differences in non-adult health, and its impact on health and disease later in the life course. No rural-urban differences in growth and development and their impacts on morbidity and mortality were identified through logistic regression and correlation analysis. One possible explanation for this homogeneity stems from the high economic status of the individuals included in this analysis, which could have buffered potential detrimental effects of urban living. This evidence highlights the complexity of urban and rural health and the necessity of parsing out impacts of economic status on health.

Neonatal hair as a record of maternal and fetal exposures

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This presentation is part of the symposium *Integumentary Anthropology: Examining the Exterior*. Biological material comprising the integumentary system, or produced by it, can be analyzed for biomarkers that reveal information about real-time or past biology of the individual from whom it was collected. As a keratinized matrix that preserves concentrations of – among other things – proteins, hormones, and heavy metals in circulation at the time of its growth, hair can be analyzed to interrogate endogenous physiology and exogenous influences on individual biology.

Neonatal hair, grown mostly *in utero*, can provide a window to understand influences on fetal physiology during gestation, including nutrition, environmental exposures, and hypothalamic-pituitary-adrenal (HPA) axis activity. We report on the analysis of neonatal hair elements and hormones in a birth cohort, and explore the relationships between aspects of the maternal and physical environment during pregnancy, and variation in the analytes measured in neonatal hair.

Consent was obtained from parents in the rural West Kiang region of Gambia to collect and analyze a sub-sample of hair shaved during infants' naming ceremony at one week of age (N: 211; 100F, 111M). Hair samples were prepared and analyzed using published enzyme immunoassay and mass spectrometry protocols for measurement of concentrations of cortisol and cortisone, and levels of calcium, copper, iron and sodium, respectively. Monthly rainfall measures, summed across trimesters of pregnancy for each infant, were used together with maternal parity and anthropometry to explore the relative contribution of these factors, across gestation, to variation in neonatal hair hormones and elements.

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Analytical validation of an enzyme immunoassay protocol to quantify hair cortisol concentrations in human hair

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Cortisol is a steroid hormone that helps mediate energy allocation during challenging conditions. As such, elevations in cortisol can be used as evidence of exposure to adverse environments. After being released by the adrenal gland, cortisol travels through the bloodstream and gets incorporated over time into the hair shaft via passive diffusion. The slow accumulation of cortisol in the hair, in addition to its non-invasive collection and easy storage, has made hair cortisol concentration (HCC) analyses a useful tool to assess long-term exposure to adverse conditions. Yet, despite its widespread use in humans, we failed to find a published validation of human hair cortisol. Here we describe our cortisol extraction from human hair and present our analytical validation of an enzyme immunoassay protocol to measure HCCs. Parallelism was calculated by running a serial dilution of our pool, and we did not find significant differences in the slopes generated by running the standards and our pool (ANOVA: t-value = 0.272, p = 0.792), indicating parallelism had been achieved. Accuracy was calculated by spiking standards with 35 µl of pool and obtained a mean recovery of 71.7% (SD = 12.33). Precision was assessed by running the same sample three times on the plate. We obtained an acceptable coefficient of variation of 12%. The results of our analytical validation, in addition to the high correlation between HCC and average salivary cortisol levels reported by previous studies, provide evidence of the reliability of this measurement as a biological marker of exposure to environmental challenges.

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Paleohistopathology of Treponemal Disease in Human Bone from Taumako, Solomon Islands (700-300ybp)

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The application of histology in paleopathological analysis of treponematosis has been limited to case studies and predominantly European individuals. However, histological examination of larger samples of archaeological human skeletal remains can provide insights into biological processes of disease and their effects on bone microarchitecture. This study investigated quantitative changes of bone microstructure in 65 adult individuals from Taumako, Solomon Islands (700-300ybp), a region of historic and continuing treponemal endemicity.

Thin sections prepared from the anterior tibia, a bone commonly involved in treponemal infection, were examined using polarised microscopy to histologically compare individuals with no visible pathology (n=40), and individuals with gummatous lesions indicative of treponemal infection (n=25). In addition to histomorphological abnormalities, individuals with treponemal infection had lower vascularity than those without the pathology (p=<0.001). Furthermore, while Haversian canal area remained consistent across both groups, overall bone porosity significantly increased (p=<0.001) with infection due to an increase in resorptive spaces and trabecularisation of cortical bone.

These results suggest that new and remodelled bone produced in response to long term treponematosis was significantly less vascular and, in being highly porous, was of poorer quality than is typically observed in non-pathological individuals. While reduced vascularity is consistent with the pathophysiology of treponematosis and effects on angiogenesis, increased porosity suggests a remodelling imbalance and increased osteoclastic activity. These are the first reported quantitative changes in bone histomorphometry in response to treponemal infection. They demonstrate our ability to better understand disease response through the lens of palaeohistopathology, beyond that of disease identification only.

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An analysis of morphological evolution in the catarrhine appendicular skeleton using methods from quantitative genetics

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Morphological differences are frequently used in evolutionary studies, but it is often difficult to determine which observed morphological changes are evolutionarily significant. Quantitative genetics provides mathematical frameworks that can be used to identify potential directional selection in morphological evolution. Lande's generalized genetic distance (GGD) is one such framework. Here, we apply Lande's GGD to examine evolutionary processes affecting the catarrhine appendicular skeleton. 45 inter-landmark distances (traits) from eight elements

(scapula, humerus, radius, ulna, os coxa, femur, tibia, and fibula) were analyzed across seven taxa: *Chlorocebus pygerythrus* (n=32), *Gorilla gorilla* (n=35), *Homo sapiens* (n=35), *Hylobates lar* (n=34), *Pongo pygmaeus* (n=30), *Pan troglodytes* (n=34), and *Macaca fascicularis* (n=35). Evidence of strong directional selection was found on the branches from the last common ancestor (LCA) of *Pan* and *Homo* to *H. sapiens*, and from the LCA of hominoids to *H. lar*. Selection gradients and responses were calculated for these branches. Large selection gradients were indicated on the femur, fibula, tibia, os coxa, humerus and radius on the branch leading to *H. sapiens*, and on the tibia, os coxa, humerus, radius, ulna and scapula on the branch leading to *H. lar*. These results are consistent with selective pressure from derived locomotor patterns and support earlier research indicating parcellation of the hominoid upper and lower limb. However, some traits that are assumed to be adaptive – such as the human tibial plateau – had selection gradients inconsistent with the morphological response, indicating these traits may be the result of processes other than direct selection.

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Central and peripheral oxytocin and vasopressin concentrations do not differ between two baboon species with divergent social systems (*Papio hamadryas* and *Papio anubis*)

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Primate social systems can be highly diverse, even among closely related species. However, it is unclear if this diversity is mediated by differences in neuroendocrine physiology. Here we focused on the closely related anubis (*Papio anubis*) and hamadryas (*Papio hamadryas*) baboons, who live in polygynandrous mixed-sex groups and multilevel polygynous societies, respectively, and measured whether these marked social and mating differences could be detected as differences in the baseline levels of oxytocin (OT) in the cerebrospinal fluid (CSF), blood plasma, and urine, and arginine vasopressin (AVP) in CSF. We collected biosamples from 84 baboons (38 hamadryas and 46 anubis) and assayed them with ELISA. Using Bayesian multilevel modelling, we found no differences in hormone concentrations between the two species. However, OT levels did vary with demographic variables, such as sex, age, and reproductive state. Specifically, OT levels were generally higher in females than in males, and peripheral OT levels in females were related to pregnancy, providing important biological validation. Levels of OT and AVP as well as OT from different sources (CSF, plasma, urine) were not correlated. In sum, we found no differences in OT and AVP levels between two closely-related baboon species, suggesting other aspects of neuroendocrine physiology are responsible for the stark differences in their social systems.

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Is there an energetic threshold during pregnancy?

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The "Energetics of Gestation and Growth" (EEG) hypothesis posits labor is initiated when the supposedly exponentially growing energetic demands of the fetus exceed the sustained maternal metabolic capacity of about 2.1×basal metabolic rate (BMR). The EGG model offers an alternative explanation for the secondary altriciality of human neonates, i.e., the greater neurological and physical immaturity compared to those of non-human primates. In contrast, the "obstetrical dilemma" attributes our secondarily altricial newborns to pelvic constraints. However, the metabolic threshold argued under the EGG framework is derived from only one study on 12 women from the UK, while data based on athletes suggest a higher maximum sustained metabolic scope at around 2.5×BMR (extrapolated to a 180-day-long endurance event such as pregnancy). Here, we show that the total energy requirements and BMR during pregnancy show considerable variability across diverse geographic and socioeconomic samples, with the maximum energetic requirement of the expectant mother ranging between 1.6 and 2.4×BMR. The higher reported metabolic levels make it unlikely that a threshold is crossed by the energetic demand of the fetus at the time of birth. Additionally, recent gestational weight gain and body composition data of human females indicate that pregnancy does not pose an energetic constraint in humans, nor does the placenta constitute a significant energetic barrier. The benefit of a presumed metabolic ceiling during pregnancy is unclear from an evolutionary perspective and the unique birth difficulties in modern humans thus require multifactorial explanations that consider the possibility of both obstetric selection and metabolic mechanisms simultaneously.

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Dominance and paternity in male mantled howler monkeys (*Alouatta palliata*) at La Pacifica, Costa Rica

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The priority of access model predicts that male primates should be dominant to monopolize access to fertile females and ultimately increase reproductive success. However, in species that live in multi-male/multi-female groups where females engage in polyandrous mating, the positive relationship between dominance rank and paternity predicted by the model is not consistently demonstrated. Mantled howler monkeys (*Alouatta palliata*) have variable group composition, females mate polyandrously, and males sometimes form dominance hierarchies, though studies using genetic markers to determine the relationship between paternity and dominance are rare in this species. We collected behavioral data on nine adult males in two mantled howler monkey study groups (groups 2 &12) at La Pacifica, Costa Rica from January to December 2010. Males in both groups formed linear dominance hierarchies. Dominance was based on agonistic interactions between dyads and calculated using David's score. We collected fecal samples noninvasively from all adult males and 22 infants and juveniles in both groups for later DNA extraction. We genotyped all individuals using 12 previously screened microsatellite markers found to be polymorphic in this population. Paternity was confidently assigned for 17/22 offspring using the program CERVUS. Preliminary results indicate that the dominant male in each group fathered 43% (group 2) and 56% (group 12) of known sampled offspring. These data suggest that while dominant males may father a higher percentage of offspring compared to