The CT Database at the University of Pennsylvania Museum.

J. Monge, P.T. Schoenemann, J. Lewis, L.D. Glotzer. Department of Anthropology, University of Pennsylvania.

The University of Pennsylvania Cranial CT Database is a collection of high resolution (sub-millimeter) CT scans of human and non-human crania from the Penn University Museum and other institutions. Because of advances in 3D imaging software, detailed anatomical studies can be accomplished without ever having to rescan (or handle) any of the specimens again. The database is designed to continually grow (it currently contains 160 scans) as new scans are obtained, and will be made available online, thereby maximizing their usefulness to researchers in anthropology, biology, and medicine worldwide.

The scans are primarily from the Morton Collection of human crania (collected in the middle of the 19th Century, curated at the U of PA Museum) from various geographic regions including Europe, Africa, Asia, parts of the Americas, and Australia. In addition, the scan archive now contains 18 chimpanzee skulls (from the American Museum of Natural History), 6 orangutans (Harrison-Hiller Collection, UPM) and 2 gorillas as well as a few other non-human primates. In the human collection, 24 specimens are sub-adult ranging in age form 8-month fetal to 8-10 years of age at death. Scans are stored both as "raw" images and in processed form using Analyze™ 7.5 image format. Information in the database includes details of the scans (# of voxels in the X,Y, and Z axes and their dimensions in millimeters) along with all data on the specimens themselves (collection, date, geographic information, and life history parameters where known).

Ancient migrations and population expansions in East Africa: Genetic evidence for Tanzanian prehistory.

H.M. Mortensen, K. Gonder, E. Tarazona Santos, J. Hirbo, S.A. Tishkoff. Dept. of Biology, University of Maryland, College Park.

East Africa, with its remarkable degree of ethnic and linguistic diversity, is best characterized as a mosaic of different cultures, subsistence patterns, and languages. Tanzania is the only region in Africa with populations currently belonging to all four of the major linguistic families of Africa (Khoisan, Afro-Asiatic, Nilo-Saharan and Niger-Kordofanian). Anthropological and linguistic data indicates successive waves of migration into Tanzania, first by Cushitic speaking peoples approximately 5000 years ago, followed later by migrations of Nilotic, and Bantu speakers who displaced and absorbed indigenous hunter/gatherers in many areas.

A large panel of ~600 Tanzanian individuals, representing 15 diverse ethnic groups, was analyzed for mtDNA control region sequence variation and a set of informative mtDNA SNPs. Populations include the Khoisan-speaking Hadza and Sandawe, Cushitic-speaking Burunge, WaFiome (Gorowa), Iraqw, and Mbugu, Nilotic-speaking Maasai, Datog, Dorobo, and Akie, and Bantu speaking Mbugwe, Gogo, Rangi, Turu, and Pare. From this data we infer long-term population size, levels of population substructure and degrees of admixture between groups. Preliminary findings concerning the relation of the traditional foraging groups (Akie, Dorobo, Hadza, and Sandawe) indicate a genetic relationship amongst Tanzanian foragers that does not necessarily correspond to linguistic affiliation. Estimated timing and direction of gene flow between diverse subsistence groups suggests that current linguistic distribution across the landscape may overlay an earlier network of indigenous hunter-gatherers.

Inference of recent gene flow following complete population isolation.

J. Mountain, M. Miyazawa, U. Ramakrishnan. Department of Anthropological Sciences, Stanford University.

Most existing tools for inferring rates of migration rely on the assumption that migration rates between two populations are constant, either throughout time or following population divergence. Investigations of human history would benefit greatly from more complex models of migration. We have investigated several models of Complete Isolation followed by Recent Migration (CIRM). Specifically, we have considered (a) two populations of identical size that diverged from a common ancestor ts generations ago, with gene flow between these populations beginning tg ($<< ts$) generations ago, (b) same as above except with two populations of dramatically different size, (c) three populations that diverged ts generations ago, one of which has contributed migrants to each of the other two for tg generations, (d) four populations, one of which has contributed migrants at different rates to each of the other three. Coalescent simulations indicate that where two populations have no identical and no similar sequences, we can readily rule out recent migration using DNA sequence data for non-recombining genetic regions such as the mitochondrial (mt) genome and the non-recombining portion of the Y chromosome. Model (c) may lead to the erroneous inference of recent gene flow. We have also characterized the parameter space (in terms of divergence times, population sizes, periods of gene flow and migration rates) wherein complete isolation followed by recent gene flow is distinguishable from no gene flow. We evaluate mtDNA data for a set of African populations in light of these results.

Using SEM to qualitatively identify structural differences in the hairs of nectar-feeding prosimians.

M.N. Muchlinski. Department of Anthropology, University of Texas at Austin.

Nectar-feeding mammals have several anatomical modifications that assist in cross-pollination. Howell and Hodgkin (1976) note structural differences in the hair and tongues of nectar feeding bats. They suggest that effective cross-pollinators may have feathered tongues, laterally scaled muzzle hair, cranial modifications such as snout elongation, and/or diminutive dentition that allow non-destructive nectar feeding and successful cross-pollination.

Within the primate order, lemurs are noted as being highly nectivorous, where monthly nectar consumption can represent over three fourths of their total feeding time. Convergent with many nectar-feeding mammals, several lemur species are documented to have brush-like feathered tongues and cranial modifications. To date, however, no one has investigated the structural variation in prosimian hairs and how variation may be related to foraging behaviors. Using a scanning electron microscope, I identified the presence of specific modifications to the hairs of 12 prosimian species. Results indicate that frugivores show a generalized hair scaling pattern where the hair slightly deviates at an angle from the main hair shaft (divaricated). Interestingly, a few seasonal nectar feeding frugivores (e.g. *Eulemur mongoz*) have extreme scale derivation. Howell and Hodgkin argue that these divaricated hair scales aid in cross-pollination among nectar feeding animals.

Although not all nectar-feeding lemurs show cross-pollinating modifications to their hair, some do. Besides the Malagasy