

Speakers

Keynote

Christina Warinner



Archaeology of the invisible: the biomolecular revolution in archaeology

Recent advances in biomolecular technologies are opening up dramatic new opportunities in the field of archaeology. Among the most exciting new technologies to emerge is that of paleogenomics - the study of ancient DNA to reconstruct past genomes and answer key questions about the human past. Although the first attempts to recover ancient DNA can be traced to the 1980s, the field underwent a technological revolution in the 2010s with the advent of high throughput sequencing and is now among the most powerful methods in the archaeology toolkit. From identifying ancient human migrations and ancestry relationships to diagnosing and tracing the spread of infectious disease to reconstructing the ingredients and flavors of ancient foods, paleogenomics is transforming our understanding of the human past. Here we introduce three paleogenomics projects our team is conducting in Nepal and explain how ancient DNA can be used answer key questions about life in ancient Nepal - including how and when ancient peoples first settled the high Himalayan valleys, the antiquity of malaria and its spread by trade, and the ancient art of brewing chaang.

Mark Aldenderfer



The High Himalayas Archaeological Project (HHARP) in Upper Mustang, 2010-2023

The High Himalayas Archaeological Project (HHARP) in Upper Mustang is an interdisciplinary project that has involved archaeologists, bioarchaeologists, geneticists, and specialists in a wide range of archaeological sciences to explore the peopling of the Himalayas and subsequent cultural and biological adaptations to life at high elevation. Over the course of the project, the team has excavated and conducted research at seven archaeological sites in Mustang and neighboring Manang. Based on this research, we now know that people entered Mustang by 1500 BCE, and through the study of ancient DNA, have found that they are ultimately descended from peoples from the Tibetan plateau. Our research has revealed a complex set of mortuary practices over time, and archaeometric studies of glass beads, metals, and other artifacts show that Upper Mustang was connected societies to South Asia as well as Central Asia and the Middle East. This presentation outlines some of the primary results of the efforts of this extraordinary team of scientists.

Talks

Ancient DNA insights into 7th century chaang brewing from Samdzong, Upper Mustang, Nepal

Maxime Borry, Mark Aldenderfer, Christina Warinner



Located some 4000 meters above sea level, in the Kali Gandaki river valley of the Upper Mustang region of Nepal, lies the sky cave of Samdzong. Archeological excavations conducted, between 2010 and 2012, revealed several tombs, among which the tomb 5, which contained human remains and cultural artifacts associated with food and beverage production. Among these artifacts, copper vessels, dated to the 6-7th century CE, are thought to be associated with the brewing and consumption of Chhaang, a typical Tibetan barley wine. After conducting DNA extraction in a dedicated ancient DNA cleanroom facility, we shotgun and target captured and sequenced these samples, to check both for plant and microbiome composition. The microbial signal present in these samples revealed an assortment of microbes associated with alcoholic fermentation, while the plant DNA matched with barley reference genomes. Taken together, these findings suggest the production of Chhaang in the Upper Mustang region in the early 7th century CE.

Ancient DNA evidence for *Plasmodium falciparum* malaria at the high-altitude site of Chokhopani in Upper Mustang, Nepal

Megan Michel, Eirini Skourtanioti, Mark Aldenderfer, Christina Warinner, Alexander Herbig, Johannes Krause



In addition to representing a major modern public health threat, the malaria-causing parasite *Plasmodium falciparum* has exerted one of the strongest selective pressures shaping the human genome. Nevertheless, debate persists over when and how *P. falciparum* emerged as a human pathogen and spread around the globe. To explore the history of this disease, we used a metagenomic approach to identify ancient DNA from malaria parasites preserved in human skeletal remains. We present the earliest identified case of *P. falciparum* malaria in an individual from the high-altitude site of Chokhopani in Upper Mustang, Nepal, dating to c. 804-765 calBCE. This site lies above the endemic range of malaria-transmitting mosquitoes in Nepal today, suggesting that the individual from Chokhopani may have acquired their infection during travel in lowland regions. As such, this represents a rare case-study in which infectious disease status sheds light on both individual mobility and trans-altitudinal connectivity in the Himalayas.

Unraveling the Genetic History of Tibetan and Tibeto-Burman Speaking Populations

Chi-Chun Liu, David Witonsky, Anna Gosling, **Ju Hyeon Lee**, Harald Ringbauer, Richard Hagan, Nisha Patel, Raphaela Stahl, John Novembre, Mark Aldenderfer, Christina Warinner, Anna Di Rienzo, Choongwon Jeong



Present-day Tibetans have successfully acclimated to the high-altitude challenges of the Tibetan Plateau, sparking significant genetic interest in comprehending their adaptation to the hypoxic environment. Unraveling the origins of present-day Tibetans is crucial for understanding their genetic adaptation. To explore the history of the formation of the Tibetan gene pool, we conducted genome-wide analysis with 33 ancient individuals dating to ca. 1420 BCE–650 CE. These individuals, most closely related to present-day Tibetans, represent an early branch within the Tibetan lineage, shedding light on the intricate history of the Tibetan gene pool. They derive most of their ancestry from groups related to Late Neolithic populations at the northeastern edge of the Tibetan Plateau. Additionally, they carry a minor genetic component originating from a distinct and ancient Paleolithic Eurasian ancestry. Unlike the Tibetan gene pool, present-day non-Tibetan Tibeto-Burman speakers residing at mid-elevations on the Plateau, exhibit the genetic clines that trace their ancestry back to Middle Neolithic populations in the Yellow River basin. Finally, we revealed the persistence of positive selection for high-altitude adaptive alleles through a comparison between ancient and present-day highlanders.