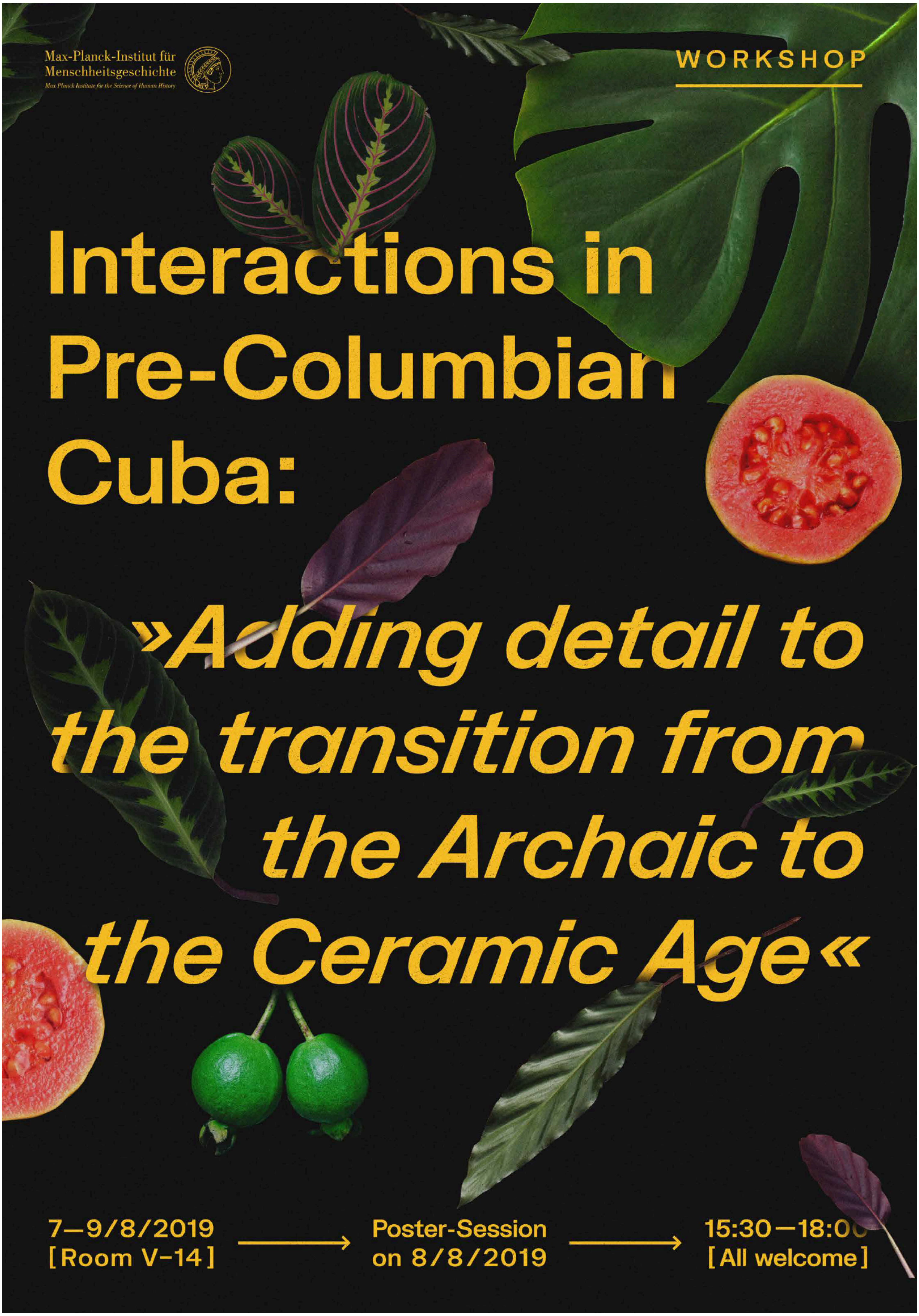

Max-Planck-Institut für
Menschheitsgeschichte
Max Planck Institute for the Science of Human History

WORKSHOP

Interactions in Pre-Columbian Cuba:

»Adding detail to the transition from the Archaic to the Ceramic Age«

7–9/8/2019
[Room V–14]

⟶

Poster-Session
on 8/8/2019

⟶

15:30–18:00
[All welcome]

Understanding the history of Cuba and its echoes in the present

Wednesday, August 7th Villa Room V.03

9:30-9:45	Registration in Rom V.03
9:45-10:00	**Johannes Krause** Welcome
10:00-10:30	**Silvia Hernandez Godoy** La ocupación humana en la cuenca hidrográfica del río Canímar, Matanzas en tiempos precoloniales: historia y actualidad. sthg71@gmail.com
10:30-11:00	**Ulises Gonzalez Herrera** Las sociedades de bajos niveles de Cuba. Preliminary title ulisesmgh1973@gmail.com
11:00-11:30	Coffee break – Library Area
11:30-12:00	**Yadira Chinique de Armas** Assessing cultural and biological differences among "Archaic Age" groups in Cuba y.chinique@uwinnipeg.ca
12:00-12:30	**William Buhay** remote talk Evidence of Late Holocene Climate Variation and Cultivation Activities near Cayo Coco, Cuba. bill.buhay@gmail.com
12:30-13:30	Lunch – Library Area
13:00-13:30	Administrative Break

13:30-14:00	**Beatriz Marcheco Teruel** Cuba: Exploring the History of Admixture using Autosomal and Uniparental Markers beatriz@infomed.sld.cu
14:00-14:30	**Enrique Gomez-Cabezas** Aborigen Genomic Ancestry: A Case Study from a Social Perspective enriquecips@ceniai.inf.cu
14:30-15:00	Coffee break – Library Area
15:00-15:30	**Ivan Roksandic** *remote presentation* Nominalizing Suffixes and the Naming Process of Taino Toponyms in the Greater Antilles i.roksandic@uwinnipeg.ca
15:30-16:00	**Mirjana Roksandic** Understanding what we don't know about the early peopling of the Caribbean Preliminary title m.roksandic@uwinnipeg.ca

Combining old and new Methods to add complexity to the Interactions in pre-contact Cuba

Thursday, August 8th Villa Room V.03

9:00-10:30	Administrative break
10:30-11:00	**Yadira Chinique de Armas** Project presentation: The Dynamic Caribbean: Tracing interactions among indigenous groups in Cuba
11:00-11:30	Coffee break – Library Area
11:30-12:00	**Kathrin Nägele** The genetic variation of pre-contact Cuba naegele@shh.mpg.de
12:00-12:30	**Rodrigo Barquera** The immunogenetic changes in pre and post contact populations from the Maya region of Mexico barquera@shh.mpg.de
12:30-13:30	Lunch – Library Area
13:30-14:00	**Zandra Fagernäs** PoopGen: Dietary species from palaeofaeces fagernaes@shh.mpg.de
14:00-14:30	**Esteban Grau Gonzales** El uso de la fotogrametría 3D, utilidad en el análisis, interpretación, reconstrucción y divulgación del patrimonio arqueológico Preliminary title estebanmatanzas@yahoo.com

14:30-15:00	Coffee break – Library Area
15:00-17:30	**Poster Session** – Library Area See Abstracts for more information
17:30 – n/a	BBQ and Music

Discussions

Friday, August 9th Villa Room V.03

9:30 – 11:30	**Discussion:** Material culture as a tool to identify differences and interactions Chairs: Ulises Gonzalez Herrera, Silvia Hernandez Godoy
11:00-11:30	Coffee break – Library Area
11:30-13:00	**Discussion:** Bioarchaeological tools to identify differences and understand interactions Chairs: Yadira Chinique de Armas, Mirjana Roksandic
13:00-14:00	Lunch – Library Area
14:00-15:30	**Discussion:** The power and limit of (ancient) DNA: Ideas and new methods for more resolution. Chairs: Kathrin Nägele, Cosimo Posth
15:30-16:00	Coffee break – Library Area
16:00-17:30	**Discussion:** Palaeoenvironmental Reconstructions and the implications for the population history of Cuba

Poster Abstracts

The Use of Ancient DNA as A Tool for the Study of Human Diversity: Mitochondrial Diversity in Mesoamerica

Komathi Sree Ponnandai Shanmugavel, Rodrigo Barquera, Diana Iraíz Hernández Zaragoza, Ernesto González Licon, Víctor Acuña Alonzo, Oana del Castillo, Lourdes Márquez Morfin, Johannes Krause.

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Ancient DNA (aDNA) has progressed from the analysis of small fragments of mitochondrial DNA from ancient contexts to the analysis of the genetic structure of ancient human populations, with the help of whole-genome, next-generation sequencing. Using ancient DNA as a tool, we analyzed the mitochondrial diversity in human populations from the classic period from Mexico, specifically from the Mesoamerican region. Those populations include Monte Alban (n=84) and Chichén Itzá (n=78) in the Maya region. The results are important to understand the population dynamics in the area and would be helpful, combined with genomic and isotope data to help reconstruct the human diversity exhibited by pre-Hispanic populations of Mexico.

Method: Mitochondrial DNA sequences were obtained after extracting ancient DNA from teeth and other skeletal elements, building libraries and capturing them with an in-solution mtDNA capture array. The resulting sequences were mapped against the human mitochondrial DNA reference HG19, and mtDNA haplogroups were called using Haplogrep and confirmed with Haplofind. Frequencies of mtDNA haplogroups and tree reconstructions were made with those results.

Conclusion: The haplogroups found are consistent with previous reports of mitochondrial diversity in Native American populations, with haplogroups A2 and B as the most frequent for both Monte Albán and Chichén Itzá. Our results shed light on the genetic diversity of pre contact Native American populations from important archaeological sites from Mesoamerica.

Unpublished results

Population continuity and disruption in the Atlantic coast: from shell-mounds to pottery

Tiago Ferraz da Silva, André Strauss, Johannes Krause, Cosimo Posth, and Tábita Hünemeier

Archaeological evidences regarding the Brazilian coast occupation during the Holocene period (~ 10k - 1k years ago) are associated with the expansion of groups fishermen/gatherers on the coast and the presence of archaeological sites the shell mounds called "Sambaquis". These sites are archaeologically recognized as cultural structures resulting from a long process of deposition of shells remains, marine fauna, and an intricate ethnic/cultural diversity.

The shell mounds builders were demographically dense societies despite the absence of agricultural practices or production of pottery vessels. The social transitions that marked the final phase of the "Sambaquian age" were the presence of the shell camps (shallow sites with "terra preta – indigenous black soil" and little portion of shell, called by DeBasis 2009 as "late Sambaquis") in the Southeast region, as well as the decline in the number of "classical Sambaquis" constructions ~2000 years before the present (BP), followed by the complete disappearance of these constructions ~ 500 BP. At the same time as the presence of the cultural characteristics associated to the Sambaquis became less evident, the cultural characteristics associated to the groups Gê from the interior, became predominant in the region, defining the end of the “Sambaquian age”. Finally, it is suggested that nowadays southern Tupi language speakers arrived in the southern Brazilian highlands at least by ~1000 BP. We aim to investigate the interactions between these groups that came from the inland to the coast and the shell mounds builders that occupied the southern Brazilian costal region for a long time before.

The use of ancient DNA in human population studies seeks to recover signals of past genetic diversity, define gene flow patterns, infer about genetic drift processes, and population reductions along a space-time assessment. However, there is a lack of genetic studies for both ancient and current South American populations including coastal populations such as Brazilian “Sambaquis”. Genomic studies of South American populations can contribute significantly to a better understanding of demographic models of global ancestry, and to the construction of demographic scenarios of subcontinental dispersal during the settlement of America.

In this context, this project aims to elucidate the demographic processes involved in the transition between the “Sambaquis” shell mound builders and the “Gê” ceramists groups from the Brazilian coast, and to verify the level of shared ancestry among them and between these ancient groups and the present indigenous populations. For this purpose, the complete mitochondrial genome (mtDNA) and genome-wide single nucleotide polymorphisms (1240K SNPs) from ancient individuals were generated and analyzed. Such data have being used to test inferences about historical demographic processes such as expansions, drastic population reductions, and historical population bottleneck among the old and extant populations.

Unpublished results

The early differentiation of Central and South Americans

Cosimo Posth, Nathan Nakatsuka, Tiago Ferraz, André Strauss, Lars Fehren-Schmitz, Johannes Krause, David Reich

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The early genetic diversification of Central and South Americans remains poorly understood because of a lack of ancient DNA that is older than a few thousand years old. Here, we report genome-wide data of 49 individuals, which form four parallel time-transects in across Belize, Brazil, the Andes (Peru and Northern Chile), and the Southern Cone (Chile and Argentina), spanning from around 11,000 to 600 years ago. We find that ancient Central and South Americans derive nearly all of their ancestry from just one of the two early branches that primarily contributed to Native Americans today. We also show that the ancestry predominant in Central and South American populations resulted from an early and rapid radiation, followed by genetic continuity in multiple regions for at least ~9,000 years. Moreover, we document two previously undocumented gene flow events between North and South America, i.e. one that provided new ancestry to southern Peruvians and northern Chileans by ~4,200 years ago and one that contributed to individuals between 11,000 and 9,000 years old from Chile, Brazil and Belize. However, both groups derive from the same ancestral source as the great majority of other Native Americans. These findings are evaluated in comparison to newly published ancient and modern American genomes to investigate when and where groups ancestral to present-day people first began to be established in each region.

Posth, Cosimo, et al. "Reconstructing the deep population history of Central and South America." Cell 175.5 (2018): 1185-1197.

Dissecting the Pre-Columbian Genomic Ancestry of Native Americans along the Andes–Amazonia Divide

Guido Alberto Gnecchi-Ruscone, Stefania Sarno, Sara De Fanti, Laura Gianvincenzo,Cristina Giuliani, Alessio Boattini, Eugenio Bortolini, Tullia Di Corcia, Cesar Sanchez Mellado,Taylor Jesus D_avila Francia, Davide Gentilini, Anna Maria Di Blasio, Patrizia Di Cosimo, Elisabetta Cilli, Antonio Gonzalez-Martin, Claudio Franceschi, Zelda Alice Franceschi, Olga Rickards, Marco Sazzini, Donata Luiselli, and Davide Pettener

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Extensive European and African admixture coupled with loss of Amerindian lineages makes the reconstruction of pre- Columbian history of Native Americans based on present-day genomes extremely challenging. Still open questions remain about the dispersals that occurred throughout the continent after the initial peopling from the Beringia, especially concerning the number and dynamics of diffusions into South America. Indeed, if environmental and historical factors contributed to shape distinct gene pools in the Andes andAmazonia, the origins of this East-West genetic structure and the extension of further interactions between populations residing along this divide are still not well understood. To this end, we generated new high-resolution genome-wide data for 229 individuals representative of one Central and ten South Amerindian ethnic groups fromMexico, Peru, Bolivia, and Argentina. Low levels of European and African admixture in the

sampled individuals allowed the application of fine-scale haplotype-based methods and demographic modeling approaches. These analyses revealed highly specific Native American genetic ancestries and great intragroup homogeneity, along with limited traces of gene flow mainly from the Andes into Peruvian Amazonians. Substantial amount of genetic drift ifferentially experienced by the considered populations underlined distinct patterns of recent inbreeding or prolonged isolation. Overall, our results support the hypothesis that all non-Andean South Americans are compatible with descending from a common lineage, while we found low support for common Mesoamerican ancestors of both Andeans and other South American groups. These findings suggest extensive back-migrations into Central America from non-Andean sources or conceal distinct peopling events into the Southern Continent.

Gnecchi-Ruscone, Guido Alberto, et al. "Dissecting the Pre-Columbian Genomic Ancestry of Native Americans along the Andes–Amazonia Divide." Molecular biology and evolution 36.6 (2019): 1254-1269.

Population structure and population history of the ancient Chachapoya from northeast Peru

Evelyn Guevara, Jukka U. Palo, Elizabeth Nelson, Thiseas C. Lamnidis, Sonia Guillén, Johannes Krause and Antti Sajantila

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Introduction. Our research focuses on the origin and population history of the human communities that inhabit the cloud forests of northeastern Peru, with both contemporary and ancient DNA data. Here we report preliminary results from the study of the ancient genetic diversity among the Chachapoya. We have produced ancient DNA data from 34 individuals spanning three archaeological periods, Late Intermediate (1000-1475 C.E.), Late Horizon (1475-1532 C.E.) and Early Colonial Period (1532-1560 C.E.).

Objectives. We are addressing a long-standing question on the origin of the Chachapoya people given the fact that culturally they have received influence from Andean and Amazonian societies in ancient times. Additionally, the study aims to assess whether the high diversity levels we have observed in the Chachapoya area nowadays (1) reflects an ancient demographic signature or the result of more recent phenomena.

Methods and preliminary results. DNA was extracted from 43 ancient individuals belonging to eight Chachapoya sites and one Cajamarca site. Double stranded next-generation sequencing libraries (Half-UDG) were generated for all individuals which subsequently were shotgun sequenced following standard protocols.

In PCA plots, the Chachapoya individuals fall between Andean and Amazonian populations, which is also supported by MDS plots based on f_3-outgroup statistics. The samples, spanning three archaeological periods tend to overlap spatially in PCA plots.

Conclusions. The results are in line with the cultural context, which shows that attributes from both, Andean and Amazonian regions are present in the Chachapoya area. The diachronic approach used in his study has revealed that the genetic composition of the populations in this area has remained constant despite population shifts during Inca times.

Guevara E.K., Palo J.U., Guillén S., and Sajantila A. 2016. MtDNA and Y-chromosomal diversity in the Chachapoya, a population from the northeast Peruvian Andes-Amazon divide. American Journal of Human Biology 2016 Nov; 28(6):857-867. DOI: 10.1002/ajhb.22878

A unified protocol for simultaneous extraction of DNA and proteins from archaeological dental calculus

Zandra Fagernäs, Maite Iris García-Collado, Jessica Hendy, Courtney Hofman, Camilla Speller, Irina Velsko, Christina Warinner

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Ancient dental calculus is a rich source of DNA, proteins, metabolites and microfossils, all of which offer complementary lines of evidence for archaeological studies. However, calculus is often found in small quantities and destructive sampling should be minimized. A protocol allowing for simultaneous extraction of several types of biomolecules from one single sample would thereby be advantageous, in order to maximise the information that is gained from this finite resource. Here, we evaluate a new unified protocol for simultaneous extraction of DNA and proteins from one single sample of archaeological dental calculus. The protocol is evaluated on samples from a range of ages and estimated preservation statuses, as well as on two different amounts of starting material, and compared against a standard protein-only and DNA-only protocol. Protein recovery was not affected by the unified protocol, but a lower starting amount of calculus used was found to increase yield. DNA recovery was significantly decreased through the unified protocol, but the yield was >50% of the yield from the DNA-only protocol. Significantly less basic amino acids were recovered through the unified protocol, indicating that proteins with high hydrophilic amino acid content may be lost to the aqueous fraction, which is mainly used for DNA purification. The reconstructed microbiome and proteome are not significantly affected by extraction protocol, and the unified protocol was not found to affect the level of contamination. In conclusion, the unified protocol was not found to introduce any biases in genetic analyses, and only minor biases in proteomic analyses. The unified protocol is thereby preferred over performing two separate extractions, to minimise destructive analyses and maximize information yield.

Unpublished results

Head, Shoulders, Knees, and Toes: A Large Scale, Systematic Invesigation of DNA Preservation in Medieval Skeletal Elements

C. Parker , S. Friederich , A. B. Rohrlach , W. Haak , K. I. Bos , J. Krause

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Ancient DNA (aDNA) analyses necessitate the destructive sampling of precious archaeological material. The pars petrosa (the portion of the temporal bone that houses the inner ear) is currently the most sought after skeletal element, as it tends to yield higher proportions of endogenous DNA, even from climatic regions that have been previously deemed unsuitable for aDNA analysis. However, the micro-structure of the inner ear is also in high demand for morphological studies or may otherwise be unavailable for sampling. In light of this, a systematic investigation that compares host DNA preservation across skeletal elements would be beneficial. Here we present a comprehensive survey of endogenous human aDNA preservation in multiple sampling sites from each of 10 skeletal elements stemming from 11 individuals excavated from the abandoned 12th century cemetery of Krakauer Berg, Germany and using high-throughput, automated, single-stranded library preparation and Illumina short read sequencing. Our analysis shows that while the dense areas around the cochlea of the pars petrosa retain the highest percentage of endogenous DNA on average, there are a range of other elements that also yield sufficient aDNA for a variety of applications. Our analyses utilize both standard bioinformatics packages and modern statistical approaches to consider several aspects of aDNA preservation including: endogenous human DNA content, contamination levels, and library complexity. This ranked listing of skeletal elements will provide investigators a better perspective on DNA preservation across the skeleton and aid in sample selection in a wide range of aDNA studies, especially for incomplete or fragmentary individuals.

Unpublished results

Pleistocene North African genomes link Near Eastern and sub-Saharan African human populations

Marieke van de Loosdrecht, Abdeljalil Bouzouggar, Louise Humphrey, Cosimo Posth, Nick Barton, Ayinuer Aximu-Petri, Birgit Nickel, […], Jean-Jacques Hublin, Svante Pääbo, Stephan Schiffels, Matthias Meyer, Wolfgang Haak, Choongwon Jeong & Johannes Krause

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North Africa, connecting sub-Saharan Africa and Eurasia, is important for understanding human history. However, the genetic history of modern humans in this region is largely unknown before the introduction of agriculture. After the Last Glacial Maximum modern humans, associated with the Iberomaurusian, inhabited a wide area spanning from Morocco to Libya. The Iberomaurusian is part of the early Later Stone Age and characterized by a distinct microlithic bladelet technology, complex hunter-gathering and tooth evulsion.

Here we present genomic data from seven individuals, directly dated to ~15,000-year-ago, from Grotte des Pigeons, Taforalt in Morocco. Uni-parental marker analyses show mitochondrial haplogroup U6a for six individuals and M1b for one individual, and Y-chromosome haplogroup E-M78 (E1b1b1a1) for males.

We find a strong genetic affinity of the Taforalt individuals with ancient Near Easterners, best represented by ~12,000 year old Levantine Natufians, that made the transition from complex hunter-gathering to more sedentary food production. This suggests that genetic connections between Africa and the Near East predate the introduction of agriculture in North Africa by several millennia. Notably, we do not find evidence for gene flow from pre-Holocene European hunter-gatherers into the ~15,000 year old North Africans as previously suggested based on archaeological similarities. Finally, the Taforalt individuals derive one third of their ancestry from sub-Saharan Africans, best approximated by a mixture of genetic components preserved in present-day West Africans (Yoruba, Mende) and East Africans from Tanzania (Hadza). In contrast, modern North Africans have a much smaller sub-Saharan African component with no apparent link to Hadza. Our results provide the earliest direct evidence for genetic interactions between modern humans across Africa and Eurasia.

van de Loosdrecht, Marieke, et al. "Pleistocene North African genomes link near Eastern and sub-saharan African human populations." Science 360.6388 (2018): 548-552

The first Anatolian Epipaleolithic Genome suggests a local origin for the first farmers of central Anatolia

Michal Feldman, Eva Fernández-Domínguez, Luke Reynolds, Douglas Baird, Jessica Pearson, Israel Hershkovitz, Hila May, Nigel Goring-Morris, Marion Benz, Julia Gresky, Raffaela A. Bianco, Andrew Fairbairn, Gökhan Mustafaoğlu, Philipp W. Stockhammer, Cosimo Posth, Wolfgang Haak, Choongwon Jeong, Johannes Krause

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Some of the earliest evidence of farming was found in central Anatolia. These early farming communities later expanded into Europe and largely replaced local hunter-gatherers. The lack of genetic data from pre-farming Anatolians has so far limited our understanding of the Anatolian Neolithisation process. In particular, it has been unclear whether farming was adopted by indigenous hunter-gatherers in Central Anatolia or imported by settlers from earlier farming centres. Here we present the first genome-wide data from an Anatolian Epipaleolithic hunter-gatherer who lived ca 15,000 years ago, as well as from Early Neolithic individuals from Anatolia and the Levant. We find a high degree of genetic continuity throughout the Neolithic transition. In addition, we detect two distinct waves of gene flow entering Anatolia during the late Pleistocene/early Holocene: an earlier one related to Iranian/Caucasus ancestry and a later one linked to the Levant. Finally, we observe a genetic affinity between Epipaleolithic Near-Easterners and post-glacial European hunter-gatherers that suggests a genetic link between Europe and the Near East predating 15,000 years ago. Our results support models of cultural

diffusion for the development of agriculture in Anatolia with only a limited role of population movement.

Feldman, Michal, et al. "Late Pleistocene human genome suggests a local origin for the first farmers of central Anatolia." Nature communications 10.1 (2019): 1218.

Reconstructing Croatian population history with novel ancient genomes reveals diverse ancestry

Suzanne Freilich

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Migrations at the start and end of the Neolithic transition transformed the structure of European societies, as people brought with them new subsistence practices and their genetic ancestry. The Balkan Peninsula was an important crossroads for communication and trade with Anatolia, Western and Northern Europe, however limited availability of Balkan specimens means we still do not know the full extent of population interactions here. New whole genomes from Croatia were sequenced to directly reconstruct ancestry and assess evidence of genetic substructures, to better understand demographic processes of migration and impacts on genomic diversity over two time periods. Ancient DNA was sampled from the petrous bones of almost thirty individuals from the Neolithic farming settlement Beli Manastir-Popova Zemlja, and a nearby Bronze Age burial site, Jagodnjak-Krčevine. aDNA extracts were built into double-stranded libraries for shotgun sequencing to between 1 and 2X coverage. Pseudo-haploid genotypes were generated and merged with data from other ancient and modern populations for population genetic analysis. Results reveal typical Anatolian Neolithic affinities among the farmers, while Bronze Age people display steppe-related ancestry and the presence of a western hunter-gatherer component. Individuals from Popova Zemlja dating to later time periods exhibit diverse ancestral signatures, suggesting more complex interactions in this region. In addition, first and second degree relatives were identified in association with divergent grave goods. This study reveals a complex genomic and social landscape developing with the expansion of steppe pastoralists into Europe, consistent with other studies of this period. Further genetic and complementary stable isotope analyses will elucidate relationships within and between these groups to shed more light on the interaction between genotype, phenotype and nutrition against a backdrop of increasing mobility and social organisation.

Unpublished results

Uniparental markers show sex-biased admixture in ancient Pacific populations

Kathrin Nägele, Cosimo Posth, Frederique Valentin, Stuart Bedford, Monica Tromp, Patrick Roberts, Johannes Moser, Julia Gresky, Adam Powell, Russell Gray, Johannes Krause

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Analyses of uniparental markers have shown that present-day populations across Remote Oceania received mitochondrial DNA (mtDNA) largely of East Asian origin while the majority of Y-chromosome lineages derive from Near Oceania. Ancient DNA time transects across different regions of the Southwest Pacific offer the opportunity to elucidate the timing and formation of this genetic landscape shaped by sex-biased admixture. Here, we report uniparentally inherited mtDNA and Y-chromosomes of ancient individuals from Vanuatu, Tonga and French Polynesia in Remote Oceania, as well as from the Solomon Islands and Papua New Guinea in Near Oceania. We confirm that the first settlers of Remote Oceania associated with the Lapita culture and the spread of Austronesian languages approximately 3,000 years before present (yBP) carried mtDNA haplogroup B4a1a1, the so-called ‘Polynesian motif’. We also present the first Y-chromosome haplogroup for a Lapita individual, O1a1a1a, further supporting the East Asian origins of the Austronesian expansion. We identify the arrival of Near Oceanic ancestry and signatures of sex-biased admixture as early as 2,500 yBP in Vanuatu. While autosomal DNA analyses of ancient individuals provide greater resolution in reconstructing population history, uniparental markers still offer valuable insights into admixture dynamics and especially where DNA preservation is not sufficient for genome-wide analyses.

Posth, Cosimo, Nägele, Kathrin et al. "Language continuity despite population replacement in Remote Oceania." *Nature ecology & evolution* 2.4 (2018): 731.