

Fort Worth, TX

November 4, 2023

University of North Texas

Health Science Center



Primate Behavior
Socioecology



Human Variation
Forensics



Paleoanthropology
Paleoprimateology

TABA 2023

17th Annual Meeting of the Texas Association of Biological Anthropologists



**PROGRAM OF THE 17TH ANNUAL MEETING OF
THE TEXAS ASSOCIATION OF BIOLOGICAL
ANTHROPOLOGISTS**

NOVEMBER 4, 2023

FORT WORTH, TX

University of North Texas Health Science Center
Everett Hall, Research & Education Building
3500 Camp Bowie Blvd, Fort Worth, TX

TABA Scientific Program Committee

Scott Maddux, Chair
Bernadette Perchalski
Lauren Gonzales
Elizabeth Cho
Kate Lesciotto
Angela Achorn
Kaelyn Dobson

Local Arrangements Committee

Scott Maddux, Chair
Bernadette Perchalski
Lauren Gonzales

CONFERENCE LOCATION & PARKING

The 2023 Annual Meeting of the Texas Association of Biological Anthropologists will be held on the 1st floor of the Research & Education (RES) Building on the campus of the University of North Texas Health Science Center (3500 Camp Bowie Blvd, Fort Worth, TX).

Free visitor parking is available in Parking Lot 6 located off of Clifton Street. Visitor parking passes will be distributed at registration. The conference may be accessed by going down the stairs at the north end of the parking lot.

Public transportation is available from Fort Worth Central Station (downtown) via the Trinity Metro #002 “Camp Bowie” bus and the “Dash” electric bus (ridetrinitymetro.org/routes-schedules).



From I-30

SCHEDULE OF EVENTS

Friday, November 3, 2023

7:00 pm Social Gathering at [The Flying Saucer](#) on Sundance Square (111 E 3rd St Fort Worth, TX 76102). *Drinks only. Many restaurants nearby.*

Saturday, November 4, 2023

First floor, Research & Education (RES) Building, UNTHSC Campus

Morning

8:00-9:15 Registration; poster set-up
9:15-9:30 Welcome Address
9:30-10:30 Podium Session I: Environmental Pressures Past & Present
10:30-11:00 Coffee break
11:00-12:00 Poster Session I: Anatomy in Anthropology
12:00-1:30 Lunch Break

Afternoon

1:30-2:30 Poster Session II: Human Health & Ethnoprimateology
2:30-3:45 Podium Session II: Museums, Genetics, and Social Dynamics
3:45-4:00 Break
4:00-5:00 Poster Session III: Primate Genetics & Behavior
5:15-6:00 Business Meeting
6:00-6:30 Student Presentation Awards & Closing Remarks
6:30-9:00 Social Gathering at [Maple Branch Craft Brewery](#) (2628 Whitmore St, Fort Worth, TX 76107). [Food Menu](#).

PODIUM & POSTER PRESENTATIONS

Podium Session I: Environmental Pressures Past & Present

Everett Hall (RES 100)

- 9:30 Neolithic decline or reorganization?: A paleodemographic and environmental perspective of Northern China from Neolithic Age to Iron Age (6000 BCE to 0 CE).** MARK SIMON, QIAN WANG
- 9:45 Climatic adaptation in the human nose: An investigation using 3D morphometrics and computational fluid dynamics.** LYNDEE A. WARD, HASINTHA H.A.K. PATABENDIGE, ELIZABETH O. CHO, TODD R. YOKLEY, BRIAN H. DENNIS, SCOTT D. MADDUX
- 10:00 Environmental and genetic influences on the skeletal health of the Cayo Santiago rhesus macaques.** GEORGE N. FRANCIS, QIAN WANG
- 10:15 Source level and attenuation of titi monkey duets in a rainforest habitat.** SILVY M. VAN KUIJK, ANTHONY DI FIORE

Poster Session I: Anatomy in Anthropology

Kiva Lobby (RES first floor)

11:00 - 11:30 Oral presentations
11:30 - 12:00 Authors present for questions

- 1. Accessory bones in the skulls of rhesus macaques (*Macaca mulatta*) from Cayo Santiago.** ALINA MCCLOUD, GEORGE FRANCIS, QIAN WANG
- 2. The ontogeny of sexual size monomorphism in Verreaux's sifaka (*Propithecus verreauxi*).** GABRIELLE L. BUENO, REBECCA J. LEWIS
- 3. Modeling airflow dynamics during the nasal cycle *in silico*: Implications for variation in human nasal form and function.** BAONHU TRAN, LYNDEE A. WARD, HASINTHA H.A.K. PATABENDIGE, VIVEK C. NAIR, ELIZABETH O. CHO, TODD R. YOKLEY, BRIAN H. DENNIS, SCOTT D. MADDUX
- 4. Body mass estimation based on bi-iliac breadth and femoral head diameter.** MADISON L. RODRIGUEZ, ALYSSA C. GONZALEZ, DEBORAH L. CUNNINGHAM, DANNY J. WESCOTT

TABA Conference Program 2023

5. **Thermoregulatory implications of sexual dimorphism in human torso morphology.** CAROLINE COUNTS, KATHERINE MCBROOM, CHLOE BOETTGER, ELIZABETH O. CHO, ALBERT YURVATI, CARA OCOBOCK, LIBBY COWGILL, SCOTT D. MADDUX
6. **Estimating vertebral column length from contiguous vertebrae segments for anatomical stature reconstruction.** KATELYN R. KALLMAN, AARYN M. ARNOLD, ALYSSA LOREDO, ROBERT C. MCCARTHY, DANIEL J. WESCOTT, DEBORAH L. CUNNINGHAM
7. **The quantification of non-metric traits in the human skeleton.** EMILY K. BREEZE, KATELYN B. KNIGHT, STEPHANIE A. BAKER, PATRICK J. LEWIS
8. **Reconstructing aquatic environments: Through the eyes of turtle remains at Spring Lake.** MYRIAH A.J. ALLEN

Poster Session II: Human Health & Ethnoprimateology

Kiva Lobby (RES first floor)

1:30 - 2:00 Oral presentations
2:00 - 2:30 Authors present for questions

9. **Investigation/identification of pathologies found in the Sam Houston State University Southeast Texas Applied Forensic Science Facility.** COURTNEY KLEINDL, AMAYAH BROWN, JAMIE BAGLEY, ERICA FROSCH, BRANDON TREVINO, MELISSA HANSEN, STEPHANIE BAKER, PATRICK LEWIS
10. **A comparative study of pathological observations and socioeconomic backgrounds.** ELIANA B. GUTIERREZ, HAIDEE V. HERNANDEZ
11. **mCT to analyze asymmetries from trauma to the nasomaxillary suture.** JAMIE L. BAGLEY, PATRICK J. LEWIS, AMAYAH BROWN, ERICA FROSCH, COURTNEY KLEINDL, BRANDON TREVINO, STEPHANIE BAKER, MELISSA HANSEN
12. **Development of *ex vivo*, salivary Bacteria Killing Assay for humans.** TOMASZ J. NOWAK, JEFFREY GASSEN, SEAN PRALL, RAJ PATEL, ALEXES THURMAN, DANIEL ARANA, VARSHINI KRISHNAN, MICHAEL P. MUEHLENBEIN
13. **Environmental influences on gut function: Market integration, pathogen exposure, and children's intestinal fatty-acid binding protein (I-FABP) in Amazonia.** THANMAYI PARASU, ELIZABETH KIM, SAMUEL S. URLACHER

TABA Conference Program 2023

14. **Measurement of intestinal fatty-acid binding protein (I-FABP), a marker of gut function, in dried blood spots using ELISA.** ELIZABETH Y. KIM, THANMAYI PARASU, SAI S. SAGIREDDY, TIFFANY F. LUAN, KAMILA MONTENEGRO, SRIHAN SOMEPALLI, JEFFREY GASSEN, TOMASZ J. NOWAK, SALLY P. WEAVER, ERICH BAKER, MICHAEL P. MUEHLENBEIN, SAMUEL S. URLACHER
15. **Childhood physical activity patterns among small-scale populations.** MARCELA PFAFF-NASH, JOSH SNODGRASS, KAREN L. KRAMER, MARTINA KONECNA, LARA R DOUGAS, HERMAN PONTZER, LAWRENCE S. SUGIYAMA, SAMUEL S. URLACHER
16. **Lemur-human interactions and beliefs among individuals living around Marotandrano Special Reserve, Northeast Madagascar.** ELIETTE NOROMALALA, FARATIANA RAFIANINANTSOA, HERRIMANN D. TEHINDRAZANARIVELO, KATHRYN ALESSI, KARA I. GABRIEL
17. **The incidental primate interface: A systematic review of primate research conducted outside of protected areas.** ALEXANDRA C. SHELDON, THAD Q. BARTLETT

Podium Session II: Museums, Genetics, & Social Dynamics

Everett Hall (RES 100)

- 2:30 **Biology, anthropology, and medicine on display: Three Philadelphia museums adapt to the 21st Century.** SHELLEY L. SMITH
- 2:45 **Unlocking museum collections: promises and challenges of museomic studies in African galagids.** LUCA POZZI, ANNA PENNA, MARY E. BLAIR, HSIAO-LEI LUI, ELSA PETERS, LOGAN KISTLER
- 3:00 **Genotyping-in-thousands to assess twin chimerism in wild saddleback (*Leontocebus weddelli*) and bearded emperor tamarins (*Saguinus imperator subgrisescens*) from Amazonian Peru.** RACHEL VOYT, SAMANTHA LOPEZ CLINTON, KATERINA GUSCHANSKI, RAQUEL BALLESTEROS, GIDEON ERKENSWICK WATSA, SUMITHA HUNJAN, ANTHONY DI FIORE, AARON SANDEL, MRINALINI ERKENSWICK WATSA
- 3:15 **Female mountain gorillas form enduring social relationships.** RILEY N. DERBY, WINNIE ECKARDT, TARA S STOINSKI, ROBIN E MORRISON, AARON A SANDEL
- 3:30 **A perceived wild: American's interactions with innately wild animals.** KAELYN DOBSON

Poster Session III: Primate Genetics & Behavior

Kiva Lobby (RES first floor)

4:00 - 4:30

Oral presentations

4:30 - 5:00

Authors present for questions

18. **A Bioinformatic Pipeline for SSR Identification and Development using Publicly Available Genome Assemblies.** DI FIORE, ALICE GIUNCHI, CRISTINA JASSO, FILIPPO AURELI
19. **No strong sex-bias found in dispersal patterns of *Colobus vellerosus* fragment groups.** SYDNEY M. SELF, TERESA D. HOLMES, PASCALE SICOTTE, NELSON TING, EVA C. WIKBERG
20. **Group composition influences on vocalization counts in *Alouatta palliata*, *Ateles geoffroyi*, and *Cebus imitator* at Camaquiri Conservation Initiative (CCI) field site.** KAYLA M. TELLEZ, JILL D. PRUETZ
21. **Variation in ranging behaviors in *Colobus vellerosus* in relation to population density.** EMILY GLOTFELTY, BISMARCK OWUSU ANTWI, ROBERT KORANTENG, CHARLES ODUM, EVA C. WIKBERG
22. **Identification of ecological and locomotor indicators of semi-terrestriality in anthropoid primates.** INDYA J. THOMPSON, BERNADETTE A. PERCHALSKI, SCOTT D. MADDUX, LAUREN A. GONZALES
23. **An assessment of hypotheses for the maintenance of polymorphic color vision in a group of wild *Ateles belzebuth*.** SAM RETTKE, D. MAX SNODDERLY, ANDRÉS LINK, ANTHONY DI FIORE
24. **Predicting performance of diverse color vision genotypes of wild primates when foraging for food.** MAX SNODDERLY, DELISA RAMOS, ANDRES LINK, ANTHONY DI FIORE

ABSTRACTS

alphabetical order by first author

Reconstructing aquatic environments: Through the eyes of turtle remains at Spring Lake

MYRIAH A.J. ALLEN¹

1. Department of Anthropology, Texas State University, San Marcos, Texas

Located in San Marcos Texas, at the base of the Balcones escarpment sits Spring Lake (41HY160), both a lake and an archaeology site. The dam, built in 1849, helped create the present-day lake which is home to several types of animals (e.g., fish, mammals, birds, etc.) and five native turtle types (i.e., musk, box, sliders, snappers, and softshell turtles). Researchers are currently exploring the possibilities of a prehistoric dam near Spring Lake, which could have created a prehistoric lake/wetland ecosystem where the lake sits today. This poster presents the preliminary results of faunal analysis on the archaeological turtle remains found during excavations at the Spring Lake site. This analysis utilizes aquatic ecological information on Texas turtles and compares the archaeological turtle record to the present types of turtles seen today at the lake to help recreate the aquatic environments that could have been present at Spring Lake thousands of years ago.

Using mCT to analyze asymmetries from trauma to the nasomaxillary suture

JAMIE L. BAGLEY¹, PATRICK J. LEWIS^{2,3}, AMAYAH BROWN¹, ERICA FROSCHE¹, COURTNEY KLEINDL¹, BRANDON TREVINO¹, STEPHANIE BAKER⁴, MELISSA HANSEN⁵

1. Sam Houston State University College of Osteopathic Medicine, Conroe, TX
2. Honors College, Sam Houston State University, Huntsville, TX
3. Southeast Texas Applied Forensic Science (STAFS) Facility, Sam Houston State University, Huntsville, TX
4. Department of Anthropology, Texas State University, San Marcos, TX
5. Sam Houston State University, Huntsville, TX

Even mild trauma to the head can result in long-term health complications or death. Prior research suggests that head trauma alters the major cranial sutures in predictable patterns. As such, understanding how trauma impacts sutures more broadly may have both medical and forensic applications. Here we expand on previous research by quantifying the effects of trauma on sutures of the face. Five skulls from the Southeast Texas Applied Forensic Science facility (STAFS) at Sam Houston State University were CT scanned at The University of Texas at Austin CT lab. Two crania had blunt force trauma, two had trauma from car accidents, and one was a control with no known trauma. We tested for asymmetry in right and left nasomaxillary sutures. The nasomaxillary suture images were analyzed with 3Dslicer software. The suture widths were measured in three

successive slices in the coronal plane and those measurements were averaged. Measurements were taken at regular intervals along both the right and left sutures and compared statistically. Preliminary results from the t-tests exhibited highly significant differences between the nasomaxillary suture's right and left sides ($p > 0.001$) in blunt force trauma crania. However, no significant differences between the sides were found in the car accident and control crania. Ultimately, mCT imaging is a valuable tool for evaluating the bony anatomy of postmortem specimens exhibiting trauma. Further research on a larger sample, using the method developed here, will better characterize the microanatomy of trauma on the facial sutures.

The quantification of non-metric traits in the human skeleton

EMILY K. BREEZE¹, KATELYN B. KNIGHT¹, STEPHANIE A. BAKER², PATRICK J. LEWIS¹

1. Department of Biology, Sam Houston State University, Huntsville, TX
2. Department of Anthropology, Texas State University, San Marcos, TX

Non-metric traits in anthropology are defined as anatomical variations in the human skeleton that cannot be measured through usual means as their occurrence cannot be predicted. Identification of these non-metric traits can play a crucial role in positively identifying individuals when traditional methods like DNA analysis or dental records are unavailable. Therefore, the objective of this project is to quantify the occurrence of common non-metric traits in both the cranial and post cranial bones to look for any observable patterns. To do so, 64 specimens were obtained from the Southeast Texas Applied Forensic Science facility (STAFS) and observations were recorded for 12 cranial traits and 7 post cranial traits. Results indicate that some traits had a higher occurrence rate than others. This included the presence of a supraorbital notch (54.69%) and/or supranasal suture (60.94%) in the cranium as well as the presence of a bifid spinous process in the cervical vertebrae (89.06%) and/or a clavicular nutrient foramen (78.13%) in the postcranial observations. However, this cannot hold true for all cases due to the irregular and unpredictable occurrence of non-metric traits. In future studies, additional data will be examined to assess whether certain non-metric traits are more prevalent among reported donor ancestries or specific sexes.

The ontogeny of sexual size monomorphism in Verreaux's sifaka (*Propithecus verreauxi*)

GABRIELLE L. BUENO¹, REBECCA J. LEWIS¹

1. Department of Anthropology, The University of Texas at Austin, Austin, TX

Sexual size dimorphism, exhibited by many primates, can develop through variation in growth rate, growth duration, or a combination of the two. Adult Verreaux's sifaka (*Propithecus verreauxi*) exhibit sexual size monomorphism, but whether the sexes experience the same developmental trajectory to reach this same adult body size is unknown. We used generalized additive mixed models to examine the growth rate and duration of 14 morphometric variables

collected from a population of wild Verreaux's sifaka at Kirindy Mitea National Park in Madagascar between 2006 and 2019 (n=211 captures). Terminal adult weight was reached at age six for both sexes, later than other populations. Females exhibited longer growth duration in body, hindlimb, thigh, and forelimb lengths, and faster growth rates in hindlimb and forelimb lengths. Males exhibited longer growth duration in thigh and bicep circumferences, and faster growth rates in bicep circumference. Males reach terminal skeletal length earlier, but terminal musculature later, than females. Adult females had significantly longer hindlimb length than males, while adult males had significantly larger thigh circumference, bicep circumference, and a higher intermembral index. Because most of the intersexual differences appeared in adulthood, they may be associated with sex differences in infant carrying and intrasexual competition: as vertical clingers and leapers, adult female sifaka may need longer legs to compensate for dorsal infant carrying, while adult males may benefit from larger thigh and bicep muscles in male-male contest competition over mates. These results demonstrate that the path to adulthood can vary greatly depending on sex and life history.

Thermoregulatory implications of sexual dimorphism in human torso morphology

CAROLINE COUNTS¹, KATHERINE MCBROOM¹, CHLOE BOETTGER¹, ELIZABETH O. CHO¹, ALBERT YURVATI², CARA OCOBOCK³, LIBBY COWGILL⁴, SCOTT D. MADDUX¹

1. Center for Anatomical Sciences, University of North Texas Health Science Center, Fort Worth, TX
2. Texas College of Osteopathic Medicine, University of North Texas Health Science Center, Fort Worth, TX
3. Department of Anthropology, University of Notre Dame, South Bend, IN
4. Department of Anthropology, University of Missouri, Columbia, MO

Ecogeographic variation in human body form is widely attributed to Bergmann's and Allen's rules, which relate thermoregulatory efficacy to the ratio of body surface area (SA) compared to internal body volume (V). Within the anthropological literature, these rules are most commonly operationalized via Ruff's "Cylindrical Model", which posits that ecogeographic variation in SA/V ratio is primarily influenced by differences in body breadth dynamics rather than stature. Importantly, the cylindrical model employs bi-iliac breadth (BIB) as a proxy for overall body breadth. However, as BIB is one of the few non-sexually dimorphic measurements in humans, its use in the cylindrical model may underestimate the impact of sexual dimorphism in torso shape on SA/V ratio. Accordingly, this study collected multiple anthropometric measures of body breadth from a sample of 30 (15 male, 15 female) living human subjects. Following theoretical predictions, males and females were not significantly different for BIB ($t=0.466$, $p=0.645$). Conversely, males were found to have significantly wider upper torsos compared to females, as evidenced by both bi-acromial breadth ($t=3.952$, $p=0.0005$) and chest circumference ($t=9.085$, $p<0.0001$). Indeed, males were also found to exhibit significantly larger bi-acromial/bi-iliac breadth ratios ($t=2.804$, $p=0.009$), confirming significant differences in overall torso shape between males and females. Cumulatively, these results suggest the Cylindrical Model may underestimate the influence of

sexual dimorphism in torso shape on thermoregulatory function. These findings thus support suggestions that males and females inhabiting the same geographic/climatic region likely achieve comparable thermoregulatory outcomes through slightly different anatomical and physiological mechanisms.

Funding: National Science Foundation #2203808 (Cho), #2020096 (Ocobock), #2020506 (Cowgill), #2020715 (Maddux).

Female mountain gorillas form enduring social relationships

RILEY N. DERBY¹, WINNIE ECKARDT², TARA S STOINSKI², ROBIN E MORRISON^{2,3}, AARON A SANDEL¹

1. Department of Anthropology, University of Texas at Austin, Austin, TX
2. Dian Fossey Gorilla Fund, Musanze, Rwanda
3. Human Evolutionary Ecology Group, Department of Evolutionary Ecology, University of Zurich, Zurich, Switzerland

Strong, affiliative relationships are important across social mammals, and in many species, relationships between female kin form the basis of group life. Relationships are expected to be weaker in cases where females disperse or do not cooperatively defend resources. Mountain gorillas (*Gorilla beringei beringei*) seem to support this, as females can emigrate multiple times throughout their life and do not jointly defend the abundant vegetation they feed on. Unsurprisingly, mountain gorillas form variable or weak relationships with other females and seemingly prioritize relationships with adult males. But prior studies may have misinterpreted relationships due to a focus on grooming and due to understandable limitations of small sample sizes and short study periods. Here, we examine proximity and grooming between 46 adult female mountain gorillas in five groups over 5 to 13 years. We analyze 2m proximity relationships between 321 individual dyads to determine (1) if proximity relationships are preferential, and (2) if they endure across time. Most females formed at least one preferential proximity relationship (43 of 46), which lasted a mean of 2.2 years. Additionally, 5.6% of dyads (n=18/321) formed enduring proximity preferences that exceed four years with the longest lasting at least 12 years. Maternal kin had the most enduring relationships and were most likely to groom each other, although grooming was rare overall. The enduring proximity relationships between some female gorillas in our sample are similar in length to those of female baboons and male chimpanzees, which suggests that these relationships are social bonds. Our study highlights a need to refine definitions of social bonds and potentially reassess their evolutionary function.

A Bioinformatic Pipeline for SSR Identification and Development using Publicly Available Genome Assemblies

ANTHONY DI FIORE^{1,2}, ALICE GIUNCHI³, CRISTINA JASSO⁴, FILIPPO AURELI⁵

1. Department of Anthropology, The University of Texas at Austin, Austin, TX

TABA Conference Program 2023

2. Estación de Biodiversidad Tiputini, Universidad San Francisco de Quito, Quito, Ecuador
3. Instituto de Neuroetología, Universidad Veracruzana, Veracruz, México
4. Instituto de Investigaciones en Matemáticas Aplicadas y Sistemas, Universidad Nacional Autónoma de México, Ciudad de México, México
5. Instituto de Neuroetología, Universidad Veracruzana, Xalapa, México

Despite the growing use of single nucleotide polymorphism data in population genomics, simple sequence repeat (SSR, or “microsatellite”) markers remain useful for certain applications (e.g., studies of parentage, dispersal, and genetic structure in wild populations). For many years, the development of SSRs relied on generating and sequencing gDNA libraries selectively-enriched for microsatellite repeats, which requires high-quality gDNA as a starting material. Today, publicly-accessible repositories -- such those maintained by NIH/NCBI -- include genome assemblies for thousands of taxa (including dozens of nonhuman primates), which allows the use of *in silico* screening to identify promising loci. We developed a flexible bioinformatics pipeline to mine genome assemblies for SSRs, select those likely to show polymorphism, and design suitable primers for PCR amplification. Using the pipeline, we identified tens of thousands of microsatellites from the genomes of 13 platyrrhine species belonging to 10 of 19 currently-recognized genera. From the set of loci discovered in one species, *Ateles geoffroyi*, we screened ~35 in a wild population from the Mexican Yucatan. More than 80% of the newly-identified markers were variable in an initial small sample of subjects, and 13 of the markers we then selected for genotyping the larger population yielded an average of ~5.7 alleles/locus. Several of these loci also were polymorphic in small samples of two other atelins, *Ateles belzebuth* and *Lagothrix poeppigii*. Overall, our results demonstrate the potential of genome mining to efficiently identify large numbers of polymorphic loci for population genetic studies of non-model organisms.

Funding: CONTEX Research Grant #2018-119A, Texas Global Faculty Research Grant, The University of Texas at Austin

A perceived wild: American's interactions with innately wild animals

KAELYN DOBSON¹

1. Department of Anthropology, Texas State University, San Marcos, TX

Americans have a relationship with wilderness, nature and wild animals uncommon to other locales. The typical interface with wild animals is highly dependent on human control and the ability to individually determine the purpose of the interaction. Wild animals in zoological facilities are often considered wild and dangerous, caged creatures but in the same breath perceived as easily touched, held and kept as pets. Wildlife in parks is commonly counted as a part of the entertainment value and are often perceived to be approachable, pet and captured. Wild animals ranging from ferrets to tigers are kept as pets in households by Americans, claiming most any animal can be a domesticated version of its wild nature. The relationships Americans often have with wild animals conflict with themselves and with the nature of the animals. These interactions occur with wild animals on a daily basis, but why? What makes Americans perceive animals in

these ways? Why is this the engagement Americans have with wildlife? What could be done to impact and improve human-wildlife relationships? I dive into the possible foundations of where these perceptions about wildlife may be derived and how they could be altered for better outcomes for both human and animal actors. Personal experiences with American interfaces are shared with a context of change. I glance at the history of wildlife relations in America, the continued connections we have with wild animals and possibilities for the future.

Environmental and genetic influences on the skeletal health of the Cayo Santiago rhesus macaques

GEORGE N. FRANCIS¹, QIAN WANG¹

1. Department of Biomedical Sciences, Texas A&M University School of Dentistry, Dallas, TX

The Cayo Santiago Rhesus macaques (*Macaca mulatta*) are a unique primate population associated with known demographic, familial, and skeletal data. The island habitat (400m by 600m) promotes naturalistic behaviors in a free-ranging yet observable setting, which combine to produce a primate colony with compelling translational potential. This study investigates environmental and genetic influences on aging, pathology, and development using the derived skeletal collection. In total, skeletons of 2789 individuals (Age range: 0 – 31yrs), housed in the Caribbean Primate Research Center (CPRC) and the New York University-CPRC collection, were examined for signs of pathology and aging, and measured for bone mineral density and size dimensions. A myriad of pathologies were found within the colony, including neoplasms (0.22%), osteoarthritis (5.41%), osteomyelitis (1.01%), and periosteal reactions (10.68%). Sex differences were found for oral, degenerative, and inflammatory diseases ($p < 0.05$). Familial disparities were concentrated in the craniofacial region, including crowding, antemortem tooth loss, temporomandibular joint arthritis, and periapical cavities ($p < 0.05$). Certain skeletal pathologies varied according to colony nutritional quality. Periodontitis decreased between age-cohorts as quality increased, however antemortem tooth loss, periapical cavities, and crowding increased with nutritional quality. The latter incidence may reflect the effects of diminished masticatory stress as seen in humans after epidemiological transitions. Bone mineral density was found to decrease for individuals that experienced devastating hurricane impacts ($p < 0.05$), suggesting natural disasters can accelerate the aging process. Future investigations will allow us to further elucidate drivers of skeletal aging, pathology and development as they relate to family, nutrition, and hurricane events.

Funding: The Cayo Santiago colony is supported by NIH 5P40OD012217 to Caribbean Primate Research Center. This project is supported by NSF grant #1926601 to Q. Wang.

Variation in ranging behaviors in *Colobus vellerosus* in relation to population density

EMILY GLOTFELTY¹, BISMARCK OWUSU ANTWI², ROBERT KORANTENG², CHARLES ODUM², EVA C. WIKBERG¹

1. Department of Anthropology, University of Texas at San Antonio, San Antonio, TX
2. Boabeng-Fiema Monkey Sanctuary, Boabeng, Ghana

Changing environmental conditions, such as changes in population density, can affect the intensity of feeding competition and frequency of intergroup encounters. In crowded areas, animals may alter ranging patterns to increase access to resources while minimizing intergroup contests; especially for groups that are likely to lose an intergroup contest. We compared previously collected ranging data from 2000-2009 on up to eight social groups of *Colobus vellerosus* at Boabeng-Fiema, Ghana with newly collected data from 2023 on four groups to explore whether population density and a group's competitive ability are related to ranging patterns. During this period, the population density increased from 104.17 individuals/km² to 190.10 individuals/km². We examined variation in home range size, proportion of overlap, daily travel distance, and forest strata use across groups and population density conditions. Larger groups had longer daily travel distances and larger home range sizes in both low population and high population density conditions. Further, groups spent more time in low forest strata in the higher population density condition. While these findings suggest that individuals may cope with environmental changes through increased usage of lower forest strata, we still need to determine whether these behavioral changes are sufficient for maintaining health, survival, and reproduction in today's rapidly changing environments.

A comparative study of pathological observations and socioeconomic backgrounds

ELIANA B. GUTIERREZ¹, HAIDEE V. HERNANDEZ¹

1. Department of Anthropology, Texas State University, San Marcos, TX

Key determinants such as healthcare accessibility, nutritious food availability, and living conditions significantly impact individuals' health and skeletal pathologies. We examine how socioeconomic factors influence the skeletal health of non-US born and US-born populations. Twenty donors from the Texas State Donated Skeletal Collection (TXSTDSC) were selected, equally divided between non-US born and US born individuals. Selection criteria included age, birth country, childhood socio-economic status, and adult socio-economic status, resulting in a balanced age range of 28 to 94 years. Vertebral column examinations revealed various pathologies, including lipping, lesions, compression fractures, fusion, enthesophytes, Schmorle's Nodes, osteophytes, and eburnation. Statistical analysis, utilizing an unpaired t-test for independent groups of non-US born and US-born individuals, showed no statistical significance. Graphical representations comparing the two groups reinforced the similarities in the number of observed pathologies. These results challenge prior assumptions and suggest no direct correlation between pathologies in non-US born and US-born individuals. Nevertheless, this study holds implications for forensic casework, emphasizing the need to consider skeletal health and socioeconomic factors during analyses. Potential limitations contributing to the lack of statistical significance include the donor pool's socio-economic background, limited sample size, the absence of healthcare and food accessibility issues, or insubstantial observed differences within our methodology's scope. This

study highlights underrepresentation within skeletal collections, advocating for inclusivity and future research with larger sample sizes and exploration of donors' professions to deepen insights into the socioeconomics and skeletal health intersection.

Estimating vertebral column length from contiguous vertebrae segments for anatomical stature reconstruction

KATELYN R. KALLMAN¹, AARYN M. ARNOLD¹, ALYSSA LOREDO¹, ROBERT C. MCCARTHY², DANIEL J. WESCOTT¹, DEBORAH L. CUNNINGHAM¹

1. Department of Anthropology, Texas State University, San Marcos, TX
2. Department of Biological Sciences, Benedictine University, Lisle, IL

Stature estimation from skeletal elements is used in bioarchaeological, forensic, and paleoanthropological analyses. Several regression formulae exist for estimating stature from long bones and while these estimates typically have high accuracy, knowledge of sex and ancestry is necessary to achieve the best results. Anatomical stature, on the other hand, is independent of such knowledge as sex and population differences in stature are naturally included in the final estimate. As anatomical stature estimates require linear measurements of all skeletal elements that contribute directly to stature, incomplete skeletons make this assessment problematic. The axial skeleton, being unpaired, is especially susceptible to incompleteness. Here, we focus on total vertebral length (TVL), a large portion of the axial skeleton's contribution to an estimate of stature, as vertebrae are common missing elements in all bioanthropological contexts in which a stature estimate is desired. Using 62 (38 male, 24 female) individuals from the Texas State Donated Skeletal Collection (TXSTDSC), an ethically-sourced and well-documented human skeletal collection, we measured the midline height of C2-L5 following Raxter et al. (2006) and correlated four vertebral segments (C2-C7, T1-T6, T7-T12, L1-L5) to TVL. All four segments produced TVL estimates with an approximately 3.5% error. The correlations (R^2) for each segment are 0.48, 0.51, 0.56, and 0.53 with absolute errors of 17.6 mm, 17.2 mm, 16.6 mm, and 18.8 mm for C2-C7, T1-T6, T7-T12, L1-L5 segments, respectively. The study demonstrates that estimations of vertebral column length can be used when not all vertebrae are present.

Measurement of intestinal fatty-acid binding protein (I-FABP), a marker of gut function, in dried blood spots using ELISA

ELIZABETH Y. KIM¹, THANMAYI PARASU², SAI S. SAGIREDDY², TIFFANY F. LUAN², KAMILA MONTENEGRO², SRIHAN SOMEPALLI², JEFFREY GASSEN³, TOMASZ J. NOWAK³, SALLY P. WEAVER⁴, ERICH BAKER⁵, MICHAEL P. MUEHLENBEIN³, SAMUEL S. URLACHER³

1. Department of Biology, Baylor University, Waco, TX
2. Human Evolutionary Biology and Health Lab, Baylor University, Waco, TX
3. Department of Anthropology, Baylor University, Waco, TX.
4. Waco Family Medicine, Waco, TX.

5. Department of Computer Sciences, Baylor University, Waco, TX.

The gut plays a pivotal role in the evolutionary trajectories of both humans and non-human primates (NHPs), influencing aspects such as metabolism, life history, and overall health. Despite this recognition, the study of gut function (e.g., gut permeability and absorption) has been hampered by invasive sampling methods like jejunal biopsy and venipuncture blood draws, limiting the ability to directly measure physiological aspects of the gut in diverse and vulnerable populations (e.g., children and wild NHPs). Recent research has identified intestinal fatty-acid binding protein (I-FABP) as an important gut function biomarker, indicating mucosal damage and permeability. Nevertheless, reliance on invasive blood sampling has restricted I-FABP research. Here, we validated a commercially available ELISA kit (Abcam ab234566, Cambridge, UK) for measuring I-FABP in minimally invasive finger-prick dried blood spot (DBS) samples. Our validation involved a 'Waco100' matched set ($n = 117$) of human DBS and serum samples. I-FABP was detected in all DBS samples (42.0 ± 21.2 pg/mL), with a strong linear relationship to serum values ($R^2 = 0.94$; Passing-Bablok regression). Additional tests for dilutional linearity ($111.2 \pm 8.2\%$ recovery), spike and recovery ($101.8 \pm 6.7\%$ recovery), and analyte stability under freeze-thaw and temperature variations (all effects $p > 0.05$) highlight the assay's reliability. In an initial application of the assay, we measured I-FABP in DBS from Indigenous Shuar youth in Amazonian Ecuador ($n = 311$, ages 4-12 years), revealing high mean I-FABP of 93.8 ± 44.4 pg/mL, indicative of increased gut permeability and compromised gut health. These findings highlight DBS-based I-FABP assessment as a powerful tool for studying variation in human and NHP gut function.

Funding: NSF-SPRF #SMA1606852; NIH-NICHD #R15HD106177, CIFAR Azrieli Global Scholars Program, Cooper Foundation of Waco, Bernard and Aubre Rapoport Foundation of Waco, Waco Family Medicine, and Baylor University

Investigation/identification of pathologies found in the Sam Houston State University Southeast Texas Applied Forensic Science Facility

COURTNEY KLEINDL¹, AMAYAH BROWN¹, JAMIE BAGLEY¹, ERICA FROSCH¹, BRANDON TREVINO¹, MELISSA HANSEN², STEPHANIE BAKER², PATRICK LEWIS³

1. Sam Houston College of Osteopathic Medicine, Conroe, TX
2. Sam Houston State University, Huntsville, TX
3. Department of Biological Sciences. Sam Houston State University, Huntsville, TX

Some traumas and diseases are known to alter the human skeleton in characteristic ways; how these are distributed through various populations, sexes, and age groups, however, is less clear. The large skeletal collection housed at the Sam Houston State University (SHSU) Southeast Texas Applied Forensic Science Facility (STAFS) allows for population-level questions regarding pathologies and non-metric variants to be studied. Here we undertake the first step in answering these questions with a preliminary investigation of the skeletons housed at STAFS. Skeletons were randomly selected and evaluated for non-metric variants and pathologies. Half the authors examined the appendicular skeleton while half examined the axial. Photos were taken of any non-metric variant or pathology found and were documented. In total, 21 skeletons were analyzed.

Preliminary results demonstrate that heel spurs (6), osteoarthritis (8), fused vertebrae (11), osteophytes (19), and tufting of the phalanges (4) were common. Rarer finds include Diffuse Idiopathic Skeletal Hyperostosis (DISH) (2), severe scapular degeneration (1), and fusions of both the lambdoid and sagittal sutures (4). A variety of pathologies and non-metric variant types were noted in the analysis of the SHSU STAFS collection. The examination of the collection is ongoing and the likelihood of expanding the known non-metric variants and pathologies is high. Once the entire collection has been examined additional studies will be able to assess how trauma and pathologies vary across age, sex, and ancestry. Such data will benefit both medical and forensic disciplines.

Accessory bones in the skulls of rhesus macaques (*Macaca mulatta*) from Cayo Santiago

ALINA MCCLOUD¹, GEORGE FRANCIS¹, QIAN WANG¹

1. Department of Biomedical Sciences, Texas A&M University School of Dentistry, Dallas, TX

In utero, accessory bones of the skull can form from extra ossification centers. In human and nonhuman primates, accessory bones can persist into childhood and adolescence with environmental disturbances and genetic predispositions hypothesized as potential causes. In the Cayo Santiago population, the skulls of 2623 individuals with known ages (0 to 31 years), sex, and matriline affiliation, were examined for accessory bones. Signs of accessory bones of the skull were found within the parietal (0.23%) and occipital bones (0.04%), at multiple bone sites (0.08%), and mostly at the Bregma area (2.21%). Among individuals with accessory bones at the Bregma area, male and female distribution was comparable (males = 2.63%: females = 1.84%). After 7.3 years of age, the accessory bone at the Bregma is eliminated, indicating that the feature is completely obliterated during the age of 7 and 8 years after birth in the Cayo Santiago Rhesus colony. Moreover, of the 99 known matriline (range of samples: from 1 to 243), 20 matriline have individuals presenting with the bregmatic accessory bone. Statistical comparisons between the largest 13 matriline (N>20), including matriline without the presence of accessory bregmatic bones (ranging from 0% to 9.67%), did not reveal significant differences among families ($p = 0.097$). Future investigation is warranted to understand the etiology of accessory bones, including non-metric variation, familial aggregation, or environmental exposures during growth and development.

Funding: The Cayo Santiago colony is supported by NIH 5P40OD012217 to Caribbean Primate Research Center. This project is supported by NSF grant #1926601 to Q. Wang.

Lemur-human interactions and beliefs among individuals living around Marotandrano Special Reserve, Northeast Madagascar

ELIETTE NOROMALALA¹, FARATIANA RAFIANINANTSOA², HERRIMANN D. TEHINDRAZANARIVELO³, KATHRYN ALESSI⁴, KARA I. GABRIEL⁵

1. Department of Anthropology, University of Texas at Austin
2. Groupe d'Etude et de Recherche sur les Primates de Madagascar, Antananarivo, Madagascar
3. Nator'Ala association, Antananarivo, Madagascar
4. Alumna, CUNY, Graduate Center (MALS), New York, NY
5. Primate Behavior and Ecology Program, Central Washington University, Ellensburg, WA

Lemurs face various threats. Human activities and beliefs affect lemur survival while also potentially hindering conservation efforts. Here, we explore self-reported lemur knowledge, hunting, beliefs, and perceptions in households around the Marotandrano Special Reserve (MRS), a wildlife reserve that shelters 12 lemur species. We conducted interviews with 120 households across seven villages around the western part of the MRS and collected demographic and human-lemur interaction data. Our sample was 68.3% male and 31.7% female with ages ranging from 17 to 80 years old. Most participants were Tsimihety (69.2%) or Betsimisaraka (21.7%) ethnicity, with the majority farming (90%) and having either a primary (40.8%) or secondary (30%) education. Most participants (91.7%) reported seeing lemurs in their lifetime and were most familiar with *Indri indri* (75.4%), *Varecia variegata* (70.3%), *Propithecus diadema* (50%), and *Eulemur albifrons* (40.7%), but less familiar with *Cheirogaleus major* (5.1%), *Daubentonia madagascariensis* (13.6%), *Allocebus tricotis* (15.6%), and *Hapalemur occidentalis* (19.5%). *E. albifrons* and *V. variegata* were reportedly the most hunted (35.3% and 36.1%, respectively), while *D. madagascariensis* was the least hunted. *I. indri* was perceived positively because of its resemblance to humans, while *D. madagascariensis* was believed to bring bad luck, disasters, and to kill humans. Large-bodied and diurnal lemurs were well-recognized and often hunted. These findings suggest that local beliefs result in prioritizing the protection of certain lemur species over others.

Funding: International Primatological Society and Rufford Foundation

Development of *ex vivo*, salivary Bacteria Killing Assay for humans

TOMASZ J. NOWAK¹, JEFFREY GASSEN¹, SEAN PRALL², RAJ PATEL¹, ALEXES THURMAN¹, DANIEL ARANA¹, VARSHINI KRISHNAN¹, MICHAEL P. MUEHLENBEIN¹

1. Department of Anthropology, Baylor University, Waco, TX
2. Department of Anthropology, University of Missouri, Columbia, MO

Ecoimmunology is a developing field in need of cheap and easy assays that can detect a functional measure of immunity. Bacteria Killing Assay (BKA) can be used in vertebrates to measure functional immunity. However, as blood for this assay must be fresh, working in remote areas would pose significant logistical challenges. Here, we present a salivary BKA for humans that does not require fresh samples. Human salivary BKA requires mixing saliva with a known number of live bacteria, incubating on agar plates, quantifying the remaining colonies, and comparing them to reference plates. We conducted several tests to establish a reliable protocol for collecting samples and running the assay. We determined that inappropriate storage conditions, but not

multiple freeze/thaw cycles, can alter the assay results. Results also show that the ability to kill bacteria is relatively stable across consecutive days, morning vs evening times, and between the sexes. Saliva samples are often contaminated with other microorganisms that grow on agar. We tested a heat-inactivation protocol that showed a strong correlation ($r = 0.86$) with samples that had not been inactivated. This assay can be utilized in other species, but it requires running several dilutions to calibrate. We predict that salivary and whole blood BKA will yield different results even if measured simultaneously. This would mostly be due to the different immune components and roles of saliva and blood and requires further study. Nevertheless, we believe that salivary human BKA is a reliable and accurate measure of systemic, functional immunity.

Environmental influences on gut function: Market integration, pathogen exposure, and children's intestinal fatty-acid binding protein (I-FABP) in Amazonia

THANMAYI PARASU¹, ELIZABETH KIM², SAMUEL S. URLACHER³

1. Department of Business, Baylor University, Waco, TX
2. Department of Biology, Baylor University, Waco, TX
3. Department of Anthropology, Baylor University, Waco, TX

Gut function is an important factor influencing the evolution of humans and non-human primates (NHPs), with implications for understanding variation in immunity, metabolism, life history, and health. However, our knowledge of the relationship between environment and the gut remains limited, specifically for children in low-and-middle-income countries (LMICs). Here, we investigated the relationship between environmental variables and intestinal fatty-acid binding protein (I-FABP, a leading biomarker of gut permeability and mucosal damage) among Indigenous Shuar children of Amazonian Ecuador ($N = 145$, ages 4-12 years). I-FABP levels were quantified in dried blood spots obtained from children residing in two distinct regions: Cross-Cutucú (CC; $N = 82$) and Upano Valley (UV; $N = 63$). Findings reveal significantly elevated I-FABP among CC (113.9 ± 53.9 pg/mL) compared to UV (89.6 ± 47.4 pg/mL) children ($p < 0.01$). This finding aligns with greater pathogen exposure experienced by children in the less market-integrated CC region. Initial analysis of household-level pathogen exposure variables yielded no statistically significant results, although a clear trend was detected for lower I-FABP among children from households with running water ($p = 0.068$). Ongoing analysis will examine a broader spectrum of household-level environmental variables to shed light on the complex dynamics between market integration, pathogen exposure, and gut function among humans.

Funding: NSF-SPRF #SMA1606852; NIH-NICHD #R15HD106177, CIFAR Azrieli Global Scholars Program

Childhood physical activity patterns among small-scale populations

MARCELA PFAFF-NASH¹, JOSH SNODGRASS², KAREN L. KRAMER³, MARTINA KONECNA⁴, LARA R DOUGAS⁵, HERMAN PONTZER⁶, LAWRENCE S. SUGIYAMA⁷, SAMUEL S. URLACHER^{1,8}

1. Department of Anthropology, Baylor University, Waco, TX
2. Department of Anthropology, University of Oregon, Eugene, OR
3. Department of Anthropology, University of Utah, Salt Lake City, UT
4. Department of Zoology, University of South Bohemia, Czech Republic
5. Loyola University Chicago, Chicago, IL
6. Department of Evolutionary Anthropology, Duke University, Durham, NC.
7. Department of Anthropology, University of Oregon, Eugene, OR.
8. Child and Brain Development Program, CIFAR, Toronto, Canada

Physical activity (PA) is recognized as a costly and variable component of human energy expenditure. However, reliable PA data from small-scale populations are scant – particularly for children – restricting global understandings of human phenotypic plasticity, energetics, and health. This study addresses this shortcoming by objectively assessing childhood PA among subsistence populations on three continents. Cross-sectional data were collected from 197 children (age 4-13 years), including Shuar forager-horticulturalists of Amazonian Ecuador (N = 94), Garisakang forager-horticulturalists of lowland Papua New Guinea (N = 41), and Maya agriculturalists of southern Mexico (N = 62). PA was assessed using a triaxial Actical accelerometer worn continuously at the hip for 3 to 15 days (M= 7.6). Across the sample, children exhibited a mean estimated PA energy expenditure (AEE) of 706.4 kcal/day (SD = 191.8 kcal/day), resulting in a mean estimated PA level (PAL – total energy expenditure expressed as a multiple of basal metabolic rate) of 1.6 (SD = 0.1). Population-level analyses demonstrate that Garisakang have significantly lower PAL (adjusted M= 1.58) than Maya and Shuar (adjusted M= 1.63) (p <.01). Significant differences are observed between sexes. Daily, girls engage in 85 counts/minute less on average than boys (p <.001), 25 minutes less in moderate-vigorous PA (p <.05), and 21 minutes more in sedentary PA (p <.05). These findings highlight the heterogeneity of the energetic demands of PA in small-scale populations. Existing relationships between child AEE, PAL, and body composition are further explored, particularly testing hypotheses derived from life history theory models of resource allocation.

Unlocking museum collections: promises and challenges of museomic studies in African galagids

LUCA POZZI¹, ANNA PENNA¹, MARY E. BLAIR², HSIAO-LEI LUI³, ELSA PETERS³, LOGAN KISTLER³

1. Department of Anthropology, University of Texas at San Antonio, San Antonio, TX
2. Center for Biodiversity and Conservation, American Museum of Natural History, New York, NY
3. National Museum of Natural History, Smithsonian Institution, Washington, DC

Our understanding of primate evolution and conservation is limited by our ability to obtain high-quality genetic data from wild populations. This task has been particularly challenging for small nocturnal species like the loriforms (galagos, lorises, angwantibos, and pottos). Here, we reconstructed genomic information from historical specimens to illustrate how museomics can improve taxonomic resolution and inform conservation status. We discuss how to plan a museomics study and optimize DNA extraction protocols to maximize the recovery of degraded DNA from historical specimens collected up to over a hundred years ago. Using a shotgun sequencing strategy, we performed metagenomic analyses to assess the degree of exogenous contamination, which was negligible in most samples. However, we found evidence of a broad diversity of potential blood parasites (e.g., *Plasmodium*, *Toxoplasma*, *Leishmania*). Incorporating genetic data from museum specimens enabled the most extensive geographic sampling coverage to date for West African loriforms (galagos, angwantibos, and pottos). Our results confirmed the monophyly of Asian and African lorises and known phylogenetic relationships among galagid genera, but also suggest the potential for some taxonomic revisions and cryptic diversity. Lessons learned include 1) pervasive issues of specimen mislabeling in historical collections; 2) the impacts of specimen age and type on DNA concentration and sequencing success; 3) insights on the presence of blood parasites; and 4) resolution of long-lasting questions about lineage diversity and biogeography. Taken together, these results attest to the enormous potential of museomic approaches for advancing our understanding of galago evolution, ecology, and conservation.

Funding: National Science Foundation (BSC-2120691/1926105/1926215)

An assessment of hypotheses for the maintenance of polymorphic color vision in a group of wild *Ateles belzebuth*

SAM RETTKE¹, D. MAX SNODDERLY^{2,3}, ANDRÉS LINK^{3,4}, ANTHONY DI FIORE^{1,3,5}

1. Department of Anthropology, The University of Texas at Austin, Austin, TX
2. Department of Neuroscience, The University of Texas at Austin, Austin, TX
3. Estación de Biodiversidad Tiputini, Universidad San Francisco de Quito, Quito, Ecuador
4. Departamento de Ciencias Biológicas, Universidad de los Andes;
5. Primate Molecular Ecology and Evolution Laboratory, University of Texas at Austin, Austin, TX

Spider monkeys are large-bodied frugivorous platyrrhines that can live in social groups of over 50 individuals, but frequently split into multiple subunits that range and forage independently. Like most platyrrhines and some strepsirrhines, they possess polymorphic color vision due to allelic variation at a single *M/LWS* locus; heterozygous females are trichromats, while males and homozygous females are dichromats. Four mechanisms – heterozygote advantage, frequency-dependent selection, mutual benefit of association, and niche divergence – have been proposed to explain the maintenance of the opsin polymorphism. We tested predictions of three of these mechanisms in a group of white-bellied spider monkeys (*Ateles belzebuth*) that has been monitored at Tiputini Biodiversity Station in Amazonian Ecuador since 2005. To investigate the possibility of heterozygote advantage, we compared the interbirth intervals and number of offspring produced

for dichromat versus trichromat females. We found no differences in these crude measures of reproductive output, suggesting that the conditional advantages of trichromacy may not translate to higher fitness. To assess niche divergence, we examined the foraging behavior of dichromat versus trichromat females, but found no differences in observations of feeding on major food types. Lastly, we evaluated whether dichromat females might benefit from associating with a trichromat. Preliminary results suggest that dichromats are no more likely to forage on fruit when trichromats are present than when they are in subgroups composed of dichromats alone. Future work may consider other aspects of fitness and fine-scale foraging behavior to better understand how multiple visual phenotypes have been maintained in this population.

Funding: NSF BCS-1638822, Harry Frank Guggenheim Foundation, National Geographic Society, and The University of Texas at Austin.

Body mass estimation based on bi-iliac breadth and femoral head diameter

MADISON L. RODRIGUEZ¹, ALYSSA C. GONZALEZ¹, DEBORAH L. CUNNINGHAM¹, DANNY J. WESCOTT¹

1. Department of Anthropology, Texas State University, San Marcos, TX

Body mass is an important biological parameter for understanding the evolution and life history of humans and has the potential to aid in positive identification in medicolegal death investigations. This study investigates the accuracy of the stature-bi-iliac breadth (ST-BIB) method by Schaffer and the femur head diameter (FHD) equations by Ruff and colleagues. Skeletal remains with documented stature and body weight from the Texas State University Donated Skeletal Collection were used and include 333 individuals (135 female and 197 male) ranging in weight from 32.6 to 219.0 kg (with n=165 “high” BMI [pre-obese/obese]). As expected, both methods underestimated the body mass of high-BMI individuals by 45.1 kg and 42.5 kg for the FHD and ST-BIB, respectively. Individuals with a moderate BMI between 18.5 and 24.9 were also underestimated by both methods by an average of 4.94 kg for FHD and 5.8 kg for ST-BIB. Both methods overestimated body mass of low (>18.5) BMI individuals by 19.89 and 20.36 kg for FHD and ST-BIB, respectively. Interestingly, the differences in the estimates for all BMI categories are not statistically different between the methods. Both methods are relatively accurate for individuals with a moderate BMI, but significant deviations occur for higher and lower BMI category individuals. Because FHD requires a single measurement and ST-BIB requires measuring pelvic breadth and estimating stature, FHD equations are preferred. Methods of determining BMI status from the human skeleton are needed in order to improve accuracy of body mass estimates in a modern U.S. population.

No strong sex-bias found in dispersal patterns of *Colobus vellerosus* fragment groups

SYDNEY M. SELF¹, TERESA D. HOLMES², PASCALE SICOTTE³, NELSON TING⁴, EVA C. WIKBERG¹

1. Department of Anthropology, University of Texas at San Antonio, San Antonio, TX
2. Alumna, Department of Anthropology, University of Calgary, Calgary, AB
3. College of Arts and Sciences, Concordia University, Montreal, QC
4. Department of Anthropology, University of Oregon, Eugene, OR

The dispersal of individuals from their originating natal group into another group or area plays a fundamental role in shaping the structure of social groups and maintaining gene flow between populations. This study examined the degree of sex-biased dispersal within *Colobus vellerosus*, a critically endangered colobus species, living in five smaller forest fragments adjacent to the Boabeng Fiema Monkey Sanctuary (BFMS) in Ghana. Male-biased dispersal is the most common in primates overall, and previous research on *C. vellerosus* in the main forest Boabeng has revealed patterns of obligate male dispersal and facultative female dispersal. If dispersal is also male-biased in the fragments, we would expect lower adult male-to-male relatedness than adult female-female relatedness within groups. We extracted DNA from 196 fecal samples (range: 3-8 samples per fragment), which we genotyped at 10 Short Tandem Repeat loci. There was a large range of variation in same-sex within-group relatedness values, indicating a lack of strong sex-biased dispersal. These findings suggest that there may be less of a sex-bias in dispersal in the fragment populations, while female philopatry may be more common in the Boabeng population. It is possible that these newly recolonized fragments contain males and females who engaged in long-distance dispersal from the source population (Boabeng), and future research will further investigate this possibility. The ability for both sexes to disperse over longer distances has can have positive implications for recolonization of surrounding forest fragments and population persistence over time.

The incidental primate interface: A systematic review of primate research conducted outside of protected areas

ALEXANDRA C. SHELDON¹, THAD Q. BARTLETT¹

1. Department of Anthropology, University of Texas at San Antonio, San Antonio, TX

Ethnoprimateology seeks to better understand the world in which humans and other-than-human primates coexist. Today, there are few primate habitats untouched in some way by humans but research sites remain largely within protected areas. We conducted a systematic review to understand the breadth of primate research being conducted outside of protected areas. We included any article on first-hand primate research conducted outside of a protected area. Publications where research took place across multiple sites were included in our review as long as at least one site fit our inclusion criteria. We excluded research with captive primates, or where the location of the primates was unspecified. Out of 300 articles, 262 (87%) were published after 2000, indicating a sharp increase in ethnoprimateological research since the inception of ethnoprimateology two decades ago. The most common genus represented in the articles was *Macaca* (36%, N = 404), followed by *Cercopithecus* and *Papio* (all <10%). This aligns somewhat with general trends in primate research at all types of sites. 68 research sites were in India, followed by Brazil and Indonesia (>20, N = 360). 36% of articles reported a “mosaic” site (mix of site

types), 28% of research took place at an urban site and 14% at a temple. Given that all research was conducted outside of protected areas, these results are in line with ethnoprimate research. With the majority of primate species considered endangered, it is important to understand human-primate interfaces and the effects they have on all species involved.

Neolithic decline or reorganization?: A paleodemographic and environmental perspective of Northern China from Neolithic Age to Iron Age (6000 BCE to 0 CE)

MARK SIMON¹, QIAN WANG¹

1. Department of Biomedical Sciences, Texas A&M University School of Dentistry, Dallas, TX

During the “Neolithic Decline” (circa 3000–2200 BCE), the population decline detected in Eurasian human populations was previously attributed unilaterally to global climatological shifts. Modern ecological and anthropological frameworks, however, are being developed through interdisciplinary and multiscale analyses to better describe the human-environment interaction and reorganization during the Neolithic Age and proceeding Bronze and Iron Ages. In this study, 92 archaeological sites from Northern China dated from 6000 BCE to 0 CE containing 22,726 human remains were surveyed. Preliminary results demonstrated that there was no significant difference in the minimum number of individuals (MNI) or the ratio of females to males between intervals measured every 250 years (Kruskal-Wallis ANOVA: $p=0.2165$ and $p=0.08191$, respectively). Additionally, estimated χ^2 -values indicated no differences in estimated age groups between 250-year intervals (Children $p=0.8999$, Adolescents $p=0.3942$, Young Adults $p=0.2029$, Middle Adults $p=0.9848$, Old Adults $p=0.1423$). However, there was a marked negative turning point of MNI at archaeological sites at 3500-3000 BCE that aligned with Holocene Event 3, or the beginning of the Neoglacial, suggesting the negative effects of the new environmental regime and altered epidemiology. The well-studied Quaternary geologic records, ecotone diversity, and archaeological richness of Northern China make it an ideal location to develop dynamic models of environmental changes and human populations through time and space. These models will be of importance during the current period of climate change and pandemics and hold potential for guiding policymaking and informing both positive and negative changes in human, animal, and environmental health in the present and future.

Funding: NSF #2040388 to Q. Wang and S. DeWitte.

Biology, anthropology, and medicine on display: Three Philadelphia museums adapt to the 21st Century

SHELLEY L. SMITH¹

1. Department of Sociology and Anthropology, University of Texas at Arlington, Arlington, TX

The Academy of Natural Sciences of Philadelphia, founded in 1812, is the oldest natural history museum in the U.S. The University of Pennsylvania is home to the Penn Museum, an archaeology/anthropology museum founded in 1887. The museum of The College of Physicians of Philadelphia became the Mütter Museum in 1863 following T.D. Mütter's donation of his sizeable collection. In July 2023, I visited these three museums, with a primary focus on the traveling exhibit, "Skin: Living Armor, Evolving Identity." The "Skin" exhibit was co-created by Nina Jablonski and the California Academy of Sciences design team and was subsequently modified by the Science Museum of Minnesota to become a traveling exhibit. It is an excellent example of the infusion of anthropology, both biological and cultural, into a natural history museum environment. The Penn Museum serves as an example of the decolonization movement underway in modern museums; very little biological anthropology content is on display. The Mütter, while popular with the public (and uncomfortably packed during my visit), prohibits photography inside the main exhibits and is currently conducting an ethics review. The efforts of these three old museums to remain relevant and responsive to modern ethical sensibilities demonstrate the transformations underway in 21st museums. I argue that biological anthropologists should remain actively engaged to promote positive change in anthropology and natural history museums and to ensure that our discipline remains represented in these critical public venues.

Funding: UTA Faculty Senate and Department of Sociology and Anthropology

Predicting performance of diverse color vision genotypes of wild primates when foraging for food.

MAX SNODDERLY¹, DELISA RAMOS¹, ANDRES LINK², ANTHONY DI FIORE¹

1. University of Texas at Austin, Austin, TX
2. Universidad de los Andes, Bogota, Columbia

Most diurnal Neotropical primates have polymorphic color vision that can result in multiple types of dichromats and trichromats living in the same social group. We have modeled how well these genotypes would be predicted to distinguish dietary fruits from the visual background of leaf tops and leaf bottoms as a classification problem implemented by support vector machines (SVMs). We measured reflectance spectra of fruits and leaves, and irradiance spectra of incident light to compute quantum catches of genetically diverse cones of three sympatric primates in Amazonian Ecuador: *Ateles belzebuth*, *Lagothrix lagothrica*, and *Pithecia aequatorialis*. We constructed MacLeod-Boynton chromaticity spaces for each genotype and trained SVMs to classify fruits and leaves based on color, then added a third dimension for luminance. For metrics of performance, we used classification accuracy and also the area under ROC curves (AUC), which allowed calculation of 95% confidence intervals (CIs, range 0-1). In the absence of luminance information, in direct sunlight trichromats are predicted to distinguish fruit from leaf tops with accuracies of 91-96% compared to 59-73% for dichromats; CIs of the AUCs do not overlap. When luminance was incorporated, predicted performance of trichromats did not improve, but

predicted accuracy for dichromats increased to 71-79%; some CIs overlapped with trichromats. For the more common (and more difficult) discrimination of fruit vs leaf bottoms, predicted accuracy based on color decreased to 76-92% for trichromats and 64-71% for dichromats; CIs had small amounts of overlap that varied among genotypes. Adding luminance information had less effect on predicted accuracy for trichromats, but increased predicted accuracy for dichromats to 66%-82%; now CIs of dichromats overlapped extensively with those of trichromats. Thus, dichromats may be able to use luminance information to minimize the potential advantage that trichromats have in a critical foraging discrimination.

Funding: NSF IOS-0843354, NSF BCS 1638822, and The University of Texas at Austin.

Group composition influences on vocalization counts in *Alouatta palliata*, *Ateles geoffroyi*, and *Cebus imitator* at Camaquiri Conservation Initiative (CCI) field site.

KAYLA M. TELLEZ¹, JILL D. PRUETZ¹

1. Department of Anthropology, Texas State University, San Marcos, TX

Vocal communication is crucial for primates to determine territory, mates, and group composition. A primate's effectiveness to determine friend or foe through short calls and long calls has evolved to become a beneficial adaptation. I studied the vocalization frequencies from different group compositions in three neotropical primates present at the Camaquiri Conservation Initiative (CCI) in Costa Rica to determine if group size influences vocal call counts. The three primates; howler monkeys (*Alouatta palliata*), spider monkeys (*Ateles geoffroyi*), and capuchin monkeys (*Cebus imitator*) were included in 1-hour scan sampling behavioral observations with 2-minute intervals. In addition to behavioral observations, all-occurrence data was recorded for vocalizations within each observed group. I found that different average vocalization counts were exhibited between-primate species throughout the day. Howler monkeys on average had the highest vocalization counts (212 calls), followed by capuchins (91 calls), and spider monkeys vocalized the least (64 calls). My finding that vocal counts differ between neotropical primate species supports the hypothesis that vocalizations are dependent on a primate's societal group. Within-species, the hypothesis of group size influence wasn't supported and there was no correlation between group size and vocalization frequency. Multiple group sizes exhibited a large range of vocal counts, but the sample sizes observed did not provide sufficient data to support or reject the proposed hypothesis. The within-species results suggest that group composition does not influence vocalization counts, but with between-species data future studies can be conducted to determine species-specific vocalization influences.

Funding: The Gavin Brink Memorial Fund

Identification of ecological and locomotor indicators of semi-terrestriality in anthropoid primates.

INDYA J. THOMPSON¹, BERNADETTE A. PERCHALSKI¹, SCOTT D. MADDUX¹,
LAUREN A. GONZALES¹

1. Department of Physiology and Anatomy, UNTHSC, Fort Worth, TX

Semi-terrestriality, the utilization of both arboreal and terrestrial environments, is commonly discussed in the primatological literature but inconsistently defined, limiting its study in fossil taxa. This project aims to fill that gap by investigating the ecological and locomotor variables that characterize semi-terrestrial taxa. 18 semi-terrestrial and 17 arboreal anthropoid taxa were identified from the literature. Ecological data were collected from mammalian demographic and environmental databases and locomotor data were collected from the literature. Two stepwise canonical variate analyses (CVA) were run (ecological and locomotor) to identify factors that discriminate between semi-terrestrial and arboreal primates. The ecological CVA retained population size, social group size, and percentage of leaves in the diet as variables. CV1 (55.8%) differentiated semi-terrestrial platyrrhines from arboreal and semi-terrestrial catarrhines. CV2 (26.9%) distinguished semi-terrestrial platyrrhines and catarrhines cluster away from their arboreal counterparts. The locomotor behavioral CVA retained bridging, leaping, quadrupedal walking, climbing, scrambling/clambering and bimanual suspension as variables. CV1 (62.3%) separated semi-terrestrial platyrrhines from semi-terrestrial catarrhines, while CV2 (31.5%) distinguished both semi-terrestrial taxa from arboreal taxa. These results indicate select ecological and locomotor variables can reliably identify semi-terrestrial taxa, helping to improve our understanding of this enigmatic behavior. Future studies should likely include measures of specific bony features to investigate potential morphological indicators of semi-terrestrial behaviors.

Modeling airflow dynamics during the nasal cycle *in silico*: Implications for variation in human nasal form and function

BAONHU TRAN¹, LYNDEE A. WARD¹, HASINTHA H.A.K. PATABENDIGE², VIVEK C. NAIR², ELIZABETH O. CHO¹, TODD R. YOKLEY³, BRIAN H. DENNIS², SCOTT D. MADDUX¹

1. Center for Anatomical Sciences, University of North Texas HSC, Fort Worth, TX
2. Department of Mechanical and Aerospace Engineering, University of Texas at Arlington, Arlington, TX
3. Department of Sociology and Anthropology, Metropolitan State University, Denver, CO

Investigations into how morphological variation within the human nose influences intranasal airflow dynamics have been limited due to an inability to control for nasal mucosal congestion during the nasal cycle. Here, we combined a newly developed *in silico* method for controlling nasal mucosal congestion with Computational Fluid Dynamics (CFD) analyses to assess the functional impacts of the nasal cycle on intranasal heat and moisture exchange. Three nasal models with varying congestion levels were generated from a male human head computed tomography

(CT): asymmetrical (left/right = 90/10%), mid-cycle (left/right = 50/50%), and fully decongested (left/right = 0/0%). Morphological assessments of mucosal surface area-to-airway volume (SA/V) ratios reveal that the decongested model exhibited a substantially lower SA/V ratio (0.57) than the mid-cycle (0.72) and asymmetrical (0.74) models. Afterwards, CDF analyses were performed on each model to evaluate the amount of heat and moisture transferred to cold-dry (-5°C, RH=0%) inspired air. Consistent with anatomical and functional expectations, the fully decongested model demonstrated the lowest levels of inspiratory heat and moisture transfer during CFD modeling upon reaching the nasopharynx (28.2°C, 66.1% pulmonary humidity) than the mid-cycle (29.2°C, 68.4% PH) and asymmetrical (29.4°C, 69.6% PH) models. These results suggest that the nose's overall air-conditioning capacity likely remains relatively stable through the nasal cycle regardless of morphological variation within the nasal cycle. Thus, it may be the distinction between the semi-congested nasal cycle versus complete mucosal decongestion (as seen during strenuous exercise) that confounds functional interpretations of variation in nasal morphology.

Funding: National Science Foundation (#2203808), Texas Center for Health Disparities (RF00241 & RI40241), and the Association for Anatomy Innovations Program.

Source level and attenuation of titi monkey duets in a rainforest habitat

SILVY M. VAN KUIJK¹, ANTHONY DI FIORE¹

1. Department of Anthropology, The University of Texas at Austin, Austin, TX

Passive acoustic monitoring (PAM) is a practical tool for studying primate vocal communication over large spatial or temporal scales. However, for optimal research design and performance, effective use of PAM requires baseline knowledge on the characteristics of the species-specific vocalizations and acoustic properties of the primate's habitat. We determined the source level (amplitude at 1m from the monkeys) for duet vocalizations given by pair-living red titi monkeys (*Plecturocebus discolor*) and the attenuation rate of these duets in an Amazonian rainforest environment to estimate at which distances from an autonomous unit we can expect to record high quality data. Using duets extracted from audio recordings collected within the territory of a single titi monkey pair at the Tiputini Biodiversity Station (TBS), we estimated that the source level of titi duets was ~105 dB re 20 µPa at 1m in the frequency range that contains the loudest elements of the duet (700-1400 Hz). We used playback experiments to determine that the attenuation of duets at TBS averages 8 dB per doubling of distance. Because loss of amplitude with distance due to spherical spreading alone is ~6 dB/doubled distance, excess attenuation in this particular rainforest habitat is estimated as ~2 dB/doubled distance. Loud calls captured in recorded audio are generally considered high quality when the signal-to-noise ratio (SNR) is > 10. With an average ambient noise level at TBS of ~40 dB, to obtain high quality data duets would need to be recorded within a ~130m radius around the recording device.

Funding: The University of Texas at Austin.

Genotyping-in-thousands to assess twin chimerism in wild saddleback (*Leontocebus weddelli*) and bearded emperor tamarins (*Saguinus imperator subgriseus*) from Amazonian Peru

RACHEL VOYT¹, SAMANTHA LOPEZ CLINTON^{2,3}, KATERINA GUSCHANSKI^{2,4}, RAQUEL BALLESTEROS, GIDEON ERKENSWICK WATSA³, SUMITHA HUNJAN⁵, ANTHONY DI FIORE^{1,6}, AARON SANDEL¹, MRINALINI ERKENSWICK WATSA^{3,5}

1. Department of Anthropology, University of Texas at Austin, Austin, TX
2. Department of Ecology and Genetics - Animal Ecology, Uppsala University, Uppsala, Sweden
3. Field Projects International
4. Ashworth Laboratories, University of Edinburgh, Edinburgh, United Kingdom
5. San Diego Zoo Wildlife Alliance, Escondido, CA
6. Estación de Biodiversidad Tiputini, Universidad San Francisco de Quito, Quito, Ecuador

Callitrichines are a radiation of small-bodied primates characterized by a suite of unique life history traits, including the regular production of twins or other multiples. During embryonic development, twins exchange hematopoietic stem cells via inter-placental anastomoses and maintain these cell lines through adulthood, each twin growing up as a genetic chimera of the other. Studies of this phenomenon, however, are concentrated on captive populations of only a few species and have focused on mixed-sex chimerism, providing limited knowledge of how chimerism presents more generally. We examined twin chimerism in wild saddleback (*L. weddelli*) and emperor tamarins (*S. i. subgriseus*) from the Estación Biológica Río Los Amigos in Amazonian Peru. We sequenced hair and blood samples from 32 twin pairs (n = 14 *L. weddelli*; n = 18 *S. i. subgriseus*) at 211 SNP loci via genotyping-in-thousands by sequencing (GT-seq). We used hair sample reads to determine the “self” genotype at each locus, and blood sample reads to calculate hematopoietic chimerism. After removing uninformative loci and samples that did not amplify, we could estimate chimerism for 18 individuals (six *L. weddelli*; 12 *S. i. subgriseus*) from 11 twin pairs (four *L. weddelli*, seven *S. i. subgriseus*) using 2 to 27 loci (mean = 10.7 loci) per individual. Mean chimerism ranged from 54 to 87% in *L. weddelli* and 0 to 100% in *S. i. subgriseus* individuals, fitting within values found for mixed-sex twin chimerism in other callitrichines. Our results suggest that GT-seq could be a valuable method for characterizing chimerism in additional species.

Funding: The Leakey Foundation, The University of Texas at Austin, The Texas Academy of Science, The Explorers Club

Climatic adaptation in the human nose: An investigation using 3D morphometrics and computational fluid dynamics

LYNDEE A. WARD¹, HASINTHA H.A.K PATABENDIGE², ELIZABETH O. CHO¹, TODD R. YOKLEY³, BRIAN H. DENNIS², SCOTT D. MADDUX¹

TABA Conference Program 2023

1. Center for Anatomical Sciences, University of North Texas Health Science Center, Fort Worth, TX
2. Department of Mechanical and Aerospace Engineering, University of Texas at Arlington, Arlington, TX
3. Department of Sociology and Anthropology, Metropolitan State University of Denver, Denver, CO

INTRODUCTION: Ecogeographic variation in human nasal morphology is widely argued to reflect climate-mediated pressures for heating and humidifying inspired air, with taller/narrower/longer nasal passages thought to enhance heat and moisture transfers in colder environments. However, challenges in quantifying nasal soft-tissue morphology and comprehensively assessing intranasal airflow have limited empirical testing of these long-standing hypotheses. **METHODS:** To address this issue, this study employed three dimensional (3D) models of decongested nasal airways derived from cranial CT scans from a mixed-sex sample of 21 living individuals of West African and/or European ancestry. A total of 260 semi-landmarks were collected on each nasal model to quantify nasal morphology, followed by Computational Fluid Dynamics (CFD) analyses to assess intranasal temperature and humidity transfers during inspiration of cold-dry air (-5°C , $\text{RH}=20\%$). Multivariate regression was then employed to test for statistical associations between nasal morphology and intranasal heat and moisture transfers. **RESULTS:** A significant association between nasal shape and the temperature and humidity of inspired air entering the nasopharynx after passing through the nasal cavity ($R^2=0.582$, $p<0.0001$) was identified. Consistent with theoretical expectations, the resulting 3D shape vector indicates that taller/narrower/longer nasal passages are associated with greater transfers of heat and moisture to inspired air. **CONCLUSIONS:** This study thus provides strong empirical support for hypotheses regarding ecogeographic variation in nasal form and function. Future studies investigating how nasal morphology influences specific aspects of intranasal airflow (e.g., directionality, velocity) which ultimately mediate heat and moisture transfers are needed to develop a more comprehensive understanding of nasal airflow biomechanics.

Funding: This research was supported by Texas Center for Health Disparities Grant #RF00241 via NIMHD #5U54MD006882-10.