

nuclear encoded. Of the nuclear encoded subunits, four are typically found as protein isoforms which show tissue-specific and developmental patterns of expression in mammals. COX subunit VIII consists of a ubiquitously expressed isoform, encoded by *COX8L*, and an isoform that is expressed in heart and skeletal muscle, encoded by *COX8H*. Previous research suggests that the gene duplication leading to the COX8 isoforms, preceded the origin of mammals, but that *COX8H* is not expressed in humans and macaques. By obtaining the full-length cDNA of a functional *COX8H* gene from *Eulemur fulvus* and *Ateles belzebuth*, we show expression of the gene does occur in primates. Therefore, loss of *COX8H* expression occurred during primate evolution, in the catarrhine primates. Furthermore, we show that *COX8H* is an unprocessed pseudogene in humans, located on chromosome 11 adjacent to the 26S proteasome p40.5 gene, in the same relative position as in species with a functional *COX8H* gene. Significantly, loss of expression of *COX8H* is not an isolated event, but appears related temporally to previously documented increased rates of evolutionary change for other genes of the electron transport chain in anthropoid primates. Selected adaptive changes in brain oxidative metabolism may have facilitated the evolution of the large energy-dependent primate neocortex. Whether changes in *COX8* gene expression patterns are related to this neocortical expansion remains to be determined.

#### **Relationship between collagen fiber orientation, age and mechanical adaptation of the human mid-shaft femur.**

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Collagen fiber orientation is an aspect of a bone's microstructure that influences its mechanical properties. Although its spatial distribution is hypothesized to reflect loading during life, its variability in a modern human sample is essentially unknown. Using a large (n = 70) adult autopsy sample, variability in collagen fiber orientation within the mid-shaft femur was examined in relation to age and sex.

Montaged images of entire 100-micron thick cross-sections were obtained using circularly polarized light microscopy (CPLM) under standardized lighting conditions. An automated routine divided images into 48 segments according to anatomical position. Average grey values (reflective of orientation) were quantified for each segment, and one-way ANOVA with Tukey HSD post-hoc

tests were applied to assess differences between segments.

Collagen fiber orientation appears non-randomly distributed across the mid-shaft femur, though no single 'human' pattern was identified. Individual variation, unexplainable by age, sex or body size, overwhelms most population level trends. Differences between age and sex groups suggest a strong correspondence between collagen fiber orientation and tissue type distributions. Minimal consistencies demonstrated here may reflect mechanical forces induced at the femoral mid-shaft. However, the myriad of other factors influencing collagen fiber orientation patterning, including disease states, growth trajectories, and metabolic and nutritional status need to be explored further. Only then, in conjunction with studies of other structural and material properties of bone, will we elucidate the linkages between microstructure and functional adaptation.

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#### **Kennewick man revisited: group affiliation and Native American Origins.**

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Since the discovery in 1996 at Kennewick Washington, "Kennewick Man" has been a target for fierce political and scientific debate. The question of whether or not his remains are those of a Native American, who lived in the Columbia Plateau some 9,500 B.P., has attracted not only the attention of the anthropological community, but also the attention of the world at large. The present study seeks to test the conclusions reached by J.C. Chatters (1999, 2000, 2001) and J.F. Powell and J.C. Rose (1999), in which it is argued that "Kennewick Man" is more closely affiliated with Polynesians, Ainu, and Jomon rather than modern Native Americans. To test such conclusions, a multivariate statistical analysis by way of principal components was performed on 11 common measurements of the human cranium utilizing data taken from the T. Hanihara and W.W. Howells world craniometric databases. Prehistoric data were also taken from the literature. In total, the study used 38 sample population groups representing modern and some prehistoric people from North America, South America, Northeast Asia, East Asia, and Polynesia. The results obtained from the statistical analysis parallel those of previous studies. "Kennewick Man" shares some morphological similarities with Polynesians. However, there is strong evidence indicating that despite having a strong relationship with Polynesians, "Kennewick

Man" also has a strong historical-biological connection with people associated with Tierra del Fuego and Patagonia and even some prehistoric Chinese. There is no evidence suggesting a biological affiliation between "Kennewick Man" and modern Native Americans from North America.

#### **Increasing population sample sizes using global skeletal size variables.**

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Due to the scarcity of postcranial skeletons with recorded body mass in museum collections, morphological studies that incorporate body size must often draw from multiple populations within a species (demes) to generate samples large enough to yield statistically significant conclusions. Alternatively, studies may include specimens with estimated body mass, but must then incorporate confidence intervals of those predictions in their analyses. This limitation effectively prohibits evolutionary studies that analyze individual demes. This paper presents a technique for developing global skeletal size variables (GSVs), which allows researchers to increase sample sizes.

Using body mass data and multiple postcranial measurements from several primate species, it is shown that researchers can generate GSVs that scale isometrically with mass and are directly proportional to mass – both within single populations and across multiple species. Examples are presented using data from *Papio cynocephalus*, *Pan troglodytes*, *Gorilla gorilla*, *Cebus apella*, *C. albifrons*, *Saimiri boliviensis*, *Alouatta caraya*, and *Aotus azarae*. Each sample has been limited to individuals collected over small ranges of space and time to maximize the likelihood of belonging to the same deme.

Because of the nature of the relationship between these GSVs and body mass, GSVs may be used as measures of overall size in comparative studies rather than body mass. Using a GSV permits researchers to include any reasonably complete postcranial specimen in their studies rather than being limited to only those specimens that have associated mass measurements. Examples of applications of this technique to studies of primate sexual size dimorphism are provided.

#### **Spatial and genetic differentiation in an isolated tropical tree population: reconstructing primate seed dispersal.**

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Primates are important seed dispersers for many tropical plants, but their effect on the spatial distribution of dispersed species