

considerable cross-sectional area and long fibers (and thus were capable of generating high bite forces at large gapes) and that these features were adaptations for processing very resistant and large foods. This interpretation suggests that adapines fed on woody stems, mature leaves, and large fruits or nuts with tough casings. Further work to refine estimates of fiber length is necessary to evaluate this interpretation.

This study was supported by Sigma Xi, by the Duke Lemur Center's Director's Fund, and by Duke University (the Graduate School and the Department of Biological Anthropology and Anatomy).

#### **Kin biased social behavior in wild white-faced capuchin monkeys, *Cebus capucinus*.**

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It has long been known that kinship biases individuals' choices of social partners in a variety of species. However, the fine details of how individuals balance the importance of kinship against other variables such as dominance rank is less clear. It is also uncertain how kinship recognition mechanisms function in primates. In this paper, we present data from wild capuchin monkeys living in or near Lomas Barbudal Biological Reserve, Costa Rica. Analysis of genetic data for three groups of monkeys revealed a strong tendency to avoid father-daughter inbreeding ( $P < 0.0001$ , Muniz et al. 2006), though it was not clear whether fathers, daughters, or both, were responsible for the aversion. Adult females' partner choice preferences for grooming and proximity were monitored for a single group over a decade. The amount of grooming and proximity time allocated to paternal half-siblings was far more similar to that of non-kin than to that of maternal half siblings or full siblings. This suggests that females do not recognize shared paternity with other females. There were interesting fluctuations in the extent to which rank distance vs. kinship was important in the structuring of social relationships. When group size was small and the average coefficient of relatedness was high with low variance, kinship was less important than rank in determining proximity and grooming rates. When group size increased to include approximately 10 adult females, and mean matrilineal relatedness was lower with higher variance, kinship became an important determining variable and rank became less important.

#### **Correspondence and divergence among seven measures of long bone robusticity.**

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A large number of robusticity measures of long bones have been used in the literature. The best use second moments of area such as  $J$  and adjust for the effects of body size. Correlations among measures have been under-explored. We calculated correlations among seven measures of femoral, tibial, and humeral mid-shaft robusticity:  $J$  divided by bone length<sup>4</sup> and length<sup>5.33</sup>,  $J$  divided by bone length times femoral head diameter or by bone length times estimated body mass, 'residual robusticity,' 'residual strength,' and the sum of orthogonal bone diameters divided by bone length. We used a pooled-sex sample of Australians, Chinese, Inuit, Khoesan, Sami, African-Americans, European-Americans, Zulu, Neanderthals, and Gravettians (total  $n=414$ ).

Correlations among these robusticity indices sort them into families. Indices in which  $J$  or summed external diameters are divided by a function of length tend to correlate with one another ( $r = 0.898-0.986$ ), as do indices involving  $J$  or multiplied diameters divided by functions that include joint size ( $r = 0.906-0.990$ ). Correlations between these families vary by bone and are particularly low in the tibia. Residual strength (summed external diameters divided by joint size) correlates poorly ( $r = 0.112-0.838$ ) with the other indices. Adjustment by length<sup>5.33</sup> performs less well than expected. All correlations tend to be higher in the humerus than in the tibia and femur. Ecogeographic differences leave clear traces in most of the indices; as Ruff has noted, adjustment by body mass and bone length best controls for this effect.

#### **Full genome comparisons of *Mycobacterium*: Insight into the origin of tuberculosis and leprosy.**

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Resolving the origins and antiquity of the two major mycobacterial diseases, tuberculosis and leprosy, provides a framework for the study of the co-evolution of humans and the ancient obligate pathogens *Mycobacterium tuberculosis* and *Mycobacterium leprae*. Elucidating the relationships of pathogenic and nonpathogenic mycobacteria has been limited due to the lack of resolution obtained with single- or multi-locus analyses. The purpose of this study is to determine robust phylogenetic relationships and divergence times within the pathogenic mycobacteria and the genus as a whole using a genome-scale analysis.

Complete genomes of nine species/strains of pathogenic and nonpathogenic mycobacteria were obtained from Genbank and the Sanger Institute, along with their predicted protein sequences. We then identified 497 protein coding genes (~540,000 base pairs) shared by all nine genomes. Phylogenetic analyses of these data using three different methods yielded identical topologies with 100% bootstrap values for all branches. *M. leprae* is situated basal to the *M. tuberculosis* complex (MTBC), in contrast with previous studies.

Pairwise genome divergence times were obtained using the number of synonymous substitutions per site and applying the mutation rate of enterobacteria. Our results indicate that *M. leprae* and the MTBC diverged some 36 million years ago, a much deeper timescale for the origins of these pathogens than previously presumed, which suggests a coevolutionary history that begins around the time of anthropoid-prosimian divergence. Further, members of the MTBC included in this study diverged approximately 115 thousand years ago and this expansion corresponds in time with modern human evolution.

#### **Femoral head articular surface area in different human populations.**

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The articular surface area of the femoral head is a frequently used proxy measure for human body mass. In general, this area has been estimated by measuring linear dimensions, and applying these to formulas that give an approximation of the areal dimension. Here, we explore an alternative to this approach, the direct measurement of the surface area on virtual models derived from 3D surface scanning of femora.

We used a triTOS optopotometric surface scanner (Breuckmann GmbH) to digitize proximal femora of a geographically diverse sample of *Homo sapiens*. 3D models of the femora were imported into the software Rapidform™ (INUS Technology) for post-processing and taking of measurements. After delimiting the articular surface manually, we measured its area, and fitted a sphere to it by least-squares. Additionally, we located landmarks on the proximal femur and produced "classical" measurements (distances and angles).

Our preliminary results indicate that there are clear differences in the femoral head between small-sized Khoisan and large-sized Europeans. Relative to antero-posterior and supero-inferior femoral head diameters, Khoisan have relatively bigger and more spherical articular surface areas than Europeans. Thus in this particular case, intergroup allometry is inconsistent with within-group allometry, so that femoral articular surface area cannot serve as proxy for body weight in studies combining these populations. Algebraically, the cause of the paradox is the systematic difference of the ratio between the total sphere area and the actual articular surface area between the two populations.

We discuss possible reasons for this, including varying activity levels or allometric scaling.

The study was supported by the grant GZ200.093/1-VI/2004 from the Austrian Council for Science and Technology to the Department of Anthropology, University of Vienna, Austria.