseases that fall under the category of cancer and affect the body in diverse ways, and the comparative rarity of these diseases affecting the skeleton. Computed tomography (CT) provides a non-invasive method for the comprehensive analysis of remains that may reveal evidence of neoplastic disease not otherwise observable. As CT analysis becomes more readily available for archaeological projects, mummified human remains present a potential source for evidence of cancer and neoplastic disease in soft tissues as well as the skeleton.

This paper will present the results of creating a checklist specifically for the radiological analysis of mummified human remains for the identification of cancer and neoplastic disease. Checklists are used in clinical radiology to improve accuracy and completeness in analysis. Mummified human remains present specific challenges for both radiological analysis and the application of traditional anthropological analysis. This checklist was developed adapting clinical radiological and anthropological techniques in order to ensure thorough examination of mummified human remains as well as accurate and standardized recording of anomalies. Checklists such as this are important for identifying potential cases of cancer as well as for ensuring accurate differential diagnosis. The checklist is part of an ongoing radiological project surveying the presence of

ABSTRACTS

cancer in mummified human remains. As more archaeological cases of neoplastic disease are discovered, the standardization of recording anomalies, and the inclusion of full differential diagnoses in publications are essential for comparative examples and more secure diagnoses.

Sex differences in the patterning of age-related bone loss in the human hallucal metatarsal in Post-medieval rural and urban populations

LAURA A.B. WILSON¹, ISABELLE DE GROOTE² and LOUISE T. HUMPHREY³

¹School of Biological, Earth and Environmental Sciences, University of New South Wales, ²School of Natural Sciences and Psychology, Liverpool John Moores University, ³Department of Earth Sciences, The Natural History Museum

Bone tissue responds to the strains engendered during habitual activity through the processes of apposition and resorption, resulting in measurable modifications to cortex dimensions. Age-degenerative features of the metatarsals are poorly known despite the importance of metatarsal bone properties for investigating mobility patterns. We assessed the role of habitual activity in shaping the patterning and magnitude of age-related bone loss in the hallucal metatarsal using individuals from Post-medieval rural (Abingdon: ABVR) and urban (Spitalfields: SPIT) settings (N=71). Cross-sections were extracted at midshaft from micro-computed tomography scan models. Inter-population comparisons of cross-sectional geometry properties indicated that ABVR individuals had larger metatarsals that showed a) greater capacity to resist torsion and b) comparatively greater bending strength along the mediolateral plane. Cortical thickness and cortical area remained relatively constant with age in ABVR males and females suggesting a buffering-effect of higher loading regime, whereas SPIT males and females showed a decrease, with cortical area and thickness values dropping most markedly for females. An increase in periosteal bone apposition and an increase in endosteal resorption with age was evident for ABVR males and females, and less markedly for SPIT males. SPIT females showed minimal levels of periosteal bone apposition with age coupled with an increase in endosteal resorption. As a net result, SPIT females showed the most bone loss with age in the sample. At all ages, SPIT individuals showed greater variation for all cortex measurements than ABVR individuals, which could be linked to greater variability in lifestyle, including activity levels and nutritional status.

This research is supported by the Australian Research Council Discovery Program (DE150100862 granted to LABW), and the Calleva Foundation.

Colors of primate pelage: The independent evolution of sexual dichromatism in the primate order

THOMAS C. WILSON and JAMES E. LOUDON

Department of Anthropology, East Carolina University

There is a significant body of research describing the evolutionary importance of plumage coloration among avian species. However, these datasets are lacking for mammalian pelage. Furthermore, very little research has examined the variations of nonhuman primate (NHP) pelage coloration and patterning. Primatologists have noted conspicuous differences in coloration and patterning among NHPs, including neo-natal coats and sexual dichromatism. Sexual dichromatism refers to the differences in pelage coloration between the sexes of a single species. Sexual dichromatism is rare, but found among some species of lemurs, New World monkeys, and lesser apes. To illuminate the genetic mechanism of NHP sexual dichromatism, we examined published amino acid sequences for the *MC1R* and *OCA2* genes of nine NHP species across multiple genera. This dataset incorporated sexually dichromatic NHPs including white-cheeked gibbons (*Nomascus leucogenys*), Lar's gibbons (*Hylobates lar*), and black howler monkeys (*Alouatta caraya*). We also examined closely allied monochromatic NHPs including brown lemurs (*Eulemur fulvus*), long-tailed macaques (*Macaca fascicularis*), black snub-nosed monkeys (*Rhinopithecus bieti*), Mueller's gibbon (*Hylobates muelleri*), mantled howler monkey (*A. palliata*), and chimpanzees (*Pan troglodytes*). Comparisons across these species suggest the *MC1R* gene does not play a significant role in pelage coloration. In contrast, the amino acid sequence of *OCA2*, differed by ~12% for *N. leucogenys*, suggesting that this gene may regulate dichromatic pelage. To expand these genetic datasets, we analyzed socioecological variables among these species and found that smaller home-range sizes and dispersal of both sexes may have played a role in the evolution of dichromatic pelage in NHPs.

Reconsidering osteoarthritis as a skeletal age indicator

ALLYSHA P. WINBURN¹ and MICHALA K. STOCK²

¹Anthropology, University of West Florida, ²Exercise Science, High Point University

Osteoarthritis (OA) results from the breakdown of normal relationships between articular components. While biological anthropologists generally acknowledge that OA increases with age, many hesitate to use the disease to inform skeletal age estimation due to its multifactorial nature. This study investigated the utility of OA for age estimation in a modern European-American skeletal sample (n=408; Bass Collection, Tennessee). The

TMJ and all appendicular joints were examined and scored for the presence of OA. Generalized linear models (binomial) assessed the contributions of self-reported demographic data to OA, including: age; body mass index (BMI); and metabolic values for physical activities. Finally, single-variable transition analysis (TA) probit models were generated for presence/absence data at each joint surface.

Age was the only statistically significant predictor of OA in all tested joints in males, and all but two joints in females (*p*-value range: <0.001-0.036). No predictors contributed significantly to female knee OA, and BMI was the only statistically significant predictor of female ankle OA (*p*=0.036), suggesting that lower-limb OA should not be used for aging in females. For all other joints, using OA to inform age estimates appears valid. Thus, convenient age cut-offs were calculated from the TA models, representing the ages at which 90% of individuals transition to exhibiting OA (range: 29.9-55.2 years). While OA cannot be considered a primary age indicator, its presence can refine age estimates during normal skeletal analysis or provide helpful age data in incomplete or fragmentary cases. These contributions thus augment age estimation in both forensic and bioarchaeological contexts.

Financial support for this research was provided by the National Institute of Justice Graduate Research Fellowship Program in Science, Technology, Engineering, and Mathematics (Grant # 2015-R2-CX-0009).

Appropriately managing archiving and access to culturally sensitive but scientifically valuable digital imagery

JULIE M. WINCHESTER¹, TIMOTHY M. RYAN², JOSHUA WISOR², LYNN COPES³, TAMIRA K. BRENNAN^{4,5}, MARK J. WAGNER^{4,5} and DOUG M. BOYER¹

¹Department of Evolutionary Anthropology, Duke University, ²Department of Anthropology, Pennsylvania State University, ³Department of Medical Sciences, Quinnipiac University, ⁴Center for Archaeological Investigations, Southern Illinois University Carbondale, ⁵Department of Anthropology, Southern Illinois University Carbondale

Digital 3D representations of biological specimens, particularly bones, have become increasingly ubiquitous in anthropological and archaeological research. MorphoSource, a publicly accessible web database for preserving 3D data representing museum specimens, has begun to provide a model for archiving and managing scientific 3D data. Currently, almost 1,000 researchers use this platform to archive roughly 60,000 datasets, with 6,000 users accessing data. One challenging type of data is those representing human remains, especially remains that are or may be ancestral to descendent communities in the US. Special ethical considerations for both deceased and

ABSTRACTS

living individuals and groups must be taken into account when working with human remains, especially regarding privacy and providing proper context. MorphoSource is beginning to address the task of preserving data collected with public funds (e.g., NSF) and availing it to further research, while respecting the wishes of communities and obeying NAGPRA regulations. This involves providing tight and nuanced access controls to data contributors, enabling the inclusion of detailed and culturally-relevant metadata, and most importantly helping museums to appropriately manage requestor access on a case by case basis to scans that represent the physical remains in their collections while recognizing the context-dependent needs for these types of remains. Further, we present and discuss several datasets currently on MorphoSource as case studies to highlight these issues. Digital archiving of sensitive data can be significantly beneficial for all stakeholders involved, and data archive resources like MorphoSource can help ensure that appropriate access restrictions are determined and followed.

African Ancestry in the Americas: Perspectives on Afro-Puerto Rican Maternal Ancestry

TAIYE WINFUL, M.A., CASSANDRA DELDUCCO, ELSA MUELLER and JADA BENN TORRES, PHD

Department of Anthropology, Vanderbilt University

Recent studies have used the mitochondrial genome to explore patterns of common ancestry within the African diaspora in order to comment on the experiences of African peoples within the Americas. Here we compare whole mitochondrial genome data of 31 Afro-Puerto Rican individuals to previously published data from US African Americans, Haitians, Puerto Ricans, and other populations within the African diaspora. These data were used to assess diversity within and across population groups. The Afro-Puerto Ricans showed high levels of mitochondrial diversity which was comparable to what has been observed in other populations of African descent in the Americas. Roughly 74.2 % of our individuals fell into a Sub-Saharan African L type haplogroup, while the other 25.8% fell into haplogroups A2, B2 and U5, primarily associated with North and Central Native American groups and, Western Europe, respectively. A Fisher Freeman analysis was used to test for significant differences between the frequency of each haplogroup and our Afro-Puerto Rican data set. Significant differences were observed between the Afro-Puerto Ricans and the four following comparative populations: general populace of Puerto Rico, non-Hispanic African Americans from the NHANES studies, general populace of Haiti, and the general populace in St. Vincent. Based on our analysis of mitochondrial haplogroup distributions, Afro-Puerto

Rican maternal ancestry is somewhat unique suggesting different demographic histories of this community relative to other Caribbean communities. Additional analyses using larger sample sizes and Y-chromosome and autosomal markers, would be useful to further explore these differences.

Phylogenetic investigations of *Treponema pallidum* and related spirochetes

STEVIE WININGEAR and ANNE C. STONE

School of Human Evolution and Social Change, Arizona State University

Treponema pallidum is a spirochete bacterium with three recognized subspecies. These bacteria cause three globally widespread diseases. *T.p. pertenue* causes yaws, *T.p. endemicum* causes bejel (also known as endemic syphilis), and *T. p. pallidum* causes the venereal disease, syphilis. Another, closely related bacterium species, known as *Treponema carateum*, (formerly classified as *T. pallidum* subspecies *carateum*) causes pinta. Although these bacteria cause diseases, generally with different clinical manifestations, their genomes differ by less than 0.2 percent; this degree of genetic similarity makes it difficult to examine the evolutionary histories and relationships among them.

However, limited work has been done to examine the scope of genomic diversity within *T. pallidum*. Currently, only 56 assembled whole *T. pallidum* genomes are stored through the National Center for Biotechnology Information (NCBI). Due to this dearth of genomic information, the majority of phylogenetic analyses have been performed using gene sequences.

In this presentation, we detail phylogenetic analyses using all publically available *T. pallidum* genomes, including representatives of each of the three subspecies. Phylogenies constructed using whole genomic information are compared to those constructed using various gene sequences, including the *Treponema pallidum* repeat (tpr) genes. Analyses indicate the close relationship between subspecies, but still separate each into distinct clades. This exercise demonstrates the need for whole genome analyses, and broader geographic representation when attempting to elucidate evolutionary relationships between *T. pallidum* subspecies, strains, and subtypes.

Capturing 3D locomotor kinematics of modern humans to determine behavioral substrate navigation

ASHLEIGH L. A. WISEMAN¹, THOMAS O'BRIEN² and ISABELLE E. DE GROOTE¹

¹RESEARCH CENTRE IN EVOLUTIONARY ANTHROPOLOGY AND PALAEOECOLOGY, LIVERPOOL JOHN MOORES UNIVERSITY,

²RESEARCH INSTITUTE FOR SPORTS AND

EXERCISE SCIENCE, LIVERPOOL JOHN MOORES UNIVERSITY

Tracks provide evidence of hominin locomotion, yet the relationship between lower limb kinematics and the foot's interaction with the substrate remains poorly understood, inhibiting a comprehensive reconstruction of evolutionary locomotion from trackways. To determine the relationship between limb kinematics, substrate deformation and track morphology we employed 3D motion capture systems to characterize movement (hip, knee and ankle) through various types of motion (walk, fast walk, jog and bent-hip bent-knee) in modern humans across a range of substrates.

The knee and ankle displayed significant increases in joint angles when traversing across a less compliant substrate, with joint angle disparity being more severe with increasing speed. The hip was more constrained between motions. Track morphology was affected by substrate and speed, producing tracks that were both wider and longer with increasing substrate pliancy, with small discrepancies in internal morphology. As limb flexion increased joint angles were also affected, with the greatest changes found in track morphology: tracks had variable depth distributions and under-represented midfoot shapes. Hallux abduction was also found to be significantly correlated with increasing knee angle.

Discrepancies in outline metrics and internal morphology have considerable implications for biometric predictions, suggesting that biometrics cannot currently be reliably extracted from fossil tracks without a more comprehensive understanding of the interaction between movement and substrate. This study has shown that modern humans significantly alter limb kinematics to accommodate changes in substrate pliancy. It is appropriate to assume that early hominins would have adopted similar kinematic changes necessary for efficient substrate navigation.

This research was funded by Liverpool John Moores University, UK.

Act like a lady, think like a boss: Alpha status in a captive female chimpanzee (*Pan troglodytes*)

BASIA F. WISINSKI¹ and CHRISTINA CLOUTIER BARBOUR^{2,3}

¹Public Health, University of Miami, ²Wildlife, Lion Country Safari, ³Anthropology, University of Utah

Adherence to dominance hierarchies is widespread in social mammals, with higher rank often resulting in measurable effects on fitness outcomes. Where able, both sexes should compete for higher rank if the cost to do so does not outweigh the benefit. Captive environments—where animals are freed from the energetic constraints of the wild, but remain in large social groups—represent a unique opportunity to

ABSTRACTS

investigate the social behaviors that may arise in the absence of these ecological checks. Here, we report on the development of a site-specific scan sample ethogram built to determine social status in a captive female chimpanzee (*Pan troglodytes*). We review behaviors indicative of hierarchy, such as: pant-grunt use and directionality, submissive and reassurance mounting, charging and dominance displays, ascendance over preferred resources, and disruption of disputes. Data were collected on a single chimpanzee group over a 4-month period and consisted of 27 observation days. Preliminary results reveal that a female engaged in significantly more dominance behaviors than the group male, with 280 versus 56 events, respectfully. Of particular importance are pant grunts. While both individuals received these hierarchical vocalizations, group members directed them toward the female 13 times to the male's 2. Most notably, one pant grunt was delivered from the male to the female. We conclude that while the published literature asserts that *all* males of the species are dominant over their female counterparts, this does not have to be the case in captivity, where females are free to turn their interests toward politicking.

The impact of frailty in the Spanish influenza pandemic of 1918

AMANDA WISSLER

Anthropology, Arizona State University

In bioarchaeology, "frailty" has been established as a framework for interpreting skeletal lesions and to make inferences about ancient health. Previous studies have found disparate results, indicating that the relationship between frailty, lesions and increased mortality remains undertheorized and requires further examination. This project explores the impact of frailty in the Spanish Influenza Pandemic of 1918. The pandemic was an unusual epidemiological event in which the virus disproportionately killed young adults, a group that is generally the most resilient segment of the population. This study tests whether frail individuals were more likely to die during the pandemic. Data on age-at-death and skeletal indicators of stress (periostosis, femoral length, linear enamel hypoplasia, periodontal disease, and vertebral neural canal diameter) were collected from a sample of white male individuals (N=115) from the Hamann-Todd documented osteological collection and analyzed using Usher's (2000) multi-state model of morbidity and mortality. Results demonstrate that skeletal indicators of stress were associated with increased risk of mortality in those who died during the pandemic but that the strength of selective mortality during the pandemic was not significantly different from the control group. These results broaden our knowledge of past disease dynamics while supporting the traditional interpretation of skeletal lesions as

indicators of frailty. These findings also enhance our understanding of a critical epidemiological event by demonstrating that even though young adults were hit hard during the pandemic, those who died were still the most frail of their cohort.

Center for Bioarchaeological Research Pilot Grant

Interpreting skeletal growth in the past: Error and estimation of childhood growth in historic African American communities

CHRISTOPHER A. WOLFE¹ and NICHOLAS P. HERRMANN²

¹Anthropology, University of Nevada, Reno,

²Anthropology, Texas State University, San Marcos

Previous research within bioarchaeology has shown that measurements of human growth in skeletal tissue represent a suitable proxy to gauge the health and nutritional status of past populations. However, many of these studies do not address the error in approximating growth after estimating chronological age. The current study examines skeletal growth considering this bias and presents a new model to conceptualize childhood growth in the past. This study measures femoral growth in juvenile skeletal samples from three historic African American communities in Texas, Arkansas, and Georgia for evidence of stunted growth as compared to contemporaneous European American, modern American, and global populations of modern children. The heteroskedastic nature of growth in individuals of unknown age leads to a wide growth profile that would likely encompass true growth if age-at-death were known. While imprecise, the inclusion of age uncertainty in the overall growth model provides a more accurate picture of growth in the past. Results suggest that while growth stunting may occur in late infancy to early childhood, historic African American communities underwent a period of catch-up and stabilization that led to adolescent and adult measures analogous to the comparative samples. These results are contextualized within a socioecological resilience model that illuminates the plastic, yet canalized nature of growth. While age uncertainty leads to a broad, often ambiguous picture of growth in the past, this study demonstrates that interpretation of such results is possible given contextualized knowledge of historic populations and a firm grounding in the theory underpinning human growth.

Tibial torsion and pressures in the feet during walking and standing in humans: an experimental study

JESSICA S. WOLLMANN¹, AUBREE S. MARSHALL¹, MCKENZIE A. SCHRANK¹ and LAURA T. GRUSS²

¹Anthropological Sciences, Radford University,

²Biology, Radford University

Pontzer et al. (2010) reported a very low degree of tibial torsion in the Dmanisi D3901 *H. erectus* individual. Structurally, less tibial torsion may be expected to produce a more medial orientation of the foot, possibly resulting in greater stresses in the more central pedal rays during locomotion. This may explain the relatively greater robusticity in the Dmanisi MT III and IV compared to modern humans. We tested this hypothesis experimentally. Here we present pilot data for tibial torsion, foot angle, and plantar pressure data during standing and walking, in a pilot sample of 10 human subjects. Trans-malleolar axis, a proxy for tibial torsion, and foot angle were measured from photographs of each subject's foot taken from underneath. A Matscan pressure mat was used to measure plantar pressure under subjects' metatarsal heads (MT I vs. MT II-IV vs. MT V), as well as foot angle, during walking and standing. We found no relationship between tibial torsion and foot angle during standing or walking, nor between foot angle and the pattern of pressure across the metatarsals. Further data collection is underway and a larger sample size will verify these results, but our preliminary findings suggest that tibial torsion is not a major determinant of foot orientation during locomotion, and is unlikely to explain the pattern of MT robusticity in D3901. These results concur with our related osteometric study (Schrack et. al), which found no relationship between tibial torsion and metatarsal robusticity in a modern human sample.

Hadza Hunter-Gatherers Exhibit Gender Differences in Space Use and Spatial Cognition Consistent with the Ecology of Male and Female Targeted Foods

BRIAN M. WOOD¹, JACOB A. HARRIS², LAYNE VASHRO³, M. KATHERINE SAYRE⁴, DAVID A. RAICHLEN⁴, HERMAN PONTZER⁵, AMELIA SANCILIO⁶, J. COLETTE BERBESQUE⁷, ALYSSA N. CRITTENDEN⁸, AUDAX Z.P. MABULLA⁹, JAMES H. JONES¹⁰ and ELIZABETH CASHDAN¹¹

¹Anthropology, University of California, Los Angeles, ²School of Human Evolution and Social Change, Arizona State University, ³Denver Nuggets, Kroenke Sports & Entertainment, ⁴School of Anthropology, University of Arizona, ⁵Evolutionary Anthropology, Duke University, ⁶Center for Health and the Social Sciences, University of Chicago, ⁷Centre for Research in Evolutionary, Social and Inter-Disciplinary Anthropology, University of Roehampton, ⁸Anthropology, University of Nevada, Las Vegas, ⁹Dar es Salaam National Museum, National Museums of Tanzania, ¹⁰Earth Systems Science, Stanford University, ¹¹Anthropology, University of Utah

Humans think about, explore, and use landscapes like no other organism, reflecting our species' unique biological and cultural adaptations. One of these adaptations is a gendered division of foraging labor, observed in all hunter-gatherer societies. How gendered economic roles interact with ecology and shape daily movement patterns

ABSTRACTS

is not well understood. We focus on this question using 2,089 days of travel (21,761 km) by Hadza hunter-gatherers of northern Tanzania, recorded using GPS devices. A simple behavioral ecology theory proposes that travel should be influenced by the spatial distribution of food resources, and that lower resource density is expected to lead to greater travel. We test this idea and several related predictions using measures of 180 people's daily travel. Results show that Hadza men walked further per day, explored more land, followed more sinuous paths, and were much more likely to be alone while traveling. These patterns emerged early in life, before age 10, and persisted across the life course. These findings provide context for a second study of spatial cognition, which indicates a male advantage in dead-reckoning accuracy and three dimensional mental rotation, as expected given observed patterns of space use.

Max Planck Institute for Evolutionary Anthropology, Department of Human Behavior, Ecology and Culture; National Science Foundation (awards 1548143, 1062879, 0850815, 1440867, 1440841, 1329091); Leakey Foundation; National Geographic Society; John Templeton Foundation.

Out in the Cold: How cold temperatures and weather conditions influence the rate of decomposition in pig proxies (*Sus scrofa*)

KATHARINE C. WOOLLEN

Anthropology, Illinois State University

Temperature has a dramatic effect on the rate of decomposition, especially when temperatures drop to the point where decomposition is reduced or halted. Few studies have been conducted to track these changes over a period of time, and fewer still have taken into consideration other variables that might affect the rate of decomposition within cold weather settings (i.e., temperatures below 32°F). It is the goal of this study to examine how remains decompose within natural cold weather settings, so that a better representation of the postmortem interval may be eventually created when remains are subject to these kinds of conditions. Across the span of four months, i.e., early January to early May, ten partial pig specimens were exposed to the cold weather settings of central Illinois. Eight subjects were buried below ground; four at the depth of six inches, and four at the depth of 18 inches. Four samples were wrapped in white cotton t-shirts, four were wrapped in plastic garbage bags, and two were placed uncovered in a protective wire cage on the ground surface. It was determined that the cloth and plastic coverings alter the rate of cold temperature decomposition. It was also determined that an increased burial depth significantly accelerates the process of decomposition in cold temperatures. This study indicates that there are several factors that must be appreciated

when trying to understand any taphonomic variation that may occur when remains are subject to cold temperatures and weather conditions (i.e., precipitation) for an extended period of time.

Sedentism and Dietary Variation among the semi-nomadic Naduhup of the Northwest Amazon

HAROLD M. WRIGHT, MS¹, GLENN H. SHEPARD, JR., PHD² and B.A. PIPERATA, PHD¹

¹Department of Anthropology, The Ohio State University, ²Division of Human Sciences, Museu Paraense Emílio Goeldi

A growing body of literature documents declines in the health status of indigenous Amazonian populations. While these declines are often attributed to lifestyle changes, especially diet, there remains a dearth of data on dietary patterns of Amazonian populations. The goal of this study was to determine how increased sedentism affected the dietary patterns of Naduhup, semi-nomadic foragers occupying small black water tributaries in the Northwest Amazon. Data were collected in three Naduhup communities: Cabeceira da Anta, a community still heavily reliant on foraging; Embaúba, a community in transition; and, Nova Fundação, a permanent Catholic villa. Dietary data were collected using the weighed-inventory method from n=53 adults (25 men, 28 women) across the rainy, transitional, and dry seasons (July to December). Results show greater reliance on fish broths and stews in Embaúba (89.5% fish-based, 10.5% game- and insect-based dishes) and Nova Fundação (83.3% fish-based, 16.7% game- and insect-based dishes). In the foraging community of Cabeceira da Anta, there was a greater reliance on game- and insect-based dishes (55% fish-based, 45% game- and insect-based), with reliance on fish-based dishes lowest (34.1%) during the rainy season. These results indicate that sedentism, encouraged by Brazilian state and federal governments and Catholic religious authorities, has resulted in increased reliance on fish as the principle source of protein. This fundamental change in diet may place Naduhup communities in greater resource competition with adjacent riparian groups such as Tukanoans who are highly reliant on fish, with implications for food security.

Papa-B (MHC) diversity of wild bonobos (*Pan paniscus*) east and west of the Lomami River suggest different patterns of immunity

EMILY E. WROBLEWSKI¹, AARON G. ANDERSON¹, LISBETH A. GUETHLEIN², YINGYING LI³, ALEXA N. AVITTO³, PACO BERTOLANI⁴, JOHN A. HART⁵, THERESE B. HART⁵, BEATRICE H. HAHN³ and PETER PARHAM²

¹Anthropology, Washington University in St. Louis,

²Structural Biology, Stanford University School of

Medicine, ³Medicine and Microbiology, Perelman School of Medicine, University of Pennsylvania, ⁴Leverhulme Center for Human Evolutionary Studies, University of Cambridge, United Kingdom, ⁵Lukuru Wildlife Research Foundation, Tshuapa-Lomami-Lualaba Project, Democratic Republic of the Congo

Major Histocompatibility Complex (MHC) molecules bind and present peptide-antigens to T cells. *MHC* genes are characterized by extreme polymorphism and rapid evolution. Previous studies found reduced bonobo *MHC* diversity (both captive and wild), compared to that of chimpanzee and human. However, the wild populations studied (Democratic Republic of the Congo (DRC)) were located west of the Lomami River (oriented north-south). mtDNA studies indicated the Lomami has been a barrier to gene flow between bonobos residing on either side. Additional work suggests that bonobos originated in eastern DRC. Our hypothesis was that eastern bonobos are more diverse than and/or distinct from western bonobos. We isolated DNA from 94 fecal samples from 51 bonobos (differentiated by microsatellite genotype) in the eastern Tshuapa-Lomami-Lualaba (TL2) region. We PCR amplified, and then sequenced, the polymorphic exons 2 and 3 of the *Papa-B* gene. Results were compared to published genotypes from 110 western bonobos (five sites) and two eastern bonobos (Bosondjo region). We identified 15 alleles among eastern versus 21 among western bonobos. Nucleotide diversity did not differ between them, however TL2 had six unique alleles compared to 1-4 for western sites, suggesting eastern bonobos are diverse and distinctive. Eastern distinctiveness is further supported by substantial allele frequency differences for the three alleles shared by all populations. Molecular characteristics suggest that *Papa-B* interactions are biased toward adaptive immunity in eastern bonobos, and western bonobos have greater capacity for additional function in innate immunity. An important consideration is that malaria was recently identified among eastern bonobos.

National Institutes of Health R01 AI24258, R01 AI120810, and R01 AI091585

Middle Pleistocene human fossils found in China: isolated evolution or influenced by migration?

XIUJIE WU and WU LIU

Key Laboratory of Vertebrate Evolution and Human Origins of Chinese Academy of Sciences, Institute of Vertebrate Paleontology and Paleoanthropology, Chinese Academy of Sciences

During a transitional period dating from the Late Middle to early Late Pleistocene age, archaic humans existed in China, as evidenced by fossils discovered at Dali, Maba, Xujiayao, Xuchang and elsewhere. Interestingly, these early humans exhibited a mosaic of east Asian

ABSTRACTS

and contemporary western morphological characteristics. For example, a cranium from Maba possesses a Neandertal-like thick, prominently projecting supraorbital torus arching over the circular orbital profile. Moreover, the endocranial narrow frontal lobes, short flattened parietal areas and middle meningeal vessels predominating at anterior branches typify *H. heidelbergensis* and *H. erectus* features. Meanwhile, Xuchang fossil crania similarly exhibit mixed features, including European-like encephalization and supraorbital neurocranial vault morphology combined with nuchal gracilization associated with east Asian fossils. Moreover, their low, sagittally flat, inferiorly broad neurocrania possess Neandertal-like occipital and temporal labyrinthine morphology. Do these fossils reflect sole ancestral descentance from local Chinese *Homo erectus* populations or shared ancestry with migrants from the area now known as Europe? New findings suggest that many genetically diverse and mixed ancient human populations co-existed in China during this period. This diversity likely resulted from both isolated evolution of indigenous populations and genetic comingling with western outsiders arriving through multiple migration patterns. Nevertheless, part of China's evolutionary history may be independent of migrations from Europe, with morphological features shared with ancient Europeans coevolving independently in archaic humans in China.

The related studies have been supported by the grants of Natural Science Foundation of China (41630102, 41672020).

Plantar pressure distribution in *Gorilla*

ROSHNA E. WUNDERLICH¹, ANGEL ZEININGER² and DANIEL SCHMITT²

¹Department of Biology, James Madison University, ²Department of Evolutionary Anthropology, Duke University

The nature of heel strike in African apes has been the source of considerable debate, but to date there are no quantitative data on *Gorilla* heel pressures to address this issue. We examined the nature of heel strike as well as midfoot loading and toe-off mechanics in gorillas at the North Carolina Zoo and compared these to plantar pressure in *Pan*. We collected peak plantar pressures in five gorillas (ages 5-34 years) walking along an outdoor runway instrumented with an EMED-st (Novel, GmbH) plantar pressure mat. Animals were simultaneously video-recorded by four cameras. *Gorilla* exhibits high but variable heel pressures (279±101.4 kPa) and a distinct heel strike. *Pan troglodytes* usually displays a distinct heel strike with a lower peak (210±140 kPa) but can also strike the lateral border of the foot simultaneously as has been observed in *Pan paniscus*. A midfoot break is indicated by high pressures along the lateral midfoot as the heel rises. The medial midfoot exhibits less relative

pressure than in *Pan*, especially when the highly abducted toe 1 is loaded heavily, perhaps indicating contraction of the intrinsic flexors to stiffen the midfoot. Toe off is at the 2nd or 3rd digits, and metatarsal heads 1-3 consistently exhibit peak pressures significantly higher than metatarsals 4 and 5 ($p < 0.05$) as in *Pan*, but even more prominently. While *Gorilla* and *Pan* share a general pattern of touchdown and toe-off, *Gorilla* touchdown, midfoot, and forefoot walking mechanics also resemble *Homo* quite closely.

Research supported by the National Science Foundation Grant BCS-1517561

Covariance between carpal morphology and suspensory behavior in extant anthropoids, with implications for functional analysis of fossil specimens

CRAIG WUTHRICH

Evolutionary Anthropology, Duke University

The anatomy of the wrist has been instrumental in reconstructing the positional behavior of many extinct primates, but very few carpal traits have been quantitatively confirmed to consistently covary with specific locomotor modes or postures among extant species. In this study, shape traits predicted to facilitate specific positional behaviors were quantified in a broad anthropoid sample using μ CT and laser scan data and evaluated for covariance with both quantitative and categorical characterizations of positional behavior. Traits found to covary with hypothetically linked behavior(s) while accounting for allometry and phylogeny were then used to create multivariate models evaluating the efficacy of carpal morphology in estimating anthropoid behavioral repertoires.

Carpal morphology is found to strongly covary with positional behavior across the anthropoid clade. Multivariate classification accuracy of wrist posture exceeds 90% after repeated 10-fold cross-validation, and proportions of suspension, quadrupedalism, climbing, and arboreality are accurately estimated from carpal morphology of out-of-sample extant taxa. Covariance is greatest with suspensory behavior, with the carpus modified to increase mobility at the midcarpal and proximal carpal joints, enhance flexor carpi ulnaris leverage and transmission of associated forces, and stabilize the capitate joint against non-stereotypical force vectors. Covariance with arboreal-only locomotor proportions is greater than with total proportions, reflecting the need for safe and secure grasping even among the most terrestrial anthropoids. These results advance our understanding of the complex relationships among form, function, and phylogeny while guiding future behavioral reconstructions of fossil carpal specimens.

Facial masculinity-femininity and socio-economic status: A study of sub-Saharan Africans' 3D facial models

ANAS IBRAH. YAHAYA¹ and CHRISTOPHE SOLIGO²

¹Department of Anatomy, Faculty of Basic Medical Sciences, College of Health Sciences, Bayero University Kano, Nigeria. Corresponding author: ANAS IY. Email: suhhis@yahoo.com, +2348128139785, ²Anthropology Department, Faculty of Social and Historical Sciences, University College London, 14 Taviton Street, London, WC1H 0BW. Co-author: CHRISTOPHE SOLIGO. Email: c.soligo@ucl.ac.uk, 020-7679-8839

ABSTRACT

In the context of human identification, the ability to differentiate between male and female individuals is inherent especially in the face. In addition, the development of sex-specific facial characteristics has been linked to hormonal factors, which in turn have been linked to behavioural variation and environmental variables. The present study introduces a method for quantifying faces on a masculinity-femininity gradient and seeks to determine a) the extent of variation in masculinity and femininity scores between the sexes, and b) whether those scores correlate with socio-economic status. The faces of 426 participants (215 males, 211 females) from the Hausa ethnic group in Nigeria were scanned using a 3D surface laser scanner. Facial dimensions using 22 standard facial landmarks were measured in Geomagic software version 12. Principal component analysis (PCA) was performed on 35 sexually dimorphic dimensions (determined through independent two sample t-tests). The PCA generated 8 principal components (PCs), which explained most of the variation in the sample. Masculinity-femininity scores were generated from those 8 PCs using Discriminant Functions Analysis (DFA). Jack-knifing resulted in 29.2 % of the males being misclassified as female and 33.2 % of the females being misclassified as male. Hence, the average accuracy in determining sex from facial dimensions in our sample population was 68.9% (range: 66.8% -70.8%). The masculinity-femininity scores derived from the DFA were found to be associated with a summary measure of socio-economic status in women but not in men.

This research was funded by the Tertiary Education Trust Fund Nigeria (TETFund, Nigeria), No 6 Zambezi Crescent off Aguiyi Ironsi Street, Maitama, Abuja, FCT Nigeria.

Comparing intratooth isotope profiles of modern warthogs and fossil suids: a potential proxy for hydroclimate seasonality of hominin fossil sites

DEMING YANG¹, KEVIN T. UNO² and THURE E. CERLING³

¹IDPAS, Stony Brook University, ²Division of Biology and Paleo Environment, Lamont-Doherty Earth Observatory of Columbia University, ³Department of Geology and Geophysics, University of Utah

ABSTRACTS

Previous studies investigating paleoenvironments in eastern Africa have employed stable isotope analysis of enamel that often utilizes a single sample from each tooth. Alternatively, sampling a tooth along its growth axis produces an intratooth isotope profile. Carbon and oxygen isotope variability reflects changes in diet and body water over the course of tooth mineralization, which can serve as a proxy for environmental seasonality in vegetation or rainfall.

To explore whether intratooth profiles of modern suids can guide our interpretation of fossil suids, we selected third molars of modern warthogs (*Phacochoerus* spp.) from Kenya, and two fossil suids (*Metridiochoerus* and *Notochoerus*) from the early Pleistocene members of the Koobi Fora and Nachukui Formations (~2.1 – 1.4 Ma). We investigated variations in diet and body water by examining carbon and oxygen isotopes in enamel using intratooth profiles.

The $\delta^{13}\text{C}$ values of modern warthogs indicate that they have constant C_4 diets throughout the year, with very little intratooth variation ($\Delta = \sim 1\text{‰}$ to 2‰), whereas a much greater variability is observed in $\delta^{18}\text{O}$ ($\Delta = \sim 2\text{‰}$ to 5‰). Compared to modern warthogs, fossil suid diets are similarly C_4 -dominated and relatively invariant, indicating that sufficient C_4 vegetation was available throughout the year. They also have similar means and amplitudes in $\delta^{18}\text{O}$ values.

Using profiles in modern suids as an interpretive framework, fossil suid profiles can be used to reconstruct hydroclimate seasonality of hominin fossil and archeological sites. Similar methods can be extended to other modern and fossil mammals with hypsodont or continuously growing teeth/tusks.

This study is funded by the Leakey Foundation, Stony Brook University, Turkana Basin Institute, Sigma Xi and the University of Utah

Tracing gibbon phylogeography in Southeast Asia using complete mitochondrial genomes

LU YAO^{1,2,3}, ROBERT DESALLE³ and CHRISTIAN ROOS⁴

¹Anthropology, Hunter College, ²Mammalogy, American Museum of Natural History, ³Sackler Institute for Comparative Genomics, American Museum of Natural History, ⁴Primate Genetics Unit, German Primate Center

Gibbons are inadequately studied small apes and are species-rich compared to great apes. Their species-level phylogeny has been largely resolved, although certain discordances exist, perhaps because of hybridization between species. Our research draws upon wild gibbon specimens housed in museum collections around the world to expand knowledge about the phylogeography of gibbons in Southeast Asia. We used next generation sequencing techniques to sequence

the mitochondrial genomes and portions of the nuclear genome of 100 gibbon museum specimens. The reconstructed phylogeny using maximum likelihood methods traces the colonization of gibbons in Southeast Asia. We show that like orangutans and long-tailed macaques, there is a split in the groups living on the island of Sumatra, with white handed gibbons (*Hylobates lar*) occurring to the north and the mountain agile gibbon (*H. agilis*) occurring to the south. Additionally, on the island of Borneo, four taxa are present showing that *H. abbotti* is most closely related to *H. funereus*, making up the two taxa found in northern Borneo. These two species are sister group to *H. muelleri* in the southeast, and *H. albibarbis* to the southwest is sister to all Bornean species. Moreover, this research has applications for conservation biology. Most gibbon species are classified as “Endangered” or “Critically Endangered” so targeted action is acutely needed to promote gibbon conservation, and one way to achieve this is to confirm taxon identity as a basis for appropriate recognition of individuals for reproduction in captivity with a view to subsequent reintroduction into their natural habitats.

This project was funded by the Gerstner Postdoctoral Fellowship awarded to Lu Yao from the American Museum of Natural History.

Tooth Size and Vertebral Neural Canal Size as Bioarchaeological Evidence of the Developmental Origins of Health and Disease Hypothesis

SAMANTHA L. YAUSSY

Anthropology, University of South Carolina

The Developmental Origins of Health and Disease (DOHaD) hypothesis postulates that early life stresses can impact later life health outcomes. Although the available evidence of stressful events and health outcomes is limited for past populations compared to studies of modern populations, bioarchaeologists can utilize non-specific skeletal indicators to investigate the effects of stresses throughout the developmental period, thus contributing temporal depth to the DOHaD literature. This study uses tooth and vertebral neural canal size as indicators of stressful events occurring during the developmental period to assess DOHaD in Industrial-era England. The urban skeletal samples examined—Coach Lane, St. Peter’s Wolverhampton, New Bunhill Fields, and St. Bride’s Fleet Street—are dated to the 18th and 19th centuries, when England was undergoing a marked increase in urbanism and industrialization. Measurements of the lumbar vertebrae and non-polar premolars and molars, as well as data on age, sex, and socioeconomic status (SES) were incorporated into 2- and 3-way ANOVA. Results indicate that females and low SES individuals had smaller teeth compared to males and high SES individuals, whereas females, high SES individuals,

and individuals under the age of 60 had smaller neural canal sizes compared to males, low SES individuals, and individuals over 60 years of age. The tooth size findings suggest that early childhood stresses were concentrated among marginalized populations, such as women and the poor. Likewise, the neural canal results suggest stressful events continued for females throughout the childhood and early adolescent periods and may have impacted patterns of mortality in adulthood.

Supported by NSF (BCS-1649757) and the Office of the Vice President for Research at the University of South Carolina (SPARC Graduate Research Grant).

Bigger bipeds should have shorter arms: a new perspective in hominin limb evolution

ANDREW K. YEGIAN

Human Evolutionary Biology, Harvard University

Bipedalism has been a major factor in human evolution, shaping our anatomy in many ways. One such way is in interlimb proportions, with an evolutionary trajectory towards relatively shorter arms. However, there has also been an evolutionary trajectory towards larger body size and overall longer legs in hominins. Contextualizing size differences when comparing anatomy between hominins is critical to understanding how bipedalism drove changes in anatomy. Here I present a simple arm-leg scaling model from my experimental research on arm swing mechanics during walking in humans. The model, derived from mechanical first principles, predicts that longer-legged humans require relatively shorter arms to maintain similar mechanics during walking. When fossil hominins are compared to the arm-leg scaling relationship derived from experimental data, the model closely fits the evolutionary trend towards relatively shorter arms in hominins. *Homo floresiensis* offers an evolutionary test-case for the model, exhibiting a recent reversal in both leg and arm lengths. According to the model, *H. floresiensis* had precisely the arm length one would expect for a dwarfed modern human or *H. erectus*. I argue that fossil arm lengths indicate a common hominin walking form found earliest in *Australopithecus afarensis* (Lucy). Further tests of the model with bipedal theropod dinosaurs show that the same principles explain the same evolutionary trend in an unrelated bipedal taxon. Intriguingly, modern humans likely have relatively shorter arms than Lucy for the same reason *Tyrannosaurus rex* had relatively shorter arms than small theropods: size effects in the mechanics of bipedalism.

Seasonal changes in sleep duration may be adaptive among San hunter-gatherers

GANDHI YETISH and JEROME SIEGEL

Psychiatry and Biobehavioral Sciences, University of California, Los Angeles

ABSTRACTS

San hunter-gatherers average approximately 7 hours of sleep per night in the winter, but only 6 hours per night in the summer. This pattern has not been observed in most other populations worldwide, though few sleep studies have been conducted in subsistence societies to date. In the United States, short sleep duration is associated with a general lack of energy, but it is unknown if the San exhibit chronic fatigue in the summer when their average sleep duration is considerably shorter. We measured seasonal changes in alertness in the San population with the Psychomotor Vigilance Task (PVT), which measures reaction time as a proxy for general vitality. This test has been considered the "gold-standard" for quantitative assessment of alertness, as it does not require literacy or English proficiency, instructions are simple, and performance does not improve with practice. Tests were conducted with 19 San adults, 2-3 times per day for 3-5 consecutive days. This protocol was repeated in July 2016 ("winter"), November 2016 ("summer"), and March 2017 (intermediate). We found a significant seasonal effect: the slowest reaction times were in winter, when sleep duration was longest, and the fastest were in the intermediate season. Sleep duration itself was not significantly correlated with PVT score. These results suggest that San are not suffering from insufficient sleep in the summer. There is currently no established paradigm for why sleep should vary seasonally. We propose that seasonal changes in sleep may be adaptations to changing environmental conditions and weather patterns.

An assessment of the neurovascular structures of the trigeminal nerve and their relationship to tooth morphology in *Rattus sp.*, *Pithecia pithecia*, *Saimiri sciureus*, and *Chiropotes sp*

CAITLIN B. YOAKUM and CLAIRE E. TERHUNE
Department of Anthropology, University of Arkansas

The trigeminal complex provides both sensory and motor innervation to the masticatory complex and is extensively used in chewing to assess food properties and modulate bite forces. However, few studies have examined the relationship between the trigeminal complex nervous tissues and the bony canals of the mandible through which these tissues pass, and no study has directly assessed the cross-sectional area and overall volume of the nervous tissues of the masticatory apparatus in relation to tooth morphology. Using microCT data from four primate species and one rat species ($n = 20$) we examined variation in cross-sectional areas of the mental foramen, mandibular foramen, the mandibular canal below M_1 , and the corresponding nervous tissues (i.e., mandibular nerve and periodontal ligament) at these locations. These measurements were compared to the tooth morphological variables of Dirichlet's

normal energy (DNE), occlusal patch count (OPC), and average slope. Results indicate that the bony structures cannot be used as a proxy for the size of the nerve that passes through them. Nervous tissues occupied 20-70% of the mental foramen, 10-90% of the mandibular foramen, and 22-99% of the cross-section beneath the first molar. While OPC did not predict overall nerve volume, regressions showed DNE ($r^2 = 0.715$ and $p = 0.017$) and slope ($r^2 = 0.645$ and $p = 0.03$) to be good predictors for nervous tissue volume, suggesting a relationship between dental topography and innervation. These results indicate that while the nervous soft-tissues have a strong relationship to dietary adaptations, the bony morphology may not.

Relationship between chondrocranial-derived components of the nasal complex and cranial base

TODD R. YOKLEY¹, BENJAMIN JACOBSON², JILL E. SCOTT¹ and NATHAN E. HOLTON³

¹Department of Sociology and Anthropology, Metropolitan State University of Denver, ²College of Dentistry, University of Iowa, ³Department of Orthodontics, University of Iowa

The chondrocranium is an embryonic structure that spans the cranial base and extends into the facial region to form much of the nasal complex (e.g., ethmoid, nasal septal cartilage). Recent work suggests that early developmental variation in chondrocranial-derived nasal structures may strongly influence the development and morphology of the adult nasal complex. Given this relationship, aspects of the nasal complex may be correlated with the chondrocranial-derived cranial base by virtue of sharing a common developmental origin. Thus, to more completely explain nasal variation, it is important to determine whether the morphology of chondrocranial-derived structures in the nasal complex is correlated with the morphology of chondrocranial-derived structures in the cranial base. We tested the null hypothesis of independence comparing the chondrocranial-derived nasal septum (size and magnitude of deviation) to chondrocranial-derived cranial base size and shape data (symmetric and asymmetric components) using 3D coordinate landmarks from a sample of $n=70$ CT scans of adult human subjects. Our results reveal a significant correlation between the size of the nasal septum and the chondrocranial-derived cranial base, ($p < 0.001$). Despite this, septal size was uncorrelated with the symmetric ($p = 0.198$) and asymmetric ($p = 0.988$) variation in the chondrocranial-derived cranial base. Similarly, there was no correlation between septal deviation and the symmetric ($p = 0.547$) and asymmetric ($p = 0.839$) variation in the chondrocranial-derived cranial base. Our results suggest that, despite

similar embryonic origins, chondrocranial-derived nasal components (at least as represented by the nasal septum) are independent from chondrocranial-derived components of the cranial base.

Analysis of an isolated hunter-gathering population, the Pericú, and implications for the effects of isolation on hominin skeletal remains

COLLEEN B. YOUNG¹, JUAN MANUEL ARGUELLES² and BERNARDO YÁÑEZ²

¹Anthropology, University of Missouri, ²Antropología Física, DAF El Museo Nacional de Antropología

The Pericú were a group of early Amerindians who colonized the southern tip of the Baja California peninsula ~ 12,000 B.P. (Laylander and Moore, 2006). Archaeological, ethnohistoric, and biological evidence all point to the isolation of this population for most of the Holocene, thereby retaining early Amerindian morphologies. This is a preliminary analysis to evaluate body size and shape in the Pericú relative to a large global sample, and to draw conclusions for understanding the evolution of the isolated hominins, *Homo floresiensis* (LB1).

To examine body shape and size, I measured: humeral, radial, femoral, and tibial maximum length, femoral head, and bi-iliac breadth of Pericú ($N = 40$). Measurements were then compared to climatically similar, non-isolated hunter-gathering populations ($N = 504$). Results indicate that body shape, including brachial and crural indices, and bi-iliac breadth, are significantly different for the isolated Pericú ($P < 0.01$). Further, body mass, including femoral head size, is also significantly different ($P < 0.001$). The Pericú had a body mass most similar to Andaman Islanders and Negritos, and a body shape most similar to individuals in Sudan. The unique body size and proportions of the Pericú may be a product of physical isolation on the Baja California peninsula, or it may be an artifact of alternative biological or ecological factors. Future research will compare the Pericú to additional island and isolated populations in order to explore causal factors in body proportions.

This research is funded by NSF GRF and NSF GROW grant # DGE-1443129.

Influence of substrate compliance on wild primate gait kinematics

JESSE W. YOUNG¹, NOAH T. DUNHAM¹, ALLISON MCNAMARA² and LIZA J. SHAPIRO²

¹Anatomy and Neurobiology, Northeast Ohio Medical University, ²Anthropology, University of Texas at Austin

The influence of substrate compliance on gait mechanics has received little attention in previous studies of primate locomotion. Using high-speed video, we investigated how

ABSTRACTS

free-ranging platyrrhines in lowland Amazonian Ecuador adjust gait kinematics to variation in substrate compliance (N = 789 strides across eight species). We used a force gauge and stiff rope to quantify the compliance (displacement in centimeters per Newton of applied force) of a sample of 200 branches, palm fronds, and lianas representative of locomotor substrates. Substrate type and diameter explained 73% of the variance in compliance, with palms and branches tending to be more compliant than lianas (though the magnitudes of compliance differences varied across the range of diameters). We used this statistical model to estimate the compliance of the substrates utilized in each locomotor stride. The primates in our sample showed a variety of responses to increasing compliance, including decreased speeds (*Callicebus*, *Saguinus*, *Cebuella*) and – controlling for speed – increased stride lengths (*Pithecia*, *Lagothrix*), decreased stride frequencies (*Callicebus*, *Pithecia*, *Lagothrix*), increased duty factors (*Callicebus*), and increases in the average number of supporting limbs during locomotion (*Callicebus*, *Pithecia*). Overall, these changes in gait kinematics accord with biomechanical theory predicting that animals moving on compliant substrates can increase stability by reducing impact forces. Other species showed more enigmatic responses to increasing compliance, decreasing duty factors (*Ateles*) or not significantly adjusting kinematics at all (*Alouatta*, *Saimiri*). Overall, our results suggest that substrate compliance should be considered a critical parameter when evaluating primate locomotor performance and locomotor evolution.

Research supported by NSF BCS-1640552 and BCS-1640453.

Testing the effectiveness of methods for estimating biological sex from subadult skeletal remains

DOROTA ZABNICKA

Anthropology, Humboldt State University

The estimation of biological sex is one aspect forensic anthropologists and bioarchaeologists include within the biological profile of unknown decedents, and is key to a variety of research questions. Whereas methods for estimating sex of adult skeletal remains are relatively high in accuracy, these methods are often inconclusive when applied to subadults, especially prepubescent individuals, when many secondary sexual characteristics have not fully developed. Furthermore, existing methods have often been tested on samples with relatively homogenous ancestries, calling into question their reliability in more diverse populations. This project reviewed techniques used for the estimation of sex in subadult skeletal remains, and then tested the most promising methods on subadult individuals of known sex between ages 3 and 17 (n=40, 15 males, 25 females) in the Hamann-Todd Osteological

Collection housed at the Cleveland Museum of Natural History. Data collection included measurements of the dentition, cranium, long bones, ilium, talus, and calcaneus. Non-metric assessment included observations on the morphology of the eye orbits, mandible, and ilium. Whereas some of the methods showed promise in accurately estimating the sex of subadults, there was also substantial overlap in measurements/observations between sexes. This overlap may be, in part, due to the effects of stresses, such as disease and malnutrition, on skeletal development. This study identified several approaches that would benefit from further clarification of variables and methods of assessment (i.e. redefining methods reflecting a scale in variation), and a need for additional retesting on larger and more diverse samples with numerous individuals per age cohort.

Ecological niche models of human land use in Late Pleistocene Southeast Asia suggest both abiotic and biotic variables influenced human dispersal

ALEXANDRA J. ZACHWIEJA¹, FABRICE DEMETER^{2,3}, ANNE-MARIE BACON⁴, THI MAI HUONG NGUYEN⁵, ANH TUAN NGUYEN⁵, KIRA WESTAWAY⁶, PHILIPPE DURINGER⁷, JEAN-LUC PONCHE⁷, PHONEPHANH SICHANTHONGTIP⁸, THONGSA SAYAVONGKHAMDY⁹, TYLER E. DUNN⁹ and LAURA L. SHACKELFORD¹

¹Anthropology, University of Illinois at Urbana-Champaign, ²Center for Genomics, Natural History Museum, Copenhagen, Denmark, ³Homme et Environnement, Muséum national d'Histoire naturelle, Musée de l'Homme, France, ⁴Faculté de Chirurgie Dentaire, UMR5288 Centre national de la recherche scientifique, France, ⁵Institute of Archaeology, Vietnam Academy of Social Sciences, Vietnam, ⁶Department of Environmental Sciences, Macquarie University, Australia, ⁷Ecole de Observatoire des Sciences de la Terre, Université de Strasbourg, France, ⁸Department of National Heritage, Ministry of Information and Culture, Laos, ⁹Department of Medical Education, Creighton University School of Medicine

Ecological niche models (ENM) of species distributions and dispersal patterns are well established in the biological sciences. However, their use in paleoanthropological reconstructions of hominin niches is relatively recent, and has focused on out of Africa dispersals and human land use in Europe and Central Asia (Glantz et al., 2016). These studies have suggested that the most important abiotic variables for predicting human site use are moderate temperature, rainfall, and access to fresh-water. However, recent work in the biological sciences has demonstrated that models utilizing only abiotic climate factors may not provide a comprehensive picture of how a species utilizes its habitat. These studies have called for the inclusion of biotic (species-interaction) data to construct more comprehensive models (Gavin et al., 2014; Maguire et al., 2015).

Here, we used ENM to combine traditional climatic predictors of human land use with fossil estimates of human-carnivore competition (competition index) from five Late Pleistocene sites in Laos and Vietnam. Then, we constructed ENMs in the popular program MaxEnt to investigate the impact of both climate and species interactions on likely human dispersal patterns in Late Pleistocene mainland Southeast Asia. We validate ENM land-use predictions using known human occupation sites (n=20) to determine how inclusion of fossil species-interaction data may change predictions of human land use. In largely temperate Southeast Asia, models including temperature and rainfall fit well but are less informative predictors of land use (AUC = 0.94, Favorable niche space: 0.46-0.92%) compared to other abiotic (terrain, water access, vegetation) and biotic variables.

Funding for this research was provided by the University of Illinois Department of Anthropology, The Explorer's Club, and the Beckman Institute CS/AI Award

Pelvic sexual dimorphism: The relationship between sacral slope, body mass, and greater sciatic notch shape

SARAH M. ZALESKI

Anthropology, University of Florida

This study tests the hypothesis that biomechanical factors influence pelvic sexual dimorphism. I analyzed previously recorded pelvic shape data from the Hamann-Todd collection for the relationship between sacral slope (SS), body mass, and greater sciatic notch (GSN) shape. Three-dimensional landmark coordinate data for the left pelvis in 46 male and 52 female American white individuals aged 18-55 years were obtained from the Dryad repository. Geometric morphometric analyses in R Geomorph began with estimation of missing landmarks via thin-plate spline interpolation. Paired landmarks were reflected across the midplane yielding 125 total landmarks. SS was defined by the angle between the first sacral cranial endplate and a transverse plane. Body masses were retrieved from the Cleveland Museum of Natural History online database. After a Generalized Procrustes Analysis (GPA) of the entire pelvis, two-block partial least squares analyses tested the relationship between body mass, SS, and four GPA-aligned coordinates representing GSN shape. The association between body mass and GSN shape is not significant. The relationship between GSN shape and SS is moderate but significant in the total (p=0.001), female (p=0.003), and male (p=0.013) samples. Decreased SS is associated with a more posteriorly displaced GSN apex. Neither SS (t-test, p=0.757) nor the degree of SS and GSN association (compare.pls, p=0.423) significantly differ between sexes. Sex differences in body mass (t-test, p=0.023) may indicate that body mass influences GSN dimorphism, accounting for SS.

ABSTRACTS

SS affects how forces are transmitted to the pelvis. Its importance for GSN shape suggests that biomechanical factors influence GSN variation.

Exome Sequencing Reveals Patterns of Selection Across Brown Lemurs (*Eulemur*)

ANDREW J. ZAMORA¹, TIMOTHY H. WEBSTER^{3,4} and JASON M. KAMILAR^{1,2}

¹Anthropology, University of Massachusetts, Amherst, ²Organismic and Evolutionary Biology, University of Massachusetts, Amherst, ³School of Life Sciences, Arizona State University, ⁴Anthropology, University of Utah

Brown lemurs (*Eulemur spp.*), a speciose genus distributed across all Malagasy forested ecosystems, exhibit both phenotypic conservation and variation. For example, *Eulemur* species have similar overall ecologies (e.g. diets and activity patterns) but diverge in their mating systems and pelage coloration. The genome offers rich avenues for understanding the evolution of such diversity because it carries signals of natural selection shaping lineages. Exome sequencing is especially well-suited for this purpose, as it targets segments of the genome with clear phenotypic consequences. Further, the examination of non-synonymous and synonymous substitution rates (D_N/D_S) serves as a simple but powerful approach to examine selection acting on the coding regions of the genome. We sequenced a total of nine exomes from four *Eulemur* species (*E. flavifrons*, *E. ruffifrons*, *E. rubriventer*, and *E. mongoz*) and one *Propithecus* species (*P. coquereli*), to serve as an outgroup, via targeted exome capture. We mapped an average of 84.4 billion reads per sample to either the *P. coquereli* or *E. flavifrons* reference genomes. After mapping, each sample had 48.7–53.2 Mb of analyzable sequence. From these sequences, we identified 1.7 million *Eulemur* variant sites, of which 1.5 million were SNPs. With these variants, we examined D_N/D_S variation in a maximum likelihood framework. We found evidence for lineage-specific positive selection in genes associated with a variety of functions and pathways. We discuss these results in the context of known phenotypic variation across the genus and in light of the endangered status of several of the species we examined.

This work was funded via a grant from the University of Massachusetts Natural History Collections Summer Fellowship program

Lower molar endostructure in *Rudapithecus hungaricus* (late Miocene, Hungary)

CLÉMENT ZANOLLI¹, DAVID R. BEGUN² and JAY KELLEY^{3,4}

¹Laboratoire PACEA, UMR 5199 CNRS, Université de Bordeaux, Bordeaux, France, ²University of Toronto, Toronto, ON, Canada, ³Institute of Human

Origins, Tempe, AZ, USA, ⁴National Museum of Natural History, Smithsonian Institution, Washington, DC, USA

Rudapithecus is a hominid known from the 10 Ma site of Rudabánya, in Hungary, sharing features that are unique to the African ape and human clade. However, the taxonomic diversity within *Rudapithecus* and its phylogenetic relationships with other fossil and extant hominid taxa remain controversial. We used X-ray microtomographic imaging to characterize the endostructure of *Rudapithecus* lower molars and compared it with that of other European Miocene apes (*Dryopithecus* and *Ouranopithecus*), the South Asian Miocene ape *Sivapithecus*, and extant hominids. We assessed 3D tooth crown tissue proportions, enamel thickness distribution patterns and conducted geometric morphometric analyses of the enamel-dentine junction (EDJ). *Rudapithecus* has moderately thick enamel similar to *Pongo*, thicker than in *Dryopithecus* and extant African apes, but thinner than in *Ouranopithecus* and extant humans. The thickest enamel is found at the apex of the cusps, similar to *Gorilla*, while in the other extant hominids it is located more laterally along the cusps. In EDJ morphology the Miocene apes overlap with *Pongo* but not extant hominines. Among Miocene apes only, *Rudapithecus*, *Dryopithecus* and *Ouranopithecus* plot close to one another and are discriminated from *Sivapithecus*, consistent with previous analyses indicating that the European taxa form a clade. RUD 14 plots closest to *Ouranopithecus* and closer to *Dryopithecus* than to RUD 212. The difference between the two Rudabánya specimens is greater than the difference between *Rudapithecus* and *Dryopithecus*, which is consistent with previous observations suggesting the presence of more than one ape taxon at Rudabánya.

For the scans of the fossil specimens, we thank J.J. Hublin G. Röbner, A. Mazurier, R. Macchiarelli. Funding provided to CZ by the CNRS and to DRB from NSERC.

Functional morphology of chevron bones in mammals

ANNA M. ZAVODSZKY and GABRIELLE A. RUSSO
Department of Anthropology, Stony Brook University

Tail morphology and function vary considerably across mammals. While functional morphology studies have paid increasing attention to the caudal vertebrae, studies of the tail have largely ignored chevron bones – ventrally-positioned elements that articulate with the caudal vertebrae of most species, serving to protect caudal blood vessels and provide attachment sites for tail flexor musculature. Here, we systematically document chevron bone morphological variation among mammals (including primates, carnivores, and diprotodonts, among others) possessing different tail functions, including prehensibility,

terrestrial propulsion (use for pentapedal locomotion), and postural prop, during which chevron bones are presumably under different mechanical stresses and/or serve different mechanical roles. Our observations suggest that several types of chevron bones, possessing unique morphologies and differing sizes, can be identified along the tail and that they vary within and between tail regions (e.g., proximal). Preliminary scoring of these morphologies among taxa suggests that species known to employ their tails for terrestrial propulsion (e.g., *Macropus*) have chevron bones in the transitional and distal tail regions that differ from those of closely-related outgroup species, and we posit that these differences potentially reflect weight-bearing demands during pentapedal locomotion. We further qualify distinctions between prop-tailed and nonprop-tailed species, as well as between prehensile and nonprehensile-tailed mammals, including primates, and discuss the utility of metrics for quantifying specific aspects of chevron bone anatomy. This study offers new information about the functional morphology of mammalian tails, and we discuss the implications of this work for reconstructing tail function in the fossil record.

To live and die in the Ocoña Valley: the human remains from Corral Redondo, Peru

MARIA CECILA LOZADA¹, DANNY ZBOROVER² and SYLVIA CHEEVER¹

¹MAPSS, University of Chicago, ²Archaeology, Institute for Field Research

Corral Redondo, a unique ceremonial site in the Ocoña Valley of southern Peru, was previously known only through looted materials and brief reports starting from the 1940s. The remarkable collection of textiles, ceramics, shell, and metalwork of the highest quality were likely deposited there as ritual offerings. These further echo the site's premeditated position at the confluence of two rivers, a venerated focal point that stood at the heart of a valley rich with gold and silver ores. To better define the site's function and structure, in the summer of 2018 the Corral Redondo Project and field school conducted there the first systematic excavation. This demonstrated a continuous use by the Wari and Inca during the Middle to Late Horizon periods, and perhaps also by earlier cultures. Most interestingly, mummified human remains and a sacrificed adult male skeleton were also recovered, demonstrating that Corral Redondo was also used as a ceremonial burial location. In this talk we compare and contrast Corral Redondo's human remains and associated artifacts with mortuary practices elsewhere in the Ocoña Valley and the Andes. We are particularly interested in re-evaluating the early hypothesis that this was a lower-elevation *capacocha* inhumation, typically involving human sacrifice on sacred mountaintops. Additional

ABSTRACTS

lines of inquiry come from the attitudes of the current valley residents towards the site, and the rituals still conducted to ensure prosperity in contemporary mining activities.

The Corral Redondo Archaeological Project and field school were funded by Ms. Heidi King and the Institute for Field Research.

Impact forces and hindlimb vertical impulses in *Gorilla*

ANGEL ZEININGER¹, DANIEL SCHMITT¹ and ROSHNA E. WUNDERLICH^{1,2}

¹Evolutionary Anthropology, Duke University,

²Department of Biology, James Madison University

Heel strike impact transients (IT), the vertical force that develops rapidly at heel strike, are a widely reported feature of bipedal walking in humans, chimpanzees, bonobos, and orangutans. In humans, these transients are thought to cause stress fractures and osteoarthritis. The anatomy of the robust human foot, especially the calcaneus, is thought to moderate these forces. ITs appear to be less common in ape quadrupedalism, and no data exist on the presence of ITs in gorillas. We collected vertical impulse and IT data on seven gorillas ranging in age from 5 to 34 years at the North Carolina Zoo. Force and video data were collected as animals walked quadrupedally at self-selected speeds along an outdoor runway embedded with two force platforms. Peak IT magnitude, impulse, and timing were recorded for all steps. Impact transients associated with a quadrupedal heel strike were observed in 90% of all steps. This transient occurred very early in contact phase and average IT peak was $27\% \pm 14\%$ body weight. Younger gorillas had significantly higher ITs than adult gorillas, an ontogenetic pattern also observed in humans. The presence of high impulse values and impact spikes at heel strike, a pattern shared with humans, even during relatively slow quadrupedal walking further illuminates biomechanical (extended knees) and anatomical (robust calcaneus) similarities between humans and *Gorilla* and the evolution of heel-strike plantigrady and bipedalism.

Research supported by the National Science Foundation Grant BCS-1517561

Gut microbiota in the full gastrointestinal tract of a ring-tailed lemur (*Lemur catta*)

YAN ZENG¹, XUEQIN NI¹, DONG ZENG¹, LILI NIU², JIABO DENG², YANG LI¹ and YI ZHOU¹

¹College of Veterinary Medicine, Sichuan Agricultural University, Sichuan Province, Chengdu, China, ²Chengdu Wildlife Institute, Chengdu Zoo, Chengdu, China

Microbiota in the gastrointestinal tract (GIT) of herbivores are crucial for the digestion and absorption of nutrients. The spatial heterogeneity of the GIT allows a wide range of microbial

communities to inhabit it. However, most studies are limited to describing the microbiota of the large intestine indirectly through fecal samples. Therefore, little is known about the microbiota in other areas of the GIT. Here, we use samples collected at necropsy to investigate the microbial community in the full GIT (stomach, small intestine, large intestine, and faecal) of a captive ring-tailed lemur in China. A combination of denaturing gradient gel electrophoresis (DGGE) and 16S rRNA gene amplicon sequencing (V4 region) indicates that the microbiota of the stomach, small intestine, large intestine, and faecal are distinct. The highest microbial diversity was detected in the cecum. Overall, Firmicutes, Proteobacteria, and Bacteroidetes were the three most abundant phyla. Both in cecum and appendix, we found some cellulolytic bacteria *CHRISTENSENELLACEAE-R-7_group*, *TREPONEMA_2*, and *METHANOBREVIBACTER*. While *CITROBACTER* (Proteobacteria) is potentially pathogenic and detrimental to host health. Overall, this study improves our understanding of the microbial community in the GIT of the ring-tailed lemur, which may ultimately be useful for improving the care of both captive and wild populations of this endangered primate. However, additional data are necessary to fully describe the complex interactions of host and microbiota.

Chengdu Giant Panda Breeding Research Foundation (CPF2017-04)

Molecular Archaeological Research on Human Remains from the Khulhiin am and Khundiin khooloi Sites in Mongolia during the Mongol-Yuan period

NAIFAN ZHANG, DAWEI CAI, YAQI GUO, XINYUE SHAO, SIQI ZHU, YONGDI WANG, QIYAO LIANG and CHANG LI

School of Archaeology, Jilin University

In order to reveal the origins of human populations in Mongol-Yuan period, we carried out the ancient DNA analysis of seven individuals from the Khulhiin am and Khundiin khooloi sites in Mongolia. A 393 bp fragment of the mtDNA hypervariable region I (16017-16409) was amplified using three sets of overlapping primers. The identification of mtDNA haplotypes was analyzed by APLP, and AMG gene was amplified by a pair of primers for sex identification. Based on the geographic distribution of mtDNA haplogroups, and combining the results of shared sequence search, our results suggest that the populations from two archaeological sites maybe come from North Asia, Central Asia and Europe. Our results reveal vividly the complex population structure in the Mongol-Yuan period, which has the vital significance to understand the social structure, population migration and fusion between the East and West. In addition, in terms of gender identification, our test results are completely consistent with the results of physical anthropology.

Particularly, we successfully identified the gender of adolescent N2 which physical anthropology failed to recognize. This result shows the reliability and accuracy of genetic testing, as well as the advantages of ancient DNA analysis.

Paleodemography of the Hamingmangha Site - a Neolithic Settlement Abandoned after a Disaster

QUANCHAO ZHANG¹, QIAN WANG², HONG ZHU¹, PINGYUAN MU¹, SUNZIFENG RUAN¹, SEN YOU¹, NYAMJANTSAN OTGONTAMIR¹, YIRU WANG¹ and TAO HAN¹

¹School of Archaeology, Jilin University, ²College of Dentistry, Texas A&M University

The Hamingmangha Site is a Neolithic settlement located in Kezuozhongqi, Inner Mongolia, China, dating over 5,000 years BP, where 53 one-room dwellings were excavated, and remains of at least 181 human individuals were identified, including 97 bodies stacked in a single dwelling. Paleodemographic analysis indicated that there were three mortality clustering peaks in the juveniles, young adults, and middle-aged adults respectively, with a mean age-at-death of 26.8 years. The profile of age at death at the Hamingmangha Site was close to that of a natural living population during the Neolithic Age, suggesting a quick cause of death throughout the population. Moreover, the death toll (>181) would be higher than the low limit of the theoretical population size (159) living in this prehistoric village, if at least three members in one Neolithic household were estimated for all 53 dwellings. This may have led to the near extinction of the Hamingmangha population and total abandonment of the settlement. In addition, skeletons generally lacked signs of violence-related trauma; the way the skeletons were stacked in the houses demonstrated rapid deposition of dead bodies with personal decorations such as jade wares, which were unremoved. All of these indicate that the cause of death was not interpersonal-conflict related, but more likely a communicable disease outbreak. A comprehensive study of the Hamingmangha Site including a paleomicrobiological study, would help identify the pathogens and decipher the Hamingmangha phenomenon, and enrich our knowledge of ancient epidemics and their impact in early human community and settlement abandonment strategy.

Artificially deformed skulls from Da'an Site - Earliest Evidence and Longest in situ Practice during the Neolithic Age

QUN ZHANG^{1,3}, QIAN WANG², QUANCHAO ZHANG¹, XIAOFAN SUN¹, HEXUN CUI¹, ZINING ZOU¹, PENGZHEN LI¹ and JIAXIN LI¹

¹School of Archaeology, Jilin University, ²College of Dentistry, Texas A&M University, ³School of Humanities, Nanyang Technological University

ABSTRACTS

Artificially deformation of the head (ADH) was an old tradition used to reshape the head; its exact purposes however, are unknown. The earliest confirmed signs of ADH in modern humans were from now reburied aboriginal Australian skulls dating back to 13,000 years BP. In this study, we reported a series of ADH from a Neolithic site at Da'an, Jilin, Northeast China. Out of 25 skeletons, ten skulls carried signs of ADH, all being fronto-occipital deformation type. Ages at death of these individuals from both sexes ranged from juveniles to adolescents, young adults, and full adults. These skulls were dated to be lasting 7,000 years from 13,000 BP to 6,000 years BP during the Neolithic Age. Previous studies on cultural remains and PaleoDNA demonstrated in situ cultural and genetic continuity. All these suggest that the Da'an Site not only yields the earliest confirmed ADH case from the eastmost Old World with materials available for scientific studies, but also carries the longest duration of ADH practice at one single prehistoric site. Further studies in bioarchaeology and ethnography will deepen our knowledge of this intriguing tradition and shed light on its origin and diffusion.

Dental microwear analysis of the ancient population from Jiayi Cemetery, Northwestern China

WENXIN ZHANG^{1,2}, HEXUN CUI¹, PENGZHEN LI¹ and JIAXIN LI¹

¹School of Archaeology, Jilin University, ²School of History, Classics and Archaeology, the University of Edinburgh

The reconstruction of diet of ancient populations, especially for those living thousands of years ago, is a significant process to help us understand human's lifestyle in the past. Methods and techniques have been introduced in to make this work come true. However here is the question: how do all different methods work together to show the dietary construction?

This study thus aims to discuss the diet of an Early-Iron-Age population from Xinjiang Uygur Autonomous Region, mainly conducting an analysis on the dental microwear using the method provided by Spanish anthropologist Pérez-Pérez (1990), then compare the result with archaeological records and other research findings. A three-dimensional digital microscope (KEYENCE VHX-2000) was used to observe the lengths and orientations of striations in a 1mm² area on the buccal faces of 10 well-preserved molars belonging to individuals without serious oral diseases. Index of LH/LV was calculated and compared with modern populations whose subsistence economies and diets are known.

According to the dental microwear result, the average index of LH/LV of Jiayi population (77.5%) is comparatively close to the index of the Tasmanian aborigines (81.9%), whose diet

is mainly occupied by meat, while wild plants also contribute to their nutriment. Archaeological findings of biological remains, as well as isotopic result of another population in the same cultural background both show the similar tendency, while the heavy and oblique tooth wear indicates the hard trait of the food kind. Further comparison on individuals is still on plan to be conducted later.

This study was funded by Chinese Scholarships Council.

High Altitude Adaptation and the Evolutionary History of *EPAS1* Gene in Tibetan Population

XINJUN ZHANG¹, KELSEY WITT¹, XIN JIN³, ASAN ASAN³, RASMUS NIELSEN⁴ and EMILIA HUERTA-SANCHEZ²

¹School of Natural Sciences, University of California, Merced, ²Department of Ecology and Evolutionary Biology, Brown University, ³Shenzhen Headquarter, BGI, ⁴Department of Integrative Biology, University of California, Berkeley

Modern humans have settled in some extreme environments since migrating out of Africa. One example is Tibetans, who have adapted to the hypoxic environment of high altitudes. The *EPAS1* gene, which regulates physiological responses to the variation in oxygen supply, was previously identified as being under strong positive selection in Tibet. This beneficial haplotype also matched closely with the *EPAS1* haplotype in Denisovans, an archaic human group from 40,000 years ago, suggesting that this haplotype was introduced through adaptive introgression. However, questions remain regarding the actual source population of the *EPAS1* haplotype, as well as the timing of admixture.

In this study, DNA sequences (30x depth) including the *EPAS1* region from 148 Tibetan individuals were obtained, with altitude ranging from 3000 to 4800 meters above sea level. We identified a positive correlation between altitude difference and *EPAS1* mean Fst between groups within Tibet, which may indicate a direct correlation between the selection on *EPAS1* and change in oxygen level. To further clarify the history of *EPAS1*, we applied SPrime method and identified two introgressed segments in *EPAS1* region. By comparing the genetic divergence between Neanderthals and Tibetan *EPAS1* haplotype, we confidently suggested that an archaic population highly alike the Denisovan, not Neanderthals, admixed with East Asian populations including Tibetans, and introduced the *EPAS1* beneficial haplotype. In addition, we fit to the observed distribution of introgressed haplotype lengths, and estimated an approximate time of admixture.

Mandibular shape variation within hylobatid species is not consistent with genetic diversity

JULIA M. ZICHELO

Sackler Educational Laboratory for Comparative Genomics and Human Origins, American Museum of Natural History

Intraspecific neurocranial shape variation within extant hominoids has been shown to reflect patterns of neutral genetic diversity. Taxa which are more cranially diverse, are also more genetically diverse. This suggests that neutral evolutionary processes drive cranial shape variation within hominoid species. Here we tested for this pattern in hylobatid mandibular shape variation. We expect the mandible—unlike the neurocranium—to be subject to strong selective and developmental pressures due to mastication. We analyze 3D geometric morphometric mandibular shape variation within five hylobatid species (*Hylobates klossii*, *H. moloch*, *H. pileatus*, *H. lar* and *Symphalangus syndactylus*) and compare the sum of eigenvalues to nucleotide diversity (π) within each species. Interestingly, mandibular shape variation within different species is fairly consistent across taxa, which contrasts with their levels of genetic diversity which vary substantially between hylobatids. This suggests that selection and developmental plasticity have played a major role in generating shape variation in the hylobatid mandible. The exception is the *Hylobates lar* group, which shows increased intraspecific mandibular shape variation in comparison to other taxa. *H. lar* also shows the highest level of genetic diversity within all hylobatids included here. Our results imply that—unlike the neurocranium—mandibular shape variation cannot be used as a reliable proxy for historical population inferences, due to functional pressures substantially obscuring this signal.

Anatomical convergences in adult Gorilla and Pongo males

ADRIENNE L. ZIHLMAN and CAROL E. UNDERWOOD

Anthropology, University of California, Santa Cruz

Prior to 10 million years ago, *Gorilla* and *Pongo* shared a common ancestor of moderate body size that differed in body structure and locomotor skill from these two modern ape genera. Details about this common ancestor are unknown. Though once isolated, each branch evolved away from the common ancestor and from each other in anatomy and behavior. *Gorilla* adapted to life in equatorial forests in Africa, and *Pongo* to tropical rainforests in Asia. *Gorilla* and *Pongo* males converged in large body size, extreme sexual dimorphism, and distinct morphologies that denote “prime adult male”—for *Gorilla*, “silverback male” and “flanged male” for *Pongo*. Quantitative dissection data (n=4) illustrate that anatomical markers of sexual dimorphism in

ABSTRACTS

body composition, mass and linear proportion, although distinct in each species, have similar functions that are superimposed upon their divergent locomotor adaptations. This comparison of *Gorilla* and *Pongo* demonstrates that extreme male body size and sexual dimorphism reflect shared selective pressures in males from these African and Asian ape genera. Formidable size reduces vulnerability from terrestrial predators or conspecific males. Large bodies have large guts for digesting high fiber foods and "space" to store body fat. Sexually dimorphic anatomical markers define and identify high rank or prime males, and females apparently prefer them. Anatomical features such as limb lengths and muscle distribution underpin locomotor distinctiveness. Convergent body size and anatomies of these two ape genera are outcomes of more than 10 million years of independent evolution on each branch.

Divergence between humans and chimpanzees at the cellular level

TRISHA M. ZINTEL, DELANEY DUCEY, JASON PIZZOLLO and COURTNEY C. BABBITT

Biology, University of Massachusetts Amherst

Intercellular signaling facilitated by cell adhesion is vital for many biological processes, such as synapse formation in the brain or metastasis of cancerous cells, and consequently represents a potential mechanism by which functional differences among primates may have evolved. However, it is unclear how variation at the cellular level contributes to the well-characterized differences in organism-level phenotypes among primates. Previous work has identified that gene expression differences in cell adhesion pathways exist between humans and chimpanzees. Here, we determined differentially expressed (DE) genes between human and chimpanzee brain samples via RNA-Seq and followed up with a comparative cell biology approach to investigate differences in cellular phenotypes using cell lines from each species (2-3 individuals per species). We found 3,648 significantly DE genes between the brains of each species that were significantly enriched ($p < .05$) for several pathways related to cell adhesion either directly, e.g. "focal adhesion", or indirectly, e.g. "glioma", a neural cancer pathway for which 13 of the 19 DE genes are specifically involved in cell adherence to the extracellular matrix. We then assayed the capability of skin fibroblasts to adhere to plastic when challenged with flowing liquid. We found that chimpanzee fibroblasts adhered sooner and remained adherent for a significantly longer period of time than human fibroblasts (t-test, $p < .05$). Additional investigation into neural cells derived from induced pluripotent stem cells

(iPSCs) from both species will allow us to further characterize differences in cell adhesion capable of influencing interspecies differences in neural processes.

The National Chimpanzee Brain Resource is supported by the NIH (NINDS).

Intergenerational Fitness Effects of Early Life Adversity in Baboons

MATTHEW N. ZIPPLE¹, ELIZABETH A. ARCHIE^{2,3}, JENNY TUNG^{1,3,4,5}, JEANNE ALTMANN^{3,6} and SUSAN C. ALBERTS^{1,3,4}

¹Department of Biology, Duke University,

²Department of Biological Sciences, Notre

Dame, ³Institute of Primate Research, National Museums of Kenya, ⁴Department of Evolutionary Anthropology, Duke University, ⁵Duke Population Research Institute, Duke University, ⁶Department of Ecology and Evolutionary Biology, Princeton University

In both human and nonhuman primates, early life adversity can affect an individual's health, survival, and reproduction for years or even decades after the adverse experience. Whether early life adversity has intergenerational effects on direct measures of offspring fitness is largely unanswered. Here we present a prospective, longitudinal study of a wild, long-lived primate, the yellow baboons of the Amboseli ecosystem, Kenya. We previously showed that early life adversity dramatically shortens females' own lifespans in this population, in some cases by as much as a decade. Here, we demonstrate that early life adversity also negatively affects the survival of these females' juvenile offspring ($n=169$ females; $n=689$ offspring), independent of the environmental conditions faced by the juveniles themselves. Specifically, focal offspring whose mothers experienced a close-in-age sibling ($p=0.02$) or maternal loss ($p=0.009$) during the mother's early life are less likely to survive. These effects are linked to reduced viability of those mothers ($p=0.03$), who appear to be less able to successfully rear surviving young towards the ends of their lives. Together, our findings demonstrate that adversity experienced by baboons in one generation can have strong effects on the survival of offspring in the next generation, even if those offspring did not themselves experience early adversity. They also suggest that intergenerational effects of maternal early adversity are partially mediated by poor phenotypic quality of those mothers.

This research was funded by the National Institutes of Health, the National Science Foundation, the Leakey Foundation, and the Max Planck Institute for Demographic Research.

The Hominid Anterior Inferior Iliac Spine and Why it Reflects the Unique Anatomy of our Iliac Isthmus

DEXTER ZIRKLE and C. OWEN LOVEJOY

Division of Biomedical Sciences and Department of Anthropology, Kent State University

Human ilia are short, broad, and laterally-oriented, whereas those of apes and other higher primates are tall, narrow, and posteriorly-oriented. Although these differences are well known, their developmental basis has never been fully described. We examined the emergence of the anterior inferior iliac spine (AIIS) throughout ontogeny, and analyzed the vascular anatomy of the human ilium via gross dissection. We also investigated the internal vascular tree of a mammalian quadrupedal ilium using micro CT and compared this with known vessel patterns in humans. We found that the shortening and broadening of the human iliac isthmus both reflect the same developmental mechanism that also underlies the unique human trait of an anterior inferior iliac spine formed via a separate apophysis. We posit that these vascular differences may have facilitated adoption of the unique hominid iliac morphology that promoted upright walking.

The Embodiment of Gendered Weaning Stress in the Dental Structures of Archaic Texas Hunter-Gatherers: An Analysis of Age-at-Formation of Linear Enamel Hypoplasia

CAROLINE L. ZNACHKO and LAUREN G. KOUTLIAS
Anthropology, Texas State University

While research analyzing incidences of linear enamel hypoplasia (LEH) in bioarchaeological remains is abundant, research specifically concerning dental stress in Texas Archaic populations is more limited. This study analyzed a semi-sedentary hunter-gatherer population from the Ernest Witte mortuary site (41AU36) utilized from 2700 BCE to 1500 CE. Previous research on this sample lacked modern, rigorous data collection methods and a comprehensive approach in assessing incidences of LEH. The main objective of this research was to analyze LEH in the dentition of Ernest Witte individuals to assess 1) the relationships between prevalence of LEH and change over time in the Archaic period, 2) the average and range of age-at-onset of LEH at 41AU36 in comparison with other hunter-gatherer groups, and 3) the relationship between LEH and morbidity and mortality. To address these questions, measurements of unworn crown heights and distances between each LEH and the cervico-enamel junction were collected and utilized in equations adapted from Goodman and Rose (1990) for estimation of age-at-onset. Results indicate clear and significant relationships between age-at-formation and sex and mortality, revealing earlier first incidences of LEH

ABSTRACTS

for females, and earlier age-at-onset for individuals who died as young adults. Consideration of comparative studies suggests that this patterning is potential evidence for gendered weaning practices. This study provides further insight into both populational patterns of childhood stress among individuals from 41AU36 and improves understandings of Texas Archaic hunter-gatherer responses to changes in the environment.

This research was not funded.

Among elderly Kuwaitis social support buffers functional and physiological dysregulation

KATHERINE A. ZNIDARSIC¹, ASHLEY N. EDES¹, YAGOUB AL-KANDARI² and DOUGLAS E. CREWS¹

¹Anthropology Department, The Ohio State University, ²Anthropology Department, Kuwait University

Stress generates physiological dysregulation of biomarkers leading to poor future health. In western populations, social support buffers negative effects, seen by an inverse relationship between social support and mortality. This research investigates whether social support buffers against physiological dysregulation in elderly Kuwaiti individuals (n = 253, aged 60+ years). Social support includes marital status, perceived social support, religiosity, and children living at home. Biomarkers tested include norepinephrine, epinephrine, cortisol, dehydroepiandrosterone sulfate (DHEA-S), systolic and diastolic blood pressure, waist-hip ratio, glycosylated hemoglobin (Hb_{A1c}), low-density lipoprotein cholesterol (LDL), and high-density lipoprotein cholesterol (HDL). T-tests and linear regression were used to test for associations with each biomarker. ANOVA and post-hoc analyses were used for associations between social support and each biomarker and men (n = 79) and women (n = 174) separately ($\alpha = 0.05$). Women had significantly lower DHEA-S. In men, age was negatively associated with LDL, in women, age was negatively associated with DHEA-S. Among men, being married associated significantly with lower DBP and HDL, higher perceived social support associated significantly with lower norepinephrine and DBP, being religious associated significantly with lower LDL, and children at home associated significantly with lower DHEA-S. Among women, being married associated significantly with lower norepinephrine and cortisol, having higher perceived social support associated significantly with lower DBP, Hb_{A1c}, and LDL. Social support resulted in lower levels of stress-related biomarkers for men and women, sex differences are observed. This is consistent with those observed in western societies, suggesting social support buffers stress-induced physiological dysregulation across populations.

Uncovering the institutionalized: Reconstructing the interplay of gender, sex, and social race on the lives of women institutionalized in the Mississippi State Asylum, Jackson, MS (AD 1855-1935)

MOLLY K. ZUCKERMAN

Department of Anthropology and Middle Eastern Cultures, Mississippi State University

As Grauer reflected in her 2003 piece, "Where were the women?", women, like other marginalized sub-populations in stratified societies, are often invisible or obfuscated in the historical record. This is particularly true for the Reconstruction (c. 1863-1877) and early Jim Crow-era (1877-1965) American South, especially for impoverished women and those of color. Here, I discuss findings from a critical integration of documentary, bioarchaeological, and oral history evidence surrounding the Mississippi State Asylum (MSA), Jackson, MS, in order to reconstruct the interplay of gender, sex, and social race in the lived experiences of its patients. Between 1855 and 1935, the MSA housed 35,000 patients, of whom c. 10,000 deceased while institutionalized. It convened individuals from a wide swath of socioeconomic strata and Mississippi communities, but the vast majority was identified as "Negro" by the early 20th century. Admission and discharge records from 1907 to 1912 (n=769 deaths), for instance, reveal that duration of stay prior to death varied substantially relative to patient social race, gender, and sex with "white" females (n=177) surviving an average of 13 years, but negro females (n=210) only 1.4 years. However, the wards were only racially/ spatially segregated in 1895 and mortuary programs are uniform across the burials (N=67). Bioarchaeologically, the assemblage is also equally split (40.3% male, female) by sex, as is the distribution of several stress indicators, such as LEH (n=65; 54.5% males, females affected). These lines of evidence shed light on the diversity of biosocial conditions and experiences of institutionalized women in pre-modern Mississippi.