

The Encounter of Science and History

Inaugural Symposium of the Initiative for
the Science of the Human Past at Harvard

*Cosponsored by the Broad Institute of MIT and Harvard,
the Departments of Classics and History, the Medieval
Studies Committee, and the Standing Committee on
Archaeology*

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Friday 1 November 2013
Knafel Center, Gymnasium
Radcliffe Institute for Advanced Study

Initiative for the Science of the Human Past at Harvard University
Thomas N. Benjamin, Peter Huybers, Michael McCormick, Laura Nasrallah,
Nick Patterson, David Pilbeam, David Reich, Stuart Shieber, Daniel Lord
Smail, Noreen Tuross, Walter Willett

Schedule

8:00 *Coffee and continental breakfast*

Morning Session

8:45 Welcome

9:00 **Pardis Sabeti**, Organismic and Evolutionary Biology, Harvard University, and Broad Institute of MIT and Harvard, “Evolutionary Forces in Humans and Pathogens”

Introduction by Alan Garber, Provost of Harvard University

9:30 Brief comment and discussion: Nick Patterson, Broad Institute of MIT and Harvard

9:45 **Johannes Krause**, Institute of Scientific Archaeology, University of Tübingen, “Ancient Pathogen Genomics: What we learn from Ancient and Medieval Diseases”

10:15 Brief comment and discussion: Richard M. Losick, Molecular and Cellular Biology, Harvard

10:30 *Coffee*

11:00 **Kyle Harper**, Classics, University of Oklahoma, “Population, Disease and the Fall of the Roman Empire: A Biohistory”

11:30 Brief comment and discussion: Mark Schiefsky, Classics, Harvard

11:45 *Lunch for registered participants*

Afternoon Session

1:00 **Michael McCormick**, History, Harvard, “Ancient and Medieval Climate Change and the Future of Humanity”

1:30 Brief comment and discussion: Emma Dench, Classics and History, Harvard

1:45 **David Reich**, Genetics, Harvard Medical School, “Insights into human population history from a high coverage Neandertal genome”

2:15 Brief comment and discussion: Daniel Lord Smail, History, Harvard

2:30 **Daniel Lieberman**, Human Evolutionary Biology, Harvard, “How did Early Humans Hunt?”

3:00 Brief comment and discussion: Joyce Chaplin, History, Harvard

3:15 *Coffee*

- 3:45 **Noreen Tuross**, Human Evolutionary Biology, Harvard, “Humans Move: Evidence in Isotopes”
- 4:15 Brief comment and discussion: Scott Edwards, Organismic and Evolutionary Biology, Harvard
- 4:30 **Ian Morris**, Classics and History, Stanford University, “The Science of the Human Past”
- 5:00 Brief comment and discussion: Edward M. Hundert, Division of Medical Ethics, Harvard Medical School
- 5:15 Concluding remarks
- 5:30-6:30 *Poster Session and Reception*

PAPERS: ABSTRACTS AND MORE

PARDIS SABETI works on the effect of natural selection on the human and other genomes to understand mechanisms of evolutionary adaptation in humans and pathogens.

For more go to: <http://sysbio.harvard.edu/csb/research/sabeti.html>

“Evolutionary Forces in Humans and Pathogens”

We are in the midst of a revolution in the fields of genomics and public health. The completion of the human genome sequence, the availability of genome sequences from increasing numbers of related species, the availability of genome-wide human variation data, and the ability to rapidly generate new data have created unprecedented opportunities to study human biology, evolution, and disease. These same tools are also making it possible to carry out unprecedented studies in the microbial pathogens that affect humans. My lab’s research goals are to use the rapidly emerging resources to: (1) Develop and apply methods to investigate natural selection in the human genome; (2) Study the genomic evolution of the microbial pathogens that affect humans; and (3) Build new computational tools for studies of genomics and public health. The key infectious diseases of my lab’s current studies are Lassa fever, Ebola fever, *Plasmodium Falciparum* malaria, and *Vibrio Cholerae* cholera.

JOHANNES KRAUSE works on ancient DNA, human evolution, ancient pathogen genomics, as well as comparative and evolutionary genomics.

For more go to: <http://www.geo.uni-tuebingen.de/arbeitsgruppen/ur-und-fruehgeschichte-und-archaeologie-des-mittelalters/forschungsbereich/palaeogenetik/mitarbeiter/krause.html>

“Ancient Pathogen Genomics: What We Learn from Ancient and Medieval Diseases”

Genome wide data from ancient microbes may help to understand mechanisms of pathogen evolution and adaptation for emerging and re-emerging infectious disease. Using high throughput DNA sequencing in combination with targeted DNA enrichment we have reconstructed medieval bacterial genomes of *Yersinia pestis* and *Mycobacterium leprae* from skeletal remains. Phylogenetic analysis indicates that the ancient *Y. pestis* strain from the Black Death pandemic is ancestral to most extant strains and falls very close to the ancestral node of human infectious *Y. pestis* bacteria. Temporal estimates suggest that the Black Death of 1346 – 1351 was the main historical event responsible for the introduction and worldwide dissemination of currently circulating *Y. pestis* strains pathogenic to humans, and further indicates that contemporary *Y. pestis* epidemics have their origins in the medieval era. In contrast the medieval *M. leprae* strains fall within the current genetic diversity and are found on at least two main branches in the phylogenetic tree of leprosy bacteria. Dating analysis reveals a most recent common ancestor of both all *Y. pestis* strains and all *M. leprae* strains within the last 4000 years, suggesting that both diseases may have a recent Neolithic origin. The extraordinary preservation of the *M. leprae* DNA allowed for the first time a de novo genome assembly of an ancient

organism and indicates that some bacterial DNA may survive longer than vertebrate DNA in ancient remains. This will allow tracing the history of many infectious disease-causing pathogens back to their prehistoric origin.

KYLE HARPER *is a historian of the classical world who studies social, economic, environmental and population history and the impact of climate change and disease on the history of civilization.*

For more go to: <http://cas.ou.edu/kyle-harper>

“Population, Disease, and the Fall of the Roman Empire: A Biohistory”

The later Roman Empire (ca. CE 150-600) was bookmarked by the world’s first pandemic episode (the “Antonine plague” in 165) and the first of the great bubonic plague epidemics (the “Justinianic plague” from 541). In this talk I will argue that disease played a central role in the history of the Roman Empire and that the Roman Empire played a central role in the history of disease. I will survey what we know about mortality in the Roman Empire and what we might learn in the near future thanks to the integration of the natural sciences into the study of the ancient past. I suggest some ways that documentary and bioarchaeological evidence might be synthesized in order to answer fundamental questions about the interplay between economy, demography, and environment in the Roman world.

MICHAEL MCCORMICK *studies the archaeological, natural scientific and historical evidence for the fall of the Roman Empire and the origins of Europe.*

For more go to: <http://isites.harvard.edu/icb/icb.do?keyword=k40117&pageid=icb.page188170>

“Ancient and Medieval Climate Change and the Future of Humanity”

Historians are supposed to be specialists of the written sources and focus on the past, not the future. Until very recently, historians and archaeologists generally assumed that climate was stable and could be left out of the variables that we explore to explain change in past societies. Today archaeologists and historians are expanding their evidentiary base to include the material evidence of archaeology and especially the new data from modern climate science which aims to reconstruct past climates from scientific proxies that preserve climate signals: tree rings, ice cores, etc. The rapid advance of climate science is producing amazing amounts of entirely unanticipated and increasingly precise information about unambiguous climate changes in the historical past that reveal abrupt or gradual shifts in temperatures, precipitation, and growing seasons that impacted human societies and economies over the short and long term by affecting food production, disease ecologies, and communications networks (storminess and navigation, closing of Alpine passes, etc.). When incorporating this growing scientific paleoclimate data into investigations of ancient and medieval economies and societies, we must respect the complexities of the evidence, the patterns of causation, and the differing degrees of resilience that societies displayed in the deeper past. Some examples of

recent scientific and historical investigations of ancient and medieval climate demonstrate the power of combining scientific and traditional historical evidence. Before ca. 1500 A.D., even the richest troves of written records have not sufficed for detailed climate reconstruction. They can however play an invaluable role in validating modern climate science. By working together with climate scientists to test, confirm or improve scientific reconstructions of past climate change, historians can help calibrate climate science's efforts to understand present and future trends.

DAVID REICH *studies human history, evolution and gene mapping as well as human population genetics. He was recently named one of 27 HHMI Investigators by the Howard Hughes Medical Institute.*

For more go to: <http://www.broad.mit.edu/about/associate-members/david-reich>

“Insights into Human Population History from a High Coverage Neandertal Genome”

We present the high-quality genome sequence of a Neandertal woman from Siberia. We show that her parents were related at the level of half siblings and that mating among close relatives was common among her recent ancestors. We also sequenced the genome of a Neandertal from the Caucasus to low coverage. An analysis of the relationships and population history of available archaic genomes and 25 present-day human genomes shows that several gene flow events occurred among Neandertals, Denisovans and early modern humans, possibly including gene flow into Denisovans from an unknown archaic group. Thus, interbreeding, albeit of low magnitude, was common among hominin groups in the Late Pleistocene. In addition, the high quality Neandertal genome allows us to identify almost all substitutions that became fixed in modern humans after their separation from the ancestors of Neandertals and Denisovans.

DANIEL LIEBERMAN *studies the form and function of key human features like the head and locomotion from an evolutionary perspective.*

For more go to: <http://www.fas.harvard.edu/%7Eskelton/danlhome.html>

“How Did Early Humans Hunt?”

Hunting played an important role in human evolution starting at least 2.6 million years ago, but how did early hominins hunt? Compared to other large mammal predators, hominins are slow, unsteady, lack power, and have no natural weapons such as claws and fangs. In addition, sophisticated projectile technologies are very recent: stone points were invented less than 500,000 years ago, and the bow and arrow was invented less than 100,000 years ago. Here I will make the case that the genus Homo evolved a series of adaptations to hunt through endurance running and throwing. Although these adaptations compromised the ability to climb trees effectively, they helped to contribute to a release of constraints on brain size; hence the evolution of modern humans.

NOREEN TUROSS *works on ancient isotopes, ancient DNA, and the science of archaeology in areas as diverse as Pre-Columbian civilizations, the Harvard Forest, and medieval Italy.*

For more go to: <http://www.harvardscience.harvard.edu/directory/researchers/noreen-tuross>

“Humans Move: Evidence in Isotopes”

Humans move over long distances for many reasons. Our ability to determine where and when people moved is improved by a number of dietary and hydrologically based isotopic approaches. In three examples, the movement of extant, historic and ancient peoples is found in the isotopic composition of their protein. We revisit the traveling postdoc example of the 1980's to determine how the migration across the pond (UK to US and vice versa) changes carbon isotopic composition at the compound specific level. Next, we observe the isotopic changes in 17th-century Dutch whalers as they make their circular rounds from the Netherlands to the Arctic Circle. Finally, the movement of people over a large area in southern Mexico is seen in the evidence found at one of America's most famous tombs: Tomb 7 at Monte Alban, Mexico.

IAN MORRIS *works on the ancient Mediterranean within the broader contexts of a comparative world history of antiquity and a long-term history of conflict and war.*

For more go to: <http://www.stanford.edu/dept/classics/cgi-bin/web/people/faculty/ian-morris>

“The Science of the Human Past”

Harvard's initiative for the science of the human past is one of the most positive developments in historical scholarship in many decades. Students of the past have been debating whether history is an art, a science, or a craft for more than a century, but rarely even agree on what those words mean. This has generated much confusion, but I want to suggest that there are three senses in which history really is a science. The first, which has so far produced the biggest payoffs (witnessed by many of today's papers), is the use of techniques from the natural sciences to answer historians' and archaeologists' questions. The second, which only some historians see as worthwhile, is the application of scientific principles of reasoning (such as emphasizing falsification, replicability, and quantification). The most important, though, is the third, which involves treating history as the subfield of biology that studies the behavior of our own species—meaning that history, like the rest of biology, is driven by evolutionary processes. I conclude by suggesting that we are on the threshold of a new, scientific understanding of the human past, and that this will provide the foundation for a new understanding of the human future.

DISCUSSANTS

Nick Patterson (Broad Institute of MIT and Harvard) is a geneticist at the Broad Institute, working in both population and medical genetics. He has an interest in using modern genetic data to learn about human history.

<http://www.nytimes.com/2006/12/12/science/12prof.html?partner=rssnyt&emc=rss>

Richard M. Losick (Molecular and Cellular Biology, Harvard) studies the microbial development of the spore-forming bacterium *Bacillus subtilis*.

<https://www.mcb.harvard.edu/mcb/faculty/profile/richard-m-losick/>

Mark Schiefsky (Classics, Harvard) studies the history of philosophy and science in the Greco-Roman world, especially medicine and mechanics. He has an interest in applying information technology in humanistic scholarship. <http://scholar.harvard.edu/schiefsky>

Emma Dench (Classics and History, Harvard) works on Roman imperialism and questions of identity and historiography in classical antiquity.

<http://www.history.fas.harvard.edu/people/faculty/dench.php>

Daniel L. Smail (History, Harvard) studies late medieval Europe and works on ways to bring deep historical perspectives, including not only histories but also methods, into departments of history. <http://www.history.fas.harvard.edu/people/faculty/smail.php>

Joyce Chaplin (History, Harvard) is most interested in topics where humans and nature meet. She works on American, intellectual and environmental history, as well as the history of science. <http://www.history.fas.harvard.edu/people/faculty/chaplin.php>

Scott Edwards (Organismic and Evolutionary Biology, Harvard) studies the evolutionary biology of birds and relatives through population genetics, systematics, and natural history. <http://www.oeb.harvard.edu/faculty/edwards/people/edwards.htm>

Edward M. Hundert (Division of Medical Ethics, Harvard Medical School) is a psychiatrist particularly interested in the ethical issues and moral questions of academic, medical and mentoring practices. <http://medethics.med.harvard.edu/people/hundert/>

POSTER SESSION ABSTRACTS

A New Project for High-resolution Ice Core Analysis at Colle Gnifetti, Swiss-Italian Alps in Comparison with Historical Climate Records

Pascal Bohleber (Institute for Environmental Physics [IUP], Heidelberg University and SoHP), Nicky Spaulding (Climate Change Institute [CCI], University of Maine and SoHP), Sharon Sneed (CCI, University of Maine), Dietmar Wagenbach (IUP, Heidelberg University), Paul Mayewski (CCI, University of Maine) and Michael McCormick (History, Harvard and SoHP)

Ice core studies performed on mountain glaciers in mid-latitudes can provide paleoclimate records closer to human settlements that are complementary to polar ice cores. For the European Alps, the small-scale Colle Gnifetti glacier saddle (4450m asl, Monte Rosa, Swiss-Italian Alps) is the only ice core drilling site with an annual net snow accumulation low enough to archive multi-millennial records in spite of ice thickness barely exceeding 100 m. So far, however, the interpretation of paleoclimate records from an existing Colle Gnifetti ice core array has been hampered by two primary dating concerns: (i) annual layer counting gets increasingly ambiguous beyond approximately 100 years and, (ii) age uncertainty prevents clear linkage of volcanic and mineral dust horizons to historical records. Both challenges are fundamentally connected to the rapid thinning of annual layers, and may thus be tackled by state-of-the-art laser-based impurity analyses at ultrahigh depth resolution. Here we present the first results comparing laser ablation ion-coupled plasma mass spectrometry measurements (LA) of mineral dust components with previous measurements from continuous flow analysis, already available at cm resolution. The comparison indicates that the LA yields additional high frequency information, potentially reflecting annual signals not resolved by conventional impurity analyses. From LA-based annual layer counting, we aim at obtaining a reliable ice core chronology over the last millennium and possibly beyond. Then and only then can we use the cornucopia of climate ice core signals, particularly the stable water isotope record, for cross linking with historical evidence. Moreover, LA ice core profiling may also be used to study mineral dust events, which may be associated with written accounts of “bloody rain,” including the possibility of quantifying their frequency of occurrence.

Origin and History of Domesticated Cochineal (*Dactylopius coccus*) Via Genomic Sequencing

Michael Campana, Centre for Evolutionary Medicine, University of Zurich

Domesticated cochineal (*Dactylopius coccus*) is a New-World scale insect that produces carminic acid, a potent scarlet dye used to color textiles, cosmetics and food. From the conquest of the Aztec Empire by the Spanish until the advent of laboratory-synthesized colorants in the 19th century, cochineal dye was the preeminent source of scarlet coloring. Cochineal was one of the primary exports from New Spain (after gold and silver) and played a critical role in the highland Mexican economy, where commercial production was centered. After the development of artificial red dyes, cochineal production nearly disappeared, obscuring the genetic and geographic history of the insect.

Cochineal has an unusually disjointed geographic distribution, with two populations located in the Mexican and Peruvian highlands. It is unclear whether this distribution is natural or the result of deliberate introduction of the insects in prehistory. Moreover, the ultimate geographic origin and center of domestication remains debated. Here, we investigate the history of *D. coccus* using *de novo* whole-genomic sequencing.

Inoculation: Medical Cause for Controversy? Inoculation and Final Size in the 1721 Boston Smallpox Epidemic

Marlee Chong, Harvard University IT, Harvard College '13

Today, the 1721 Boston smallpox epidemic is primarily known for the religious controversies it provoked over the introduction of inoculation in America. However, physicians and the public also opposed inoculation on medical grounds, fearing that the inoculated would infect others and worsen the epidemic. In this poster, I address the concern by asking the question: what effect did the proportion of people inoculated have on the final size of the epidemic? To answer this question, a model of the epidemic was used to simulate the final size when the proportion of people inoculated varied.

In the Swamps: Physical Geography of Antebellum Rice Cultivation

Samuel Coffin, Harvard College '14

This project explores the potential effects of physical geography on the development of rice cultivation in the antebellum South. Antebellum rice cultivation provides a unique opportunity to study the effect of physical geography on historical development, since rice cultivation required a specific geographic profile and technological investment not found in the cotton plantation economy. I focus upon two river basins in South Carolina, the "ACE" River Basin and the Waccamaw Basin, which were some of the most prominent rice-growing regions in the antebellum period. I investigate tidal levels, cited by antebellum literature as a major influence on a crop's success. As no tidal data exists for the antebellum period, I rely upon current and projected tidal levels produced by the National Oceanic and Atmospheric Administration (NOAA) for the river basins in question. Comparison of the tidal data with Census agricultural data from 1840-1860 seems to indicate regions with tidal levels lower than the supposed optimum of antebellum reckoning. A brief investigation of a secondary influence such as salinity uses the same method of contemporary data and results in the same incongruity. Further investigation may consider other effects to explain the amount of influence that physical geography exercised on antebellum rice cultivation. For instance, rice cultivation, from the colonial period onwards, remained in the hands of a few planter families. Later advances in rice cultivation may have been less effective given the immobile nature of landholdings in the South Carolina river basins.

Paleodiets, Cooking and Nitrogen Isotopes

Elizabeth Harvey (Harvard College '14), Linda Reynard (Human Evolutionary Biology [HEB], Harvard) and Noreen Tuross (HEB, Harvard)

Cooking food is an essentially human task that was developed at a yet to be determined time. The evidence of hearths is plentiful, however, during much of the Pleistocene. We test the hypothesis that cooking is relevant to the high values of nitrogen isotopes found in Neandertal remains. Previously, nitrogen isotopic values from bone collagen have been attributed to a hypercarnivorous diet of Neandertals. We test the hypothesis that the high nitrogen isotope values found in Neandertals are not solely due to meat eating, but could also be altered by food preparation. The nitrogen isotope ratios found in both beef and sweet potatoes increase with higher cooking temperature and longer cooking time. We demonstrate that by cooking at temperatures such as those found in open-hearth cooking, we produced Maillard-type reaction products that were substantially higher in nitrogen isotope values relative to uncooked controls. Paleodietary interpretations need to take at least three factors into consideration: the consumer diet, the range of isotopic values at the floral base of the food web, and the type of food preparation employed.

Rain, Records, and Tree Rings. Analyzing a Medieval French Eyewitness and Scientific Precipitation Reconstruction for Central Europe, 1465-1500 CE

Leila Hofer, Harvard College '15

This project analyzes weather descriptions in a remarkable journal written by Jehan Aubrion, a 15th-century resident of Metz, France, in conjunction with Büntgen et al.'s (2011) precipitation analysis of European oaks. Similar to Kraker (1999), this study uses a point system based on recorded wet and dry events' strength and duration, as described in the journal, to distill events into 12 categories ranging from -6 (very dry) to +6 (very wet). Events are averaged to attain yearly wetness values, and zero is assigned to years with no written record. First, these yearly values are correlated with Büntgen et al.'s French oak precipitation reconstruction, revealing a distinctly positive relationship. The two outlying years show the journal disagreeing with the reconstruction, presenting opportunities to explore how the author's perception of his environment might be colored by factors other than the weather. But this disagreement also suggests that unexpected variables, like extreme flooding described in the journal, may produce deceptive results in the reconstruction. A second category of outliers includes years with no written record. When examined together with the reconstruction, no-record years appear as neither strong indicators of average weather, nor strong indicators of the author's failure to note an anomaly, but rather, a mixture of both. These analyses augment the growing body of research underscoring written sources' contribution to understanding historic climates and their impact on human civilization.

The Chemistry of Tyrian Purple: A Novel Application of Hyperspectral Imaging

Marie Keil, Harvard College '14

Tyrian or “royal” purple dye was a marker of both wealth and status in the ancient world. The dye is also chemically intriguing, owing to its derivation from a specific genus of mollusks. Because of its chemical properties, Tyrian purple has a potentially unique fluorescent response, which would allow a novel application of hyperspectral imaging. This non-destructive analytical technique would help us understand the societal forces that led to the production of this mollusk dye on three continents. Theoretically, any dye could be identified by its unique hyperspectral “fingerprint,” if time were dedicated to the creation of high-quality comparative standards.

Climatic Contributions to Subsistence Crises, Mass Mortalities and Social Conflict in Ireland, 425-1649 CE

Francis Ludlow, Yale Climate & Energy Institute, Yale University and Rachel Carson Center for Environment and Society, University of Munich.

This poster combines historical and tree-ring records to identify climatic contributions to subsistence crises, mass mortality events, and conflict and violence across twelve centuries of Irish history, based on the Irish Annals. The Irish Annals record major historical events from the fifth to seventeenth centuries CE. Composed in monastic communities across Ireland up to the thirteenth century, and continued thereafter in the schools of hereditary professional historians employed by the Gaelic aristocracy, these sources systematically report extreme weather, harvest failure, famine and mass human and animal mortality. A broad spectrum of conflict and violence is also chronicled, from individual murders to cattle and slave raiding, to the occurrence of large land and naval battles. With more than 1.1 million words in 22 surviving texts, the Irish Annals allow a reconstruction of the annual frequency of such events presently unparalleled in Europe in its continuity and detail. Ireland also boasts a world-class oak tree-ring record spanning the past seven millennia. The width of annual rings reflects the quality of growing season climate, and years of extremely poor growth (as revealed by anomalously narrow rings) provide an independent measure of times of extreme climatic stress. Combining this record with the evidence of the Irish Annals has begun to reveal varied climatic contributions to societal stresses such as major mortality events and social conflict, with, for example, some forms of conflict occurring with increased frequency at times of anomalously low tree-ring growth. The sensitivity of medieval Irish society also varies with the intensity and type of extreme (e.g. drought vs. flooding) and varies according to evolving political and socioeconomic circumstances.

Digitizing the Roman Empire and Medieval Europe

Brendan Maione-Downing, DARMC, Harvard and Harvard College '13

In recent years, a profusion of new tools and projects have made the methods of Geographic Information Science (GIS) relevant and accessible to scholars and students investigating spatial-historical questions. *The Digital Atlas of Roman and Medieval Civilizations* (DARMC)

represents an unprecedented effort by an international team consisting primarily of Harvard undergraduates and graduate students to collect, analyze, and publish data related to the Roman Empire and Medieval Europe, broadly considered. This presentation will demonstrate how users can access a wealth of historical data through the DARMC public interface, as well as offer a look at how historical data can be used for spatial analysis through several case studies.

Giza 3D: Digital Archaeology and Scholarly Access to the Giza Pyramids

Peter Manuelian, Near Eastern Languages and Civilizations, Harvard and Anthropology, Harvard.

As part of the Giza Project at Harvard, a 3D, archaeologically accurate computer model of the pyramids, tombs, and temples at the famous Giza Pyramids, just west of modern Cairo, is being developed for teaching and research. The work is largely based on the excavations of the Harvard University–Boston Museum of Fine Arts Expedition (1905–1947). This presentation will show the computer model, and other experiments in new technologies for bringing the site back to life, for scholars, students, and the public worldwide.

A Shift Towards Endogamy: Genetic Evidence for Population Mixture in India in the Last 4000 Years

Priya Moorjani, Columbia University and University of Chicago

Most Indian groups descend from a mixture of two genetically divergent populations: Ancestral North Indians (ANI) related to Central Asians, Middle Easterners, Caucasians, and Europeans; and Ancestral South Indians (ASI) not closely related to groups outside the subcontinent. The date of mixture is unknown but has implications for understanding Indian history. We report genome-wide data from 73 groups from the Indian subcontinent and analyze linkage disequilibrium to estimate ANI-ASI mixture dates ranging from about 1,900 to 4,200 years ago. The dates of admixture are significantly more recent on average in Indo-European speaking groups in the north of India (2,100 years) than in Dravidian speaking groups in the south of India (3,100 years). In a subset of groups, 100% of the mixture is consistent with having occurred during this period. These results show that India experienced a demographic transformation several thousand years ago, from a region in which major population mixture was common to one in which mixture even between closely related groups became rare because of a shift to endogamy.

Thirsty Genes and Human Evolution: Did Environmental Selective Pressures Influence the Ability to Retain Salt?

Neil Patel, Icahn School of Medicine at Mount Sinai, NY and Harvard College '13

Public health officials around the world are attempting to implement salt reduction strategies as human salt consumption has increased to 10-20 times Paleolithic levels. Increased salt consumption may be contributing to the growing epidemic of hypertension in industrialized and developing countries. The prevalence of hypertension varies between different racial and

ethnic groups and salt sensitivity, the degree to which salt influences blood pressure, has also been observed to vary. Differential susceptibility to hypertension and differential salt sensitivity may be due to selective pressures to retain salt in the evolutionary history of humans. Within the literature, this salt retention hypothesis argues that populations in hot and humid regions would be genetically adapted to retain more salt within their bodies as large amounts of salt and water would be lost through perspiration. This hypothesis is tested using a phylogenetic generalized least squares model with data from 45 populations in the Human Genetic Diversity Project. The results demonstrated that the frequency of alleles which do not act to increase salt retention in the body decrease with increasing temperature and humidity.

Weaning Times from Archaeological Bones Using Nitrogen Isotope Ratios: The Known, the Unknown and the Unknowable

Linda M. Reynard (Human Evolutionary Biology [HEB], Harvard) and Noreen Tuross (HEB, Harvard)

Empirical observations of $\delta^{15}\text{N}$ of bone collagen by age at death from 52 archaeological sites (n=1323) document an increase over the adult mean at ages ~0-2 years. These observations are generally consistent with a hypothesis that posits a difference in trophic level between the nursing infant and the mother, involving breastmilk consumption and subsequent weaning to non-breastmilk foods. These data are most often used to infer time of weaning in past populations, for comparison of the weaning times between groups who may vary in subsistence strategies or social practices. More comprehensive and synthetic goals of determining weaning ages include the desire to understand how differences in population structure are related to subsistence shifts and inter-birth interval (e.g. agriculturalists vs. hunter-gatherers), with significant implications for the demography of past populations, or to compare the health and nutritional status of infants and juveniles between groups and over time. To accomplish these goals a robust and reliable method grounded in empirical research is needed, and this has been lacking to date.

Assessing a time of weaning from bone $\delta^{15}\text{N}$ data is not a straightforward undertaking. Other possible explanations for these age-related isotopic differences have generally not been considered in the archaeological literature, and the assumptions used to determine age of weaning are in some cases flawed, leading to difficulty in knowing with confidence when humans from archaeological populations were weaned. In the present work the existing human archaeological data are compiled and reviewed, and the problematic assumptions are identified. The aim is to outline the limits to using $\delta^{15}\text{N}$ in bone in longitudinal studies to determine weaning ages, and to highlight areas where more research is needed.

A Map of Neandertal Ancestry in Modern Humans: Insights into Human History and Biology

Sriram Sankararaman, Genetics, Harvard Medical School and SoHP

Analysis of the genomes of archaic hominins, such as Neandertals and Denisovans, has revealed that these groups have contributed to the genetic variation of modern human populations. Yet, we know little about how these ancient mixtures have shaped the genetic structure of human populations and even less about their impact on human evolution. To answer these questions systematically, we have built a map of Neandertal ancestry, i.e., a map that labels whether each region of an individual genome is descended from Neandertals.

We find multi-megabase long regions of the genome that are deserts of Neandertal ancestry consistent with rapid selection to remove genetic variants that are incompatible between Neandertals and modern humans. Chromosome X is also a desert of Neandertal ancestry with a proportion of Neandertal ancestry that is a fifth of the autosomes, also consistent with the action of hybrid incompatibility. In addition to deserts of Neandertal ancestry at a 10 Mb scale, we also see increases in Neandertal ancestry at this scale. We show that the variation in Neandertal ancestry is explained by enhanced drift in the first 300 hundred generations after gene flow. A scenario consistent with this observation is that Neandertal introgression occurred into a small band of modern humans expanding into Neandertal territory with an effective population size of hundreds.

We also find dozens of regions that harbor an excess of Neandertal ancestry and are likely to be positively selected. Such regions are enriched for genes affecting keratin filaments, sugar metabolism, vascular smooth muscle contraction and oocyte meiosis suggesting that Neandertal variants at these genes helped modern humans adapt to their non-African environments. We also find multiple genetic variants that affect risk for disease that are introgressed from Neandertals.

Letters of an Evolutionary: A Look into the Correspondence of Charles Darwin

Rachel Sapire, Harvard College '15

Darwin's correspondence with friends and other prominent scientists of the time provides a unique insight into his own scientific process, the development of his theories, and the broader Victorian society of the time. By exploring his letters, one is able to gain an understanding of his own scientific process prior to the publication of his groundbreaking books as well as the reception by other scientists at the time. Additionally, the letters and personal notes reveal the nature of the famed relationship between Darwin and Agassiz—two scientists classically thought of as members of diametrically opposed schools of thought. For my research I used a collection of primary documents, including Darwin's personal letters at the Ernst Mayr Special Collections Library and Agassiz's collections of notes. To supplement this, I used an online database put together by the Darwin Correspondence Project, which includes 15,000 letters both to and from Darwin, in order to study overall trends in his writing and how these figured into his scientific process. This was done by graphing the number of mentions of certain phrases per year over time. To gain insight into the relationship between Louis Agassiz and

Charles Darwin, I also examined a collection of Agassiz's personal notes, which document his thoughts on Darwin's work and his reactions to his publications. In the letters I looked at the number of times "sexual selection," "variation," "religious," "sexual differences," and "fitness" were mentioned. I found that all experienced a maximum immediately before the publication of *The Descent of Man*, with "variation" being discussed most frequently in the letters. After studying the documents I found that Agassiz's personal notes revealed that he respected Darwin as a friend and scientist, but ultimately disagreed with the validity of his arguments, especially his theory of sexual selection.

Tracing the Dispersal of Early *Homo sapiens* Across Africa: Evidence from the Lake Victoria Basin

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Genetic evidence indicates multiple dispersals of populations of early *Homo sapiens* across and out of eastern Africa beginning about ~70,000 years ago, ultimately colonizing new continents (e.g. Australia, North and South America) and replacing all other hominin groups (e.g., Neandertals). Although the genetic data provide a historical perspective, our understanding of the processes that lead to our global colonization remain poorly understood, particularly in the eastern African homeland of the founding population. The Lake Victoria Prehistory Project focuses on the natural and cultural history of the region around eastern equatorial Africa's largest lake, using ancient artifacts, fossil vertebrates and mollusks, volcanic ashes, and soils from ~33,000-1,000,000 years ago to document striking intervals of environmental flux that led to Lake Victoria's desiccation and rainforest fragmentation, facilitating modern human colonization of central Africa.