between all pairs of dental phenotypes into their genetic and non-genetic components to obtain estimates of shared genetic effects – i.e., pleiotropy – on patterns of dental covariation. From these analyses, we developed an appreciation for the genetic architecture underlying dental variation in baboons. In our presentation, we will provide an overview of the results of these analyses and discuss the utility of our observations for the investigation of the phenotypic evolution preserved in the fossil record.

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Functional morphology of the wrist joints of sloths and suspensory primates

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Suspensory locomotion and postures, with the forelimbs under tension and hands adopting hook-like grips, independently evolved in gibbons, spider monkeys, and sloths. Anatomical similarities of the wrist include: (1) highly curved proximal carpal joints and reduced ulnar styloid processes shared by gibbons and sloths (Jenkins & Fleagle, 1975; Mendel, 1979), and (2) half ball-and-socket midcarpal joints shared by gibbons and spider monkeys (Jenkins, 1981). All of these features are believed to increase ranges of hand movement during positional behavior. Still, the functional significance of these commonalities in carpal structure, particularly as they relate to specific hand movements, is supported by few experimental data in living animals. To this end, we radiographed the hand of anesthetized *Ateles geoffroyi*, *Choloepus didactylus*, and *Hylobates lar* in maximum ranges of radioulnar deviation and dorsi-volarflexion to examine changes in wrist joint configuration as hand positioning varies. In all taxa, ulnar deviation is accompanied by radial translation of the scaphoid and lunate on the radius, and further enhanced in primates by rotation of the capitate and hamate at the midcarpal joint. In sloths, the distal triquetrum and radius form a single, highly curved surface congruent with the scaphoid, lunate, and hamate where ulnar deviation takes place. However, the more palmar and proximal position of the cuboidal-shaped triquetrum appears to limit volarflexion compared to primates. Our experimental data suggest that different functional solutions evolved in the wrist of sloths and primates that promote mobility of the hand in specific planes.

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Testosterone mediates the association between phenotypic condition and low voice pitch in Bolivian adolescents: Implications for a costly-signaling model of male voices

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The human voice is one of the most conspicuous and dimorphic human secondary sexual characteristics; males' low fundamental and formant frequencies barely overlap with females'. Researchers often assert that low male voices are costly signals of phenotypic quality; however, no evidence currently exists linking low voices with any indicators of quality such as health or physical condition. In the present study, we examine the relationships between condition, testosterone, and vocal parameters in 91 Bolivian adolescent males. Condition is operationalized as immune function (based on secretory IgA) and energetic reserves (BMI-for-age residuals from Tsimane-specific growth curves), and "masculine" vocal parameters as having low fundamental frequency, narrow formant position, and low fundamental frequency variation. We target adolescents to capture variation in vocal parameters during the canalization period for vocal fold and vocal tract growth. Results indicate that males in better energetic condition have higher testosterone levels and lower voices, even controlling for age. Further, testosterone mediates the relationship between condition and fundamental frequency. We suggest that testosterone plays a key mediating role in the causal pathway linking phenotypic condition to lower fundamental frequency. Our results provide support for a costly-signal model of low male voices.

Biorhythm variations underlying the evolution of human life history: Evidence from tooth and bone histology

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Microstructural evidence from teeth and bone has been used to support the hypothesis that growth, metabolism, and reproduction – i.e., life history – are centrally regulated by a neuroendocrine rhythm, the Havers-Halberg Oscillation (HHO). A broad sampling of HHO rhythms across primates has fleshed out patterns of variation among species as well as among the major taxonomic groups within the order. However, intraspecific variation patterns acting as the basis for natural selection upon life history have not been thoroughly sampled. Humans are important to assess in this regard because they are a natural experiment, with an unusually high range of HHO variation; it is also obviously vital to assess modern human biology to shed light on major questions of hominin evolution.

Therefore, this study assesses dental Retzius line periodicity (a proxy for HHO cycle) and bone osteocyte density data from histological sections, sampled from humans of contemporary Malawi and South Africa. These data are analyzed against known predictors of HHO biology across anthropoids, such as body size. Given the unusual nature of human life history as compared to great apes, we predict that human intraspecific patterns will differ markedly from those of primate relatives. Regressions show that humans tend to inversely scale HHO rhythms with body size, opposite the pattern seen among anthropoid species as a whole. This suggests the unusual nature of human life history derives partly from tradeoffs between biological timing mechanisms and durations of growth, and thus the underlying physiology coordinating growth and life history in general.

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3D morphometric analyses of human ulnae

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A 3D morphometric study of 53 human right ulnae was undertaken in order to investigate the following functional morphological hypotheses related to diaphyseal bowing in this relatively straight long bone: 1.) ulnae with larger and more proximally-positioned brachioradialis attachments will show a greater degree of bowing than ulnae with smaller or more distally-placed brachioradialis attachments, and 2.) the degree of bowing in the ulna will not be correlated with the biomechanical advantage of triceps brachii, but rather will reflect the strength of the elbow flexors. Principal components of Procrustes shape data derived from 30 type II and III anatomical landmarks reveal the following. First, the vast majority (89.4%) of information in the dataset is related to size, as this is the amount of variance explained by PC1, which shares virtual identity with centroid size (r^2 = 99.7%). PC2, which explains only 1.8% of the total variance, contrasts those ulnae with large articular areas and straight diaphyses with those bearing smaller articular dimensions and bowed diaphyses. PC3 (which explains 1.4% of the total variance) is related to torsion along the bone's long axis, while PC4 (which explains 1.2% of the variance) is related to the relative position of the brachialis scar. Neither relative size nor position of the brachialis scar is correlated with PC2, although the relative moment arm size for triceps brachii is correlated with both torsion and bowing along the bone's long axis. We therefore reject our initial hypotheses and suggest avenues for further research.

The occipital lobes of Neandertal brains, orbit size, and cognition: What is the evidence for Neandertal cognitive inferiority?

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A recent article by Pearce, Stringer, and Dunbar (2013) have claimed that Neandertals did not have proportionately as large parietal association cortices as modern humans because their orbits were larger, and thus they would have had a larger visual cortex (area 17 of Brodmann) than anatomically modern humans (AMH). They thus suggest that Neandertal intelligence would necessarily have been less

evolved with respect to sociality than in AMH. We have obtained CT scans for several of the Neandertals that have occipital lobes intact (La Chapelle-aux –Saints, LaFerrassie, LaQuina, Saccopastore, Skhul V, IX, Tabun, Amud, Forbes Quarry). Analysis of virtual endocasts from these scans does not show reliable evidence to support the assertion of different brain organization in Neanderthal, in the form of enlarged visual cortices or smaller parietal cortices. Limitations of the methods used to infer visual cortex size from orbit size, as well as inferences about cortical organization from endocasts, will also be discussed.

Life history analysis for a population of *Colobus vellerosus* in Ghana, West Africa

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Matrix population models can aid effective population management by allowing us to identify the life-history stages that are under the strongest selection pressure. We compared the impact of vital rates on population change using annual demographic data to control for seasonal effects in a population of a vulnerable primate species, *Colobus vellerosus,* at Boabeng-Fiema Monkey Sanctuary (BFMS), Ghana. We collected data from individually recognizable members of 8 study groups between May 2000 and 2009. We constructed projection matrices for males and females by classifying life history data into four stages using known or estimated birth dates: infant (pre-weaning), juvenile (post-weaning to 3 years), sub-adult (3-7 years for males; 3 years to primipara for females), and adult (≥7 years for males; primipara for females). The mortality rate for males was higher than the rate for females (0.12 vs. 0.04 individuals per year respectively). This could be related to the higher philopatry of females than males in this population. This population is growing with annual rates of $\lambda = 1.37$ for females, and $\lambda = 1.17$ for males. A sensitivity analysis demonstrated that selection on survival is greater than selection on fertility for both sexes. Population growth is most sensitive to infant survival, as opposed to adult survival in other primates, which may be linked to a low predation pressure and a high infanticide risk. Continued monitoring of *C. vellerosus* at BFMS will allow us to identify population growth concerns and design approaches for successful mitigation.

Three-dimensional foot kinematics of chimpanzees and humans during bipedal locomotion

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Humans have evolved joint articular surface morphology that limits midfoot mobility during terrestrial bipedalism at the expense of arboreal locomotor capabilities. However, many pedal remains from early hominins exhibit ape-like joint morphology. Hence, a thorough understanding of ape foot mechanics during locomotion is critical to reconstructing the positional behaviors of early hominins.

In this study we measured three-dimensional kinematics of the foot in humans and chimpanzees (*Pan troglodytes*) during bipedal walking. Kinematic data were collected using a four-camera motion capture system (ProCapture, Xcitex Inc.). A 25-point leg and foot marker set was used to measure motion at the talocrural, subtalar, transverse tarsal, cuboidometatarsal, and metatarsophalangeal joints across stance phase.

We quantified the following previously unreported interspecies differences in foot kinematics. At the subtalar joint, chimpanzees exhibit roughly twice the amount of total frontal plane motion (inversion-eversion) as humans during a step. However, in chimpanzees this motion occurs almost entirely at the beginning of stance phase, as the highly inverted foot is brought into full contact with the substrate. Chimpanzees maintain a relatively static joint posture for the remainder of stance, whereas humans invert the subtalar joint prior to toe-off. Contrary to the expectations of a "midtarsal break," chimpanzees exhibit little to no dorsiflexion at the transverse tarsal joint following heel lift. Instead, chimpanzees evert the hindfoot at this joint during heel lift, causing the lateral border of the heel to leave the substrate before the midfoot. This phenonemenon was not observed in humans.

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The origins and evolution of *Mycobacterium leprae*

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Leprosy is one of the oldest human diseases and remains a public health concern in several developing countries. The causative agent of human leprosy, *Mycobacterium leprae*, underwent reductive evolution millions of years ago. The limited genetic variation among human strains of *M. leprae*, suggests a relatively recent host switch to humans from another species. We performed whole-genome sequencing of a *M. leprae* strain isolated from a West African sooty mangabey (*Cercocebus atys*). The genome comprised 3,268,076 bp, with an overall average coverage of 53x. Sequence comparisons between the mangabey strain and the reference genome (*M. leprae* TN strain from India) revealed 99.995% sequence identity. The mangabey strain differs at 153 polymorphic sites from the TN strain and at only 79 sites from the Br4923 strain from Brazil. Single nucleotide polymorphism-based phylogenetic analyses have shown that the Br4923 and mangabey strains are basal to Eurasian strains, suggesting an African origin of leprosy. We are also currently sequencing the genome of a strain of *M. lepraemurium*, the causative agent of murine leprosy. Murine leprosy shows similar clinical and histopathological manifestations as human leprosy, but unlike human leprosy, the causative agent can be cultured. Comparative and phylogenetic analyses of the strain of *M. lepraemurium* with the human and mangabey strains of *M. leprae* will help to clarify the origins and evolution of leprosy.

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Paleogenomic variation in a CC Chemokine Receptor Gene (CCR5)

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Climate plays an influential role in the distribution of diseases and their outbreaks, hosts, and vectors. Immunologically naïve populations rely on general immune system functioning such as CC chemokine receptors (CCRs) which promote chemotaxis and viral binding. In humans, CCR5 is associated with variation in susceptibility to HIV and West Nile Virus (WNV). HIV and WNV originated in Africa but have now expanded beyond the tropical zone. A 32bp deletion mutation (CCR5Δ32) in European populations in CCR5 causes increased resistance to HIV and vulnerability to severe WNV symptoms (e.g., meningitis, encephalitis). A primate-wide analysis of variation in CCR5 suggests balancing and purifying selection as well as different selective pressures in Old and New World primates. The aim of this research was to explore evolutionary human variation in CCR5 using paleogenomic data (Neandertal, Denisova; Saqqaq, a 4000 year old Paleoeskimo) from high latitude populations. Paleogenomes were expected to show similar patterns of variation to modern Eurasians due to geographically differential selection in CCRs and contributions from Neandertals to modern human immune genes. This is true for Denisova who shares with modern humans an upstream variant that may influence gene function. The Neandertal genome, however, contains three unique nonsynonymous single-nucleotide polymorphisms. The Neandertal mutations do not impact protein conformation significantly but may have a subtle effect on gene activity. Understanding evolutionary and geographic variation in genes associated with disease resistance and susceptibility are important avenues of research for epidemiological modeling.

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Reconstruction of Neolithic and Iron Age human manipulative behavior using electromygraphy

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It has been suggested that decreased humeral bilateral asymmetry detected in European females from Neolithic to Iron Age reflects grain