

Phylogeography and genetic diversity of wild bonobos (*Pan paniscus*).

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The need for better assessment of the phylogeographic pattern of genetic variation of the two *Pan* species has recently become increasingly clear due to its relevance for understanding the origin and spread of zoonotic diseases such as SIVcpz-HIV-1 complex of viruses. Furthermore, knowledge of gene flow among different populations of a species can provide information for consideration in the design of conservation plans by influencing the size, shape and number of protected areas. Compared to the common chimpanzee (*P. troglodytes*), found across the equatorial zone of the African continent, the bonobo (*P. paniscus*) has a much more restricted range and is currently only found in the central Congo Basin, between the Congo-Lualaba and Kasai-Sankuru River system. Genetically, the bonobo is by far the less studied of the two *Pan* species and previous research has been limited to individuals from two closely-situated field sites and captive individuals of unknown origin. In this study we investigate the genetic diversity and population structure of *P. paniscus* across their geographical range by sequencing 500 base pairs of the mitochondrial DNA control region using DNA extracted from non-invasively collected fecal samples of approximately 140 individuals belonging to 8 different localities within 3 major forest blocks each separated by large rivers. These results will be compared to similar data from *Pan troglodytes*, including 3 newly sampled localities from regions north of the Congo River, a zone of possible gene flow between the eastern (*P. t. troglodytes*) and central (*P. t. schweinfurthii*) chimpanzee subspecies.

MtDNA and population movements in prehistoric western North America.

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Studies of mtDNA in Native Americans have demonstrated that the majority of mtDNA types belong to one of five maternal lineages or haplogroups. The distribution of these lineages in the Americas is decidedly nonrandom. Studies of ancient and modern Native American mtDNA have also revealed a general pattern of temporal continuity in haplogroup frequencies in particular regions indicating that drift has not significantly disrupted them. Thus, the distribution of lineages can be used to infer relationships between populations.

Prior to European contact, the west coast of North America contained a virtually un-

paralleled degree of linguistic diversity and exceptionally high population densities for hunter-gatherer peoples. Some comparative linguists have suggested that many of the languages can be grouped into a few linguistic stocks of related languages. The distribution of two particular linguistics stocks—Hokan, made up of a number of languages in California and the Southwestern U.S. and Northern Mexico, and Penutian, consisting of several languages in California, Oregon and Washington—has long suggested a particular model of migration that has produced the observed distribution of speakers of various languages. This model has also greatly influenced the interpretation of the archaeological record of California. However, the linguistic validity of both stocks is still a point of considerable debate. Through the examination of mtDNA haplogroup frequencies and discrete mtDNA control region sequences from both modern Native Americans and prehistoric human burials, this study tests migration hypotheses based upon these linguistic and archaeological models. Additionally, a comparison between coastal and inland populations along the west coast of North America may suggest an ancient coastal migration to the New World.

More on the three-dimensional trabecular architecture of anthropoid primates: *Macaca fascicularis* and *Symphalangus syndactylus*.

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High-resolution imaging methods have begun to reveal the intricate nature of non-human primate cancellous bone. Fajardo and Müller (2001) presented preliminary data on the proximal femur of four anthropoid primates, including a macaque and gibbon. Here we present more data expanding our knowledge of the trabecular architecture of the anthropoid femoral neck.

The proximal femora of *Macaca fascicularis* and *Symphalangus syndactylus* specimens were scanned using a High-Resolution X-ray Computed Tomography scanner. Volumes of interest were defined within the neck, proceeding distally from the head-neck transition. The volumes of interest defined within the neck were adjusted in length for size relative to the largest specimen within the overall sample and contoured to the endosteal border. The structural variables calculated within each specimen's volumes of interest included the bone volume fraction, trabecular number, trabecular thickness, structural model index (measure of plate-like to rod-like structure of trabeculae), connec-

tivity density, and the degree of anisotropy.

The data paint an interesting picture of the trabecular bone of these two taxa that does not altogether correspond to expectations based on the locomotor behavior of these two primates. *S. syndactylus* has a slightly higher bone volume fraction of cancellous bone than *M. fascicularis* (7% higher). Consistent with our earlier findings, the cercopithecine has a higher trabecular number (>36% higher) and thinner trabeculae (>24% thinner) than the lesser ape. The negative structural model index values for both taxa indicate that their trabeculae take on the shape of spherical voids (*Syndactylus* -2.128, *M. fascicularis* -0.871). Furthermore, these two taxa exhibit strong differences in the connectivity density (*Syndactylus* 3.515, *M. fascicularis* 8.944). Unexpectedly, both taxa have a relatively high degree of structural anisotropy and the suspensory siamang (1.73) has a higher average anisotropy value than the macaque (1.51).

The evolution of brain shape in hominids.

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Results are provided for an investigation of hemispheric shape on a series of endocasts from *Australopithecus*, *Paranthropus*, *Homo erectus*, Neandertal, and extant *Homo sapiens*. Endocasts from the fossils were registered by magnetic resonance imaging (MRI) and three-dimensionally reconstructed. The endocasts for extant humans were obtained virtually from MRI of ten skulls and used to generate a mean endocast. Of 32 actual human brains, the one that was determined to be the most 'average' was used as the reference brain for projecting major anatomical and functional brain regions onto the mean human endocast. Endocasts from fossil hominids were then warped using an elastic transformation to the mean endocast from *Homo sapiens*, and the 3-D deformation fields that describe quantitatively the regional distribution of forces effecting the warping were visualized. These procedures permit identification of specific regions of hominid endocasts that change most when transformed into endocasts of modern humans. Considerable hemispheric shape change occurs between endocasts of early hominids and those of modern humans, with the largest overall deformation occurring between australopithecines and *Homo sapiens*. Much smaller differences are found for the *Homo erectus* to *Homo sapiens* transformation, and minimal differences oc-