



## **Young Investigator Symposium**

*of the Initiative for the Science of the Human Past at Harvard University,  
in collaboration with the  
Max Planck Institute for the Science of Human History, Jena, Germany*

**Harvard University  
Barker Center Kresge Foundation Room  
October 29, 2016  
8:30 am – 12:30 pm**

### **Invited Speakers:**

#### **Aurora Allshouse**

BA, Anthropology (expected Spring 2017), University of California, Davis

#### **Precision Tools: Fine-Tuning Archaeological Methods and the Role of Archaeometry in the Investigation of Early Complex Civilizations**

Due to the nature of the Paleolithic archaeological record, factors such as mobility, population dynamics, and human response to environmental changes are usually considered on a scale of thousands of years. Broad correlations between the terrestrial and marine climatic record based solely on chronological data are ideally substantiated by additional proxies such as geologic analyses or the study of faunal remains. More recently, stable isotope analysis has been used as a window into the reconstruction of changes throughout an individual's life. While not all of the methods used on Paleolithic sites may be applicable, dealing with a more recent time period offers the possibility to take advantage of many of the same methods while significantly increasing the resolution of the data set. As a case study, I propose to address issues relevant to the impact of environmental change on population dynamic during the Bronze Age in Crete. Building on the existing body of data, I will discuss how stable isotope analysis can work in conjunction with archaeology to clarify whether the dramatic cultural shift observed during the Late Minoan II is more indicative of population replacement and/or the result of acculturation related processes. From the perspective of the archaeology of complex civilizations, this integrative approach can help to move towards a more precise understanding of human adaptations to environmental stressors and mobility on a scale as small as a human lifetime.

## **Andrew Crocker**

MA, Archaeology and Material Studies (expected Spring 2017), Cornell University  
BA, Classics (Spring 2014), Michigan State University

### **Spatial Statistical Approaches to Hinterland Settlement in Iron Age Cyprus and Beyond**

By examining survey data from Cyprus using a spatial statistical measure, Moran's  $I$ , I challenge the current understandings of rural landscapes in Iron Age Cyprus. This is done by putting the results of a statistical analysis into dialogue with the reported results of other surveys from Cyprus. Furthermore, I compare these results with other surveys from the Near East, in Turkey, Iraq, and Syria, to contextualize these results and propose several possible explanations.

## **Eadaoin Harney**

PhD Program, Organismic and Evolutionary Biology (2015 – present), Harvard University  
MPhil, Human Evolutionary Studies (November 2013), University of Cambridge  
BA, Biochemistry (May 2012), Vassar College

### **Ancient Genomics of the Levant Chalcolithic**

The ancient Levant has experienced dramatic changes in population structure since the development of agriculture. Prior to and during the early Neolithic, the Levant was inhabited by populations that were highly differentiated from the rest of the Near East. By the Bronze Age, this high level of genetic differentiation had decreased dramatically, with an influx of Iran-like ancestry observed in Levantine populations. However, little is known about genetic changes in this region in the ~4,000-year interval between the Neolithic and Bronze Age periods. This study reports on genome-wide ancient DNA collected from 23 individuals from the Chalcolithic period in the Levant. This dataset approximately doubles the amount of genome-wide ancient human DNA available from the Levant. Preliminary results suggest that the Levant Chalcolithic population possessed ancestry derived from Levant Neolithic (58.2%), Iran Chalcolithic (17.0%), and Anatolia Neolithic (24.8%) populations. Additionally, analysis of Levant Bronze Age populations suggest that this Levant Chalcolithic population may represent a genetic dead end that did not contribute broadly to later groups.

## **Jonathan LoTempio, Jr.**

National Human Genome Research Institute, NIH (2015 – present), Washington, DC  
BS, Biological Sciences: Biochemistry (May 2014), University of Rochester

### **Contagion in Context: An Examination of Ancient Human and Microbial Genomics upon Admixture**

Humanity has been, and continues to be, sculpted by the exchange of genes, and microbes through human migration. Large scale human migrations have also been accompanied by the spread of disease. These disease-causing microbes do not act in isolation, but rather are part of a larger community of microbial residents (the microbiome) which are also exchanged when human populations meet. The foundational data and methods are currently available to assess the relationship between the microbiome and humans over the course of migratory admixture. Here I propose a study of microbes preserved in genetically, anthropologically, and archeologically well-characterized samples from ancient populations. A census of microbiomes in human remains along with an analysis of human genome data will provide insight into the genetic niches that these microbes, both pathogenic and beneficial, exploited and shaped in these ancient populations.

## **Matthew Luongo**

AB, Earth & Planetary Sciences, and Environmental Science & Engineering (expected Spring 2017),  
Harvard University

### **Intercomparison and Calibration of Historical Documentary and Paleo Proxy Climatic Data in Medieval Europe**

In the face of modern anthropogenic climate change, many scientists and historians look to past climatic shifts and subsequent societal reactions to gain an understanding as to how we can best respond to the current threat. Two sources of information on prior climatic conditions are historical documentary and paleo proxy climatic sources. These sources, historical and scientific, each provide rich information on past climate and have separately been the focus of many paleoclimate reconstruction studies. More recently, interdisciplinary research has sought to mesh together both historical and scientific data to gain a transformative understanding of paleoclimate, but an accurate intercomparison between historical and scientific data has been difficult to achieve. Using documentary data from the French climate historian Pierre Alexandre and proxy data from European paleo proxy sources, I attempt to intercompare and calibrate paleoclimate data from Medieval Europe. Looking at case studies of years with extreme climatic documentary reports in tandem with paleoclimate reconstructions allows for a spatial and temporal statistical analysis of both datasets. The resulting statistics will help to point out bias in each paleoclimatic data source and inform subsequent reconstructions, so as to eventually gain more accurate advice on how to respond to climate change in the modern era given prior human experience.

## **Megan Michel**

Harvard Medical School, Reich Lab Ancient DNA Technician (September 2015 – present), Cambridge, MA  
BA, Biology (Spring 2015), Oberlin College

### **Ancient DNA on the Silk Road: Sampling, Processing, and Prospects**

*Yersinia pestis*, the bacterial agent of the plague, has been responsible for three historically recognized pandemics, including the Justinianic Plague (6<sup>th</sup>-8<sup>th</sup> centuries AD). On a trip to Kazakhstan and Uzbekistan, I obtained human bone samples from six 6<sup>th</sup>-8<sup>th</sup> century Silk Road archaeological sites, which are being processed for ancient DNA analysis in a clean lab facility at Harvard Medical School. As part of my future PhD, I hope to screen both these samples and Mediterranean specimens for *Y. pestis* DNA using array-based technology or shotgun sequencing. Phylogenetic analysis of this data will be used to address two key questions in *Y. pestis* evolution: where did the Justinianic Plague originate, and what genetic and environmental factors contributed to the exceptional virulence of the Justinianic outbreak? Based on previous phylogenetic analyses of Justinianic *Y. pestis*, I hypothesize that this outbreak emerged in East Asia and was transmitted to the Mediterranean via Silk Road trade routes. I further anticipate that this study will reveal significant pathogen transmission along the Silk Road, making pathogen co-infection a possible explanation for the high virulence and mortality associated with the Justinianic epidemic.

## **Jessica Schalburg-Clayton**

MSc, Human Osteoarchaeology (August 2016), University of Edinburgh  
BA, History & Social Anthropology (April 2015), University of King's College

### **Dietary Reconstruction of Balearic Late Roman and Early Byzantine Populations: A Stable Isotope Study**

The addition of twenty-two  $\delta^{13}\text{C}$ ,  $\delta^{15}\text{N}$ , and  $\delta^{34}\text{S}$  stable isotope values expanded the already existing sample size of the site Joan Planells, a late Roman – early Byzantine necropolis found in Ibiza Town, Ibiza. This new data allowed for a more robust intra-site comparison of general dietary trends. Joan Planells was then compared to the other Balearic contemporary sites of Via Punica, S'Hort des Llimoners, and Can Reinés through statistical analysis and Food Reconstruction Using Isotopic Transferred Signals (FRUITS), a Bayesian model software.

## **Juan Vidal**

PhD Program, Archaeology (September 2014 – present), Boston University  
MA, Archaeology & Ancient Near Eastern Cultures (June 2013), Tel Aviv University  
BA, Anthropology, Archaeology & Classical Civilizations (June 2011), University of Cincinnati

### **Settlement Adaptation Strategies in the Mediterranean of the First Millennium**

The Greek Archaic Period is characterized by the expansion of the Greek territory over the Mediterranean by means of multiple waves of migration. These migrations are characterized as colonial ventures: a mother city would send off a colonial party to found an independent daughter city, which in turn may spawn yet another colonial settlement. Traditionally, these migrations are explained as a result of economic stress in the home cities, but a growing body of evidence suggests that daughter settlements seemed intent on sending off colonial expeditions early on while still experiencing economic growth or stability. The research into this phenomenon, especially in the region of Magna Graecia has reached a critical mass of archaeological, biological, historical, linguistic, numismatic, and textual data that has the potential of enabling the establishment of a cultural phylogeny of the region. This project aims to contextualize the different scales of human mobility that characterize the westward Greek expansion and their resulting settlements within their local, regional, insular and transregional spheres of interaction for the purpose of identifying socio-ecological patterns that would explain the dynamics of Greek migrations.

## **Jacob White**

MSc, Palaeopathology (Fall 2016), Durham University

BA, Anthropology: Natural Sciences (Fall 2015), University of Louisville

### **Tuberculosis, leprosy, and the disease triad: Using urbanization in the Mediterranean to investigate mycobacterial cross immunity and human niche construction**

The inverse relationship between the increase in tuberculosis and the decrease in leprosy during post-Medieval Europe is a highly disputed topic among medical historians and archaeologists. To address this problem, interdisciplinary research must be considered, such as lab-based immunology research and paleopathological studies. Moreover, the discussion will draw on concepts from evolutionary medicine such as the disease triad - genetics, pathogen load, and environmental nexus - and the concept of mutualism. This talk will focus on research the speaker conducted investigating the cross immunity hypothesis using human immune cells for *in vitro* cell culturing with tuberculosis and leprosy lysates. Then, the presentation will introduce future research trajectories for a PhD project on how mycobacterial infections influenced human population growth in the Mediterranean. The Mediterranean is chosen for this potential PhD project due to the region's abundance of archaeological samples and its importance to contemporary society. This research aims to explore interactions between intrinsic and extrinsic factors involved in tuberculosis and leprosy pathogenesis. More specifically, intrinsic factors include the increase and decrease of genetic susceptibility to mycobacteria-related disease and genetically linked autoimmune disorders such as rheumatoid arthritis, which is associated with resistance to mycobacterial infections. Extrinsic factors include demographic transitions linked to urbanization, the spread of agriculture, animal domestication, reliance on various subsistence strategies, and pathogen load. Tuberculosis and leprosy are two diseases with a significant impact on human evolution and on human health today. Understanding more about the possible interaction between these two diseases and the immune system in past populations may offer significant insights regarding the manifestations of these diseases today.

## **Sterling Wright**

Genome Sequencing Analysis Facility Lab Assistant (August 2016 – present), Austin, TX

BA, Classical Archaeology & BS, Psychology (Spring 20126), University of Texas, Austin

### **Elucidating the Long and Complicated Relationship with *Yersinia pestis***

Arguably, the Plague of Justinian and the Black Death are two of the most cataclysmic events in human history. Because contemporary historians, like Procopius, mention that many victims developed black welts, many scholars believe that *Yersinia pestis* was the causative agent for the two plagues. However, the descriptions of contemporary authors also mention how the disease was able to travel vast distances in a short period of time have led some scholars to challenge this claim. Fortunately, the advent of biomolecular technologies and their application to ancient DNA sources have provided an alternative and more reliable diagnosis method. Next-generation sequencing, for instance, has given scientists and historians molecular evidence to suggest that *Yersinia pestis* was indeed the agent for the plagues. While these methods have been helpful, there is still much work to be done. This presentation reviews the current ancient DNA research on *Y. pestis* and suggests future research that scholars should consider investigating in order to elucidate the mysterious history of the disease.