Program of the seventy-eight Annual Meeting of the American Association of Physical Anthropologists

To be held at the

Sheraton Chicago Hotel and Tower

301 East North Water Street
Chicago, IL 60611

10:00-10:15 am. **Southeast Asian primate communities: the effects of ecology and history on species richness.** H.M. HASSEL-FINNEGAN, C. BORRIES, A. KOENIG.

10:15-10:30 am. **Break**

10:30-10:45 am. **A framework for understanding thermoregulation in primates.** N.G. JABLONSKI, E.A. KELLEY, R.W. SUSSMAN, G. CHAPLIN.

10:45-11:00 am. **Sexual selection and primate extinction risk.** J.D. ORKIN, J.M. KAMILAR.

11:00-11:15 am. **Natural birth control: seasonal increases in fecal progestins affect reproductive function in wild female Phayre's leaf monkeys (*Trachypithecus phayrei*).** A. LU, C. BORRIES, N.M. CZEKALA, J.C. BEEHNER.

11:15-11:30 am. **Using macroecological methods to examine across-site variation in chimpanzee behavior**. J.M. KAMILAR, J. MARSHACK.

11:30-11:45 am. **Savanna chimpanzee (*Pan troglodytes verus*) feeding ecology at Fongoli, Senegal.** S.L. BOGART, J.D. PRUETZ.

11:45-12:00 **Sex differences in western gorilla arboreality.** D. DORAN-SHEEH1, M. ANDRIANADY, J. LODWICK

Session 24. Detecting Natural Selection in Humans. Invited podium symposium. Co-sponsored by the Human Biology Association. *Chicago 9.* Organizer: Stephen T McGarvey.

The purpose of the symposium is to present the latest evidence, prospects and challenges for detection of natural selection in human populations. AAPA members and other attendees will be interested to hear about the methods and evidence for detecting the signatures of natural selection in human populations. In addition many of AAPA members conduct fieldwork in populations with a diversity of demographic histories sometimes indicative of relative isolation. Thus, we often wonder how we might apply tools to detect natural selection to our study populations, or offer data from our study populations to research groups skilled in asking these questions and applying these new tools.

8:00-8:15 am. **Selection, drift, and geography in recent human evolution.** GRAHAM COOP, JOSEPH K. PICKRELL, SRIDHAR KUDARAVALLI, JOHN NOVEMBRE, RICHARD M. MYERS, LUIGI LUCA CAVALLI-SFORZA, MARCUS W. FELDMAN, AND JONATHAN K. PRITCHARD

8:15-8:30 am. **Issues in Detecting Natural Selection in Humans.** JOSHUA AKEY.

8:30-8:45 am. **Genetics, Selection, Perception and the Human Face.** M.D. SHRIVER, D. LIBERTON, AND K. MATTHES, J. BOSTER AND D.A. PUTS.

8:45-9:00 am. **Characterizing the effects of background selection in the human genome** RYAN HERNANDEZ AND MOLLY PRZEWORSKI.

9:00-9:15 am. **Evolution and natural selection of skin color.** E.J. PARRA

9:15-9:30 am. **Natural selection for adiposity and metabolic traits.** S.T. MCGARVEY.

9:30-9:45 am. **Natural Selection and High Altitude.** LORNA G. MOORE, MEGAN WILSON, COLLEEN G. JULIAN, ABIGAIL BIGHAM, MARK SHRIVER.

9:45-10:00 am. **Natural selection and alcohol.** H. LI, S. GU, J.R. KIDD, K.K. KIDD.

10:00-10:15 am. **Discussant,** LYNN JORDE

10:15-10:30. **Break**

Session 25. Human Biology. Human population variation and disease. Contributed papers.

Chair: Cynthia M Beall Case Western Reserve University. ***Chicago 9.***

10:30-10:45 am. **Pulmonary artery hemodynamics of high and low altitude native Ethiopian Amhara.** C.M. BEALL, B. HOIT, N.DALTON, A. GEBREMEDHIN, K.P. STROHL, S.C. ERZURUM

10:45-11:00 am. **Ancestry-associated variation in endogenous antioxidant activity during high-altitude pregnancy.** C.G JULIAN, E. VARGAS, A. BINGHAM, M. SHRIVER, J.M. MCCORD, H. YAMASHIRO, M. J. WILSON, L.G. MOORE

11:00-11:15 am. **Tuberculosis transmission and maintenance in small, low-density populations.** J.T. ACHTERBERG.

analyzed using enzyme immunoassays. Males were captured during the mating season and the subsequent birth season to measure body mass and testes size and to document chest staining. All predictions were supported by this analysis. Males with stained chests had significantly higher fT and larger testes mass. Testes mass was significantly greater during the mating season than the birth season for all males. However, the stained males exhibited less testes mass reduction during birth season. These results are consistent with the hypotheses that (1) the activity of the sternal gland is regulated by testosterone, and (2) the staining on the chest is a visual signal of testosterone levels in male Verreaux's sifaka.

Natural selection and alcohol.

H. Li[1], S. Gu[1,2], J.R. Kidd[1], K.K. Kidd[1]. [1]Department of Genetics, Yale University School of Medicine, [2]PGxHealth LLC currently.

We have previously presented strong evidence that selection has been responsible for increasing the frequency of the ADH1B*47His allele in some East Asian populations especially when in cis with a variant in the ADH1B promoter region. This amino acid substitution, Arg47His, results in a more rapid conversion of ethanol to acetaldehyde. In conjunction with a dominant-negative form of ALDH2 (also common in East Asian populations), the ADH1B*47His allele is responsible for the flushing reaction due to high acetaldehyde levels so common in East Asians after alcohol consumption. If selection were operating on elevated acetaldehyde levels—the prevailing hypothesis—there should also be evidence for selection for the dominant-negative allele at ALDH2. However, the nature of DNA variation in the region of ALDH2—extensive long range linkage disequilibrium in all haplotypes—has made direct examination of genomic signatures of selection at ALDH2 difficult/impossible to date. One possibility is that the 47His variant only became significant in elevating acetaldehyde levels in the presence of decreased ability to eliminate acetaldehyde. To further explore this possibility we have been collecting data in our lab, from the Asian literature, and from colleagues on multiple populations in East Asia to examine the joint geographic distributions of the frequencies of the relevant variants at ADH1B and ALDH2. Our new data show that the relevant frequencies at both loci increased in the eastern part of East Asia, and that both alleles increased at about the time of the emergence of agriculture.

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A genetic association study of normal variation in facial features.

D.K. Liberton[1], K.A. Matthes[1], B. McEvoy[2], R. Pereira[3], T. Frudakis[4], M.D. Shriver [1]. [1]Department of Anthropology, Pennsylvania State University; [2]Queensland Institute of Medical Research, Brisbane, Australia; [3]Catholic University of Brazil, Brasilia, Brazil; [4]DNAPrint Genomics, Sarasota, Florida.

Although facial feature variation among individuals and populations clearly suggests genetic causes, little research has focused on the genes underlying genetic variation in these traits. Given admixed populations trace their genetic ancestry to multiple parental populations that differ in facial features, they can be useful in studying the genetics of genes underlying these traits. We have tested for correlation between normal variation in facial traits and genetic ancestry, showing significant relationships. Here, selection-nominated candidate genes with known involvement in Mendelian craniofacial dysmorphologies and high allele frequency differences between West African and European populations were tested for admixture linkage to normal facial traits. The study consists of 254 subjects, ages 18-35, of West African and European genetic ancestry. 3D images of faces were acquired using the 3dMDface imaging system and 22 standard anthropometric landmarks were placed on each image. Landmark data were collected using 3dMD Patient software and analyzed using Euclidean Distance Matrix Analysis (EDMA). Each individual was genotyped at 176 Ancestry Informative Markers, allowing for proportional estimation of genetic ancestry from four parental populations.

ANOVA analyses tested for associations between the pairwise landmark distances and candidate genes, using sex, height, body mass index (BMI), and maximum-likelihood genetic ancestry estimate as covariates. Results indicate distinct patterns of facial variation associated with each gene. Next, ADMIXMAP was run using a four-population model with sex, height and BMI as covariates. Results indicate concordance between the two analyses, although ADMIXMAP has fewer significant associations as it better controls for false associations due to stratification.

Biomechanics of foot strike in habitually barefoot versus shod runners.

D. Lieberman, W. Werbel, A. Daoud. Department of Anthropology, Harvard University.

Hominins evolved to run long distances, possibly as much as 2 million years ago, and until recently, humans ran either barefoot or in soft sandals with minimal cushioning or arch support. Here we investigate whether heel strikes, characteristic of approximately 80% of modern shod runners, are typical of habitually barefoot runners. We also investigated how the foot's initial contact with the ground influences the rate and magnitude of the heel strike transient (HST), an impulse several times body weight that travels from the ground to the head in less than 10 ms, and which is thought to be a