Abstract Book

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A cross-taxon evolutionary perspective on the genetic diversity at the Middle Pleistocene Schöningen site complex

1. Wild animals and plants

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Abstract text: Though open-air sites are considered poor for deep-time DNA recovery, recent work in Schöningen, Germany shows that horse mitochondrial genomes can be retrieved and the paleogenomic record extended in such contexts. Among the fifteen excavation areas, Site 13II has yielded the largest Lower Paleolithic assemblages, dated to around 300 ka. Best known for the discovery of wooden spears associated with butchered horses, site 13II, offers rare evidence of coordinated hunting among archaic hominins. The faunal record, comprising more than 20,000 large-mammal remains, provides exceptional potential for molecular investigations of species co-occurrence within this paleolake environment.

To obtain a cross-taxon evolutionary snapshot, we generated near-complete mitochondrial genomes from six specimens representing four mammalian taxa: straight-tusked elephant, aurochs, red deer, and roe deer. Using horizontally structured sampling, petrous bone selection, and state-of-the-art laboratory and bioinformatic approaches, we placed each genome within its established mitochondrial phylogeny. Across all taxa, the mitochondrial DNA lineages occupy deeply divergent, basal positions to published datasets, providing early evolutionary anchors for lineages already established in the Middle Pleistocene. Together, these findings highlight Schöningen as a key locality for studying Middle Pleistocene genetic diversity and for dating evolutionary events within the genetic histories of extant and extinct mammals.

An Investigation of Upper Palaeolithic Gravettian Hunting-Strategies from Genomic Sex and Kinship Inference of a Woolly Mammoth Accumulation

1. Wild animals and plants

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Abstract text: Woolly mammoth bone accumulations at Gravettian and Epigravettian sites in Central Europe have been interpreted as the result of targeted hunting and the extensive use of mammoth bone as raw material for tool manufacture and construction. Reconstructing the herd dynamics of the mammoths recovered from these sites can therefore provide important insights into Upper Palaeolithic hunting behaviour. The Polish Gravettian site of Kraków Spadzista is exceptional in both the density and preservation of its mammoth remains. As part of this project, we targeted the cochlear part of a petrous bone, shown in humans to have very good DNA preservation, and which yielded 75% endogenous DNA. Here, we generate genomic data from 28 additional petrous bones from this site, providing an opportunity to investigate herd structure by reconstructing kinship patterns among the sampled mammoths. Forthcoming analyses will explore kinship patterns, potential maternal lineages, and age/sex structure, with the aim of reconstructing herd dynamics and assessing whether the accumulation reflects selective hunting, mass-kill events, or repeated exploitation of the same social groups. Integrated with the archaeological context, the genomic data can refine our understanding of human exploitation strategies during a particularly interesting time of cultural development preceding the Last Glacial Maximum.

Ancient admixed genomes reveal dual hybrid origins of red and eastern wolves

1. Wild animals and plants

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Abstract text: The complex evolutionary history of *Canis* in eastern North America has been debated for decades. Analyses of 12 ancient nuclear genomes (42,000–2,700 years ago) indicate the presence of four distinct *Canis* species in North America: coyote, gray wolf, red wolf, and eastern wolf. Red wolves originated through ancient admixture between Beringian gray wolves and wolf-like Pleistocene coyotes (*Canis latrans orcutti*). Eastern wolves arose later through hybridization between red wolf ancestors and a distinct North American gray wolf lineage that expanded southward after the Last Glacial Maximum. These ancient hybridizations are distinct from the historical (<100 years) and contemporary hybridization events that have shaped modern populations. Extant red wolves have been heavily impacted by coyote introgression over the past century, while eastern wolves currently hybridize with Eastern coyotes and, to a lesser extent, with Great Lakes wolves. Our findings not only resolve this decades-long debate by establishing a four-species framework that integrates elements of both the two- and three-species models but also underscore hybrid speciation as a powerful driver of mammalian evolution in North America.

Ancient and Modern Vole Genomes Hint at the Reorganization of Small Mammal Communities Triggered by the Last Interglacial Period

1. Wild animals and plants

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Abstract text: Recent studies have shown that warm interglacial periods, such as those during Marine Isotope Stages 7 and 5, were the main drivers of speciation and population dynamics in open-habitat small mammals. While genetic data on rodents from the Last Glaciation (115–11.7 thousand years ago) are relatively abundant, no comparable data from rodent remains predating the Last Interglacial are currently available, limiting our understanding of rodent communities of the penultimate glaciation.

Here, we present mitochondrial and nuclear genome data from vole remains recovered from the Middle Pleistocene layers of the Scladina palaeontological site. Although initially identified morphologically as common voles (*Microtus arvalis*) and root voles (*Alexandromys oeconomus*), which are typical representatives of the Last Glacial rodent assemblages, phylogenetic analyses revealed that the specimens belonged to the Kazakh vole (*M. ileaus*) and reed vole (*A. fortis*), species now restricted to Central and Southeast Asia, respectively. Effective population size reconstruction based on modern genomes confirm a much wider range of *M. ilaeus* during the penultimate glaciation. Similar demographic patterns observed in other vole species with currently restricted ranges suggest a markedly different Middle Pleistocene community composition and profound reorganisation triggered by the Last Interglacial period.

Ancient camel mitogenomes from Central Mexico shed light on the evolutionary history of camels in the Americas

1. Wild animals and plants

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Abstract text: The extinction of *Camelops*, the last Camelini native to North America, marked the end of a lineage that originated and inhabited the continent from the Middle Pliocene to Late Pleistocene. Although recent paleogenomic work from the Yukon revealed that *Camelops hesternus* was closely related to modern camels, the evolutionary history of this genus across its geographic range remains poorly understood. In this study, we analyzed ancient DNA from Late Pleistocene camel remains recovered in the suburban area of Mexico City, one of the southernmost localities for *Camelops*. From seven specimens, we successfully reconstructed three high-coverage mitochondrial genomes (>9×), using capture-enrichment methods. Comparative analyses with previously published *C. hesternus* genomes from the United States and Canada, along with modern camel species, revealed deep phylogeographic structure and the presence of two main mitochondrial subclades in North America. Our results suggest that *C. hesternus* maintained substantial genetic diversity shaped by large-scale migrations prior to its extinction. These findings expand the known evolutionary and biogeographic range of North American camels and underscore the importance of increasing sampling across their former habitat in order to reconstruct their evolutionary trajectory without a sampling bias, while raising new questions about the distribution of this extinct lineage.

Ancient DNA from a prehistoric human-like mannequin and plant diversity of the southern Siberian meadows over the past 1700 years

1. Wild animals and plants

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Abstract text: A mountainous-steppe region of the Minusinsk Basin with its favorable climatic and resource conditions has long been home to various population groups. These groups have left behind a wealth of ancient cultures and archaeological sites. One of the most representative sites is Oglakhty cemetery created by Tashtyk culture beares and dated back to the 3rd century AD. It's known for the exceptional preservation of organic remains like leather cloths, wooden utensils etc. Burial rites practiced by these people included cremation, and cremains were put into human-like mannequins made from animal skin and filled with herbaceous plants.

In this study, DNA of historical grass mixture from the mannequin excavated in 2023 was sequenced. Nearly complete chloroplast genomes of several species of Poaceae were reconstructed. This showed that 1,700 years ago, the variety of plant species in the Minusinsk Basin was similar to that of modern steppe and meadow flora. In addition to the species commonly found there today, a rare, ephemeral, and endangered grass, *Coleanthus subtilis*, was revealed. This species does not grow in the region today. As a coastal grass with a specific vegetation period, it can help to determine the location and season when the mannequins were produced.

Ancient DNA provides insight into introgression events between extinct and extant hare species

1. Wild animals and plants

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Abstract text: Introgression, also known as interspecific gene flow, is recognized as an important factor in evolution. It can result in the displacement or genetic 'absorption' of one species by another, which can lead to extinction. In this study, we analyzed ancient DNA from four specimens of the extinct Don hare (*Lepus tanaiticus*), dating back to the Late Pleistocene. To understand the possible genomic introgression from the Don hare into modern hares, we utilized whole-genome data from six modern *Lepus* species obtained from the NCBI database. For each specimen, we performed the ABBA-BABA test. Our results show that *L. tanaiticus* has varying degrees of introgression with other Lepus species, with the highest D-statistics between *L. tanaiticus* and the Mountain hare, *L. timidus*. These values changed over time, which may be explained by overlapping distribution during the Late Pleistocene. Overall, our findings suggest that introgression played a role in the evolution of modern hares. *L. tanaiticus* was replaced by *L. timidus* during the Holocene, and became extinct along with many other members of the mammoth faunal complex. The last populations of Don hares apparently existed until the early and middle Holocene, in southern Siberia and the Urals, respectively.

Ancient DNA reveals extinct equid lineages at Denisova Cave

1. Wild animals and plants

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Abstract text: Denisova Cave in Siberia, Russia was a major contact zone for Eurasian fauna during the Pleistocene. Thousands of bone remains have been recovered from the cave, providing a valuable record of the region's faunal diversity over the past 300,000 years. However, extensive fragmentation of the bones by hominins and predators has limited macroscopic identification to less than 5% of specimens. While previous studies have used collagen fingerprinting to classify these bones to the family or genus level, ancient DNA (aDNA) can provide species-level identification and offer a more fine-grained view of past diversity. Among the collagen-fingerprinted fauna at Denisova Cave, Equidae are particularly interesting candidates for aDNA analysis, as modern horses represent only a small fraction of their past diversity. In this study, we analysed aDNA from 140 Equidae bones from Denisova Cave spanning MIS 9–3. We identified multiple extinct equid lineages, including *Equus ovodovi*, a species that was once widespread across North America, Eurasia, and Africa. We also found caballine horses belonging to the divergent and genetically underrepresented Eurasian 'Clade C'. Here, we show that a diverse range of equids inhabited the Altai region in the Pleistocene.

Ancient genomes from Alpine caves shed light on past ibex populations and the impact of a major anthropogenic bottleneck

1. Wild animals and plants

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Abstract text: Species that survived strong anthropogenic pressure often show decreased genetic diversity, elevated inbreeding, and the accumulation of deleterious mutations. We investigate these effects in the Alpine ibex (*Capra ibex*), a wild mountain goat native to the European Alps, which was brought to the brink of extinction due to overhunting at the turn of the 20th century and has since recovered. To investigate the impact of this major anthropogenic bottleneck, and to understand past population structure and diversity, we obtained 44 high-quality ancient whole genomes that span the past 12,000 years from several caves across the entire Alpine range, and compared them to published, modern genomes. While the anthropogenic bottleneck appears to have diminished genetic diversity of modern compared with ancient Alpine ibex, we found that past populations had surprisingly low genetic diversity and were strongly differentiated, suggesting that many Alpine ibex populations were isolated and confined to small geographic regions for millennia. The species may thus have experienced major purging in the past, which may explain their successful reintroduction and subsequent rapid population growth in many areas of the Alps.

Ancient genomes illuminate the origins and dynamic history of East Asian cattle

1. Wild animals and plants

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Abstract text: The evolutionary history of domesticated cattle in East Asia for the last 5,000 years remains largely obscure. Here, we investigate the origins and evolution of cattle genetic diversity in China by analyzing shotgun genome sequences of 166 ancient bovines spanning a 10,000-year period, encompassing now-extinct East Asian aurochs and domesticated cattle from key archaeological cultures. East and North Asian aurochs were distinct from western aurochs, although East Asian aurochs harbored ~15% western ancestry. The first domesticated cattle in the Yellow River region derived ~10% of their ancestry from local aurochs with an uneven genome-wide distribution. Early cattle from Xinjiang were genetically distinct and partially contributed to the later northern Chinese cattle. Indicine admixture became widespread only in the Medieval period in northern China.

Ancient mollusk genomes as a window into long-term transposable element dynamics

1. Wild animals and plants

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Abstract text: DNA can persist in mollusk shells for a long time. We obtained shells of two marine gastropod species, *Littorina littorea* and *Patella vulgata*, that were collected from anthropogenic shell middens in caves in northern Spain and dated to the Upper Paleolithic (10,000 – 17,000 BP). Pilot sequencing of several individuals resulted in unexpectedly high fractions of endogenous DNA (up to 33%), indicating that (partial) nuclear genome reconstruction is feasible. To our knowledge, this has not previously been achieved for mollusks from the Paleolithic.

Currently, we are deep sequencing our most promising individual of each of the two species, as well as sequencing more individuals to a low coverage. This data will support the reconstruction of demographic history through haplotype networks, as well as guide the selection of additional individuals for deep sequencing.

Reconstructions of ancient genomes are a valuable resource for evolutionary research and will enable us to investigate long-term dynamics of transposable elements. Recent work has shown that the Dipteran *Drosophila melanogaster* experienced 12 transposable element invasions in ~200 years. In contrast, our material offers the opportunity to reconstruct transposable element histories on a much greater timescale, which would contribute to the understanding of transposable elements in mollusks.

Archaeogenomic reconstruction of ancient elephant ivory trade.

1. Wild animals and plants

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Abstract text: Since antiquity, elephant ivory has been valuable as a reflection of luxury, status and power. The long-term exploitation has pushed elephants towards extinction, and led to local extirpation of the North African elephant in the Late Roman times. Despite the cultural and economic significance, little is known about the ivory trade and the impacts of overhunting in past cultures because traditional methods only offer a course resolution of ivory sourcing and trade routes. Here, we start to reconstruct the history of the elephant ivory trade using archaeogenomics, which offers the unique resolution necessary to identify the geographic origin of ivory to population level. We demonstrate how a detailed genomic reference panel can serve to potentially identify extinct elephant populations by analysing ancient DNA from shipwreck and archaeological ivory. In collaboration with historians and archaeologists, this approach will contribute to uncovering ancient trade routes and identify lost elephant lineages, enriching our understanding of the evolutionary history of elephants and their importance in human history.

Climate-Driven Population Dynamics of Two Microtus Species in Western Carpathians: Insight from Ancient DNA

1. Wild animals and plants

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Abstract text: *Microtus arvalis* and *Microtus agrestis* are rodent species widespread in Europe present and past. Building on prior research, our study seeks to clarify unresolved aspects of the population dynamics of these taxa at the Late Pleistocene to Holocene transition in the Western Carpathians.

We generated 26 Late Pleistocene and Holocene low coverage genomes from paleontological sites across the Western Carpathians, and 39 mid- to high- coverage modern genomes from Central Europe, all identified as *Microtus arvalis.* For *Microtus agrestis* we generated 10 modern and 10 ancient genomes, plus 13 new mtDNA sequences.

We found that what was previously interpreted as a simple replacement of the Central *M. arvalis* mtDNA lineage by the Eastern lineage in fact involved admixture of these two populations during the Late Glacial. We are now modelling the parameters of this process to understand how only one lineage persisted in the region until the present day. For *M. agrestis*, we are investigating whether it experienced a substantial population decline during the Younger Dryas, or whether it was buffered from its effects by ecological or behavioural plasticity. We detected a loss of mtDNA diversity around that time and are now modelling how this signal translates into demographic change.

Confirming tusk-based morphological sex indicators in mammoths through genetic analysis

1. Wild animals and plants

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Abstract text: Woolly mammoth (Mammuthus primigenius) tusks are abundant in Siberian permafrost, yet tusk morphology often gives ambiguous sex indicators. Genetic approaches, particularly X-to-autosomal read depth ratios, provide a robust alternative but remain rarely applied to tusk material used for morphological sexing. We analyze Yakutian tusks to compare morphological and genetic sex assignments and evaluate whether tusk-based morphological criteria reliably reflect sex.

Materials and methods

We studied 22 tusks recovered from different regions of Yakutian permafrost. Preliminary sex determination was based on morphological characteristics. ADNA was extracted from tusk powder using standard aDNA protocols, and libraries were sequenced on Illumina platforms. Reads were filtered, mapped to the Loxodonta africana genome, and checked for aDNA damage. Sex was genetically determined by X-to-autosomal coverage ratios.

Results

Genetic sex identification was successful for 10 individuals: 8 females and 2 males. Several tusks yielded too little endogenous DNA for reliable sexing, highlighting variable preservation in permafrost. All genetic assignments matched preliminary morphological assessments, indicating that preserved tusk traits can reliably distinguish male and female individuals.

Conclusion

Our findings show that tusks are a viable source of ancient DNA and support the combined use of genetic and morphological data to reconstruct mammoth population structure and social organization.

Conifer macrofossil aDNA: tracing Late-Glacial and early Holocene lineages in the Eastern Alps

1. Wild animals and plants

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Abstract text: Global climate change and biodiversity loss are distinct but closely interconnected challenges. Potential responses to these changes include extinction, adaptation, or migration, but these remain difficult to predict. Demographic processes can strongly influence genetic diversity, whether through reductions such as founder effects and allele surfing, or increases due to admixture. Lake sediment archives provide opportunities for chronological and geographical studies on past population dynamics and genetic diversity of important tree species such as *Abies alba*, *Pinus cembra*, *Larix decidua*, and *Picea abies*. This study attempts to extract aDNA directly from macrofossils deposited in two mountain lakes from the northeastern Alps, to provide first insights into population dynamics from four conifers since the Lateglacial. Focusing on plant macrofossils should lead to high-coverage genomic data for single individuals, allowing detailed population genetic analyses. Our results will help to assess the impacts of future climatic and demographic changes on the genetic diversity of European mountain forests.

European small hamsters (subfamily Cricetinae) in the Late Pleistocene – biogeographical history written by ancient DNA.

1. Wild animals and plants

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Abstract text:
Late Pleistocene European small cricetids are usually assigned to grey dwarf hamster (*Nothocricetulus migratorius*), an extant species inhabiting Western and Central Asia and Eastern Europe. Instead, among the 16 samples from Late Pleistocene Central and Western Europe, the only species found was the hairy-footed hamster (*Cricetiscus sungorus*) currently occurring in northern Kazakhstan and southern Russia. Our phylogenetic reconstruction revealed one major lineage composed of all modern and some Late Pleistocene samples which coalesce around 25 thousand years ago, while older samples were located outside this clade. Such a topology suggests multiple expansions of the hairy-footed hamster to Europe, with the most recent one occurring after the Last Glacial Maximum.
In the Balkans, we found that the Late Pleistocene grey dwarf hamsters formed a distinct clade sister to the lineage formed by population from the Qurama Mountains in Uzbekistan, and not related with modern samples from Southeastern Europe. The Anatolian Holocene samples clustered with a modern population of species from the same region.
Our results indicate that steppe species, respond to past climatic and environmental changes in an individualistic manner, and generalizations about their evolutionary histories are unwarranted.

Evolutionary history and genomic vulnerability of the extinct giant deer Megaloceros giganteus

1. Wild animals and plants

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Abstract text: The extinct giant deer (*Megaloceros giganteus*) was an enigmatic megafaunal species of the Late Quaternary, defined by enormous palmated antlers reaching up to 3.5 m across, the largest among cervids. Despite its iconic status, little is known about its genomic history prior to extinction ~8 kya. We generated nuclear palaeogenomes for *Megaloceros,* including four individuals from Ireland (~11 kya; one at ~50× coverage) and five from the Upper Rhine Valley, Germany (~40 kya). Phylogenomics placed *Megaloceros* as sister to *Dama* (divergence ~3.5 Ma) and revealed gene flow with the ancestral *Cervus* lineage. Population analyses identified clear differentiation between

localities. Two genes showing strong signals of positive selection, BNIPL and SLC10A7, are associated with apoptosis regulation and skeletal development/bone mineralisation, respectively, and may relate to the species' large body and antler size. Demographic reconstructions indicate a long-term decline in effective population size, extremely low heterozygosity, extensive runs of homozygosity, an elevated burden of predicted deleterious alleles, and higher diversity in the German individuals. Together, these results suggest that *Megaloceros* entered the terminal Pleistocene in a genomically fragile state, offering new insight into the biology and evolutionary legacy of one of the largest cervids to live.

Extracting ancient DNA from plant macrofossils across the European Alps to reconstruct postglacial population dynamics

1. Wild animals and plants

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Abstract text: Plant remains preserved in lake sediment archives represent an underused source of paleogenomic information. Their relatively high abundance and stratigraphic deposition make them well suited for reconstructing past population dynamics, tracking changes in genetic diversity and examining microevolutionary processes through time. However, aDNA preservation is strongly influenced by site-specific factors-—most notably lake-water pH, which is itself controlled by local geology. Our analysis of a large number of samples from multiple conifer species preserved in lake sediments across the European Alps show that aDNA preservation is extremely low in acidic lakes (pH < 7) on siliceous bedrock. In contrast, conifer macrofossils from alkaline lakes on calcareous bedrock can yield up to 25% endogenous DNA, enabling the analysis of past population genetic patterns. Here we present an overview of results from an ongoing research project that applies optimized aDNA extraction protocols and shotgun sequencing to conifer macrofossils. These paleogenomic insights allow us to assess how past environmental changes influenced the genetic diversity of mountain forests and will support ecosystem managers in protecting multi-level biodiversity in a warming world.

Four centuries of commercial whaling eroded 11,000 years of population stability in bowhead whales

1. Wild animals and plants

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Abstract text: Bowhead whales were heavily exploited during commercial whaling between the 16th-20th centuries. Current and future climate warming poses a new threat. Assessing bowhead vulnerability to climatic change remains challenging, due to insufficient knowledge regarding responses to past climates and pre-whaling population dynamics. We integrate palaeogenomics and stable isotopes (δ13C and δ15N) of 201 Holocene bowhead fossils from the Atlantic Arctic with palaeoclimate and ecological modelling based on 823 radiocarbon dated fossils, including 140 new to this study. We find long-term resilience of bowheads to Holocene environmental perturbations, with no detectable changes in genetic diversity or population structure. Simulated commercial whaling genetic and fitness changes found that population subdivision and loss of genetic diversity are unlikely to be fully realised, despite nearly a century since whaling ceased. Furthermore, even in simulated complete population recovery scenarios, overall fitness did not return to pre-whaling levels, potentially compromising the future resilience of bowhead whales.

From Forests to Amphitheatres: Ancient DNA Traces Brown Bear Histories in the Balkans

1. Wild animals and plants

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Abstract text: The brown bear (*Ursus arctos* L.) is an iconic megafaunal survivor of Late Pleistocene extinctions. Once widespread across Europe, the species has been lost from many regions due to intensive human activities. In the Central Balkans (present-day Serbia), brown bears are now strictly protected, yet Holocene faunal assemblages show that they were regularly hunted throughout (pre)history and long inhabited local forests. As agriculture, deforestation, and human expansion reshaped these landscapes, bear populations likely experienced increasing ecological pressure. To assess how such changes influenced Holocene bears in Serbia, we generated and analysed 39 nearly complete mitochondrial genomes. These data reveal all three previously known European mtDNA lineages, along with a previously undescribed haplogroup, demonstrating that past genetic diversity exceeded that observed today. The greatest diversity was found at Viminacium, a major Roman centre with a large amphitheatre where bears were used in spectacles, suggesting that human-mediated trade and translocation significantly contributed to local genetic variation. Overall, temporal shifts in mtDNA diversity reflect not only environmental change but also long-term human influence. Ongoing analyses of ancient and modern nuclear genomes will further clarify this diversity and support effective conservation and management of brown bears in the Balkans.

Genomic Insights into the Evolutionary History of the Extinct Sabre-Toothed Cat: Homotherium latidens

1. Wild animals and plants

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Abstract text: The genus *Homotherium* represents lion-sized sabre-toothed cats that were widely distributed across Eurasia, Africa, and North America, from the Late Pliocene to Pleistocene. It had extensive temporal and geographic overlap with several hominins and survived in Eurasia until the Late Pleistocene. Despite its broad distribution, genomic data for *Homotherium* remain limited, with only one published medium-coverage genome (7X). Here, we have generated a high-coverage genome (17.8X) from a Late Pleistocene (MIS 3) *Homotherium* canine discovered on Bolshoy Lyakhovsky Island in northeastern Siberia. Given the deep divergence of *Homotherium* from living felids (~22.5 Ma), standard ancient DNA mapping approaches introduce strong reference bias, skewing allele frequencies and patterns of genetic variation. We therefore developed a pipeline to iteratively reconstruct the *Homotherium* genome, increasing the coverage from 15.2X to 17.8X. We also generated mitogenomes from two specimens: a juvenile mummy from the Republic of Yakutia (6.0X), and a specimen from Klondike, Canada (1.1X), both also radiocarbon-dated to MIS 3. These new genomes provide insights into *Homotherium* genetic diversity, inbreeding levels, long-term effective population size, and phylogenetic relationships, thereby shedding light on the evolutionary history of one of the Pleistocene's most iconic predators.

Historic Overexploitation, Genetic Erosion and Local extinction: Palaeogenomic Insights into the Decline of Eubalaena glacialis in Northeast Atlantic

1. Wild animals and plants

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Abstract text: The North Atlantic right whale (NARW, *Eubalaena glacialis*) was the primary target for early industrial whalers, particularly the Basques. Once abundant on both sides of the Atlantic, inhabiting temperate and subpolar waters, these whales are now functionally extinct in the Northeast Atlantic and critically endangered. Despite their fragmentary remains, bones are abundant in the archaeological and historical records and reveal a long history and extensive tradition connected to the exploitation of these marine resources.

Using state of the art ancient DNA techniques we characterize genetically the functionally extinct population of NARW from the Northeast Atlantic. We sequenced 17 full genomes from historical specimens from the Cantabrian Sea, dating from the 13-18th century. These data were compared with modern individuals from the Northwest Atlantic. Our results highlight differences in genetic diversity over time, shedding light on the impact of whaling on this species.

Our results suggest that NARW was panmictic, and that there was a significant decrease in diversity since the Middle Ages, with the extinction of most of the lineages present at the time. This work clearly points to the devastating effects commercial whaling had on North Atlantic Right Whales in the Cantabrian Sea and the NARW population.

Let's Talk About Sex… Ratios in The Fossil Record of Rodents

1. Wild animals and plants

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Abstract text: Genomic analyses of subfossil remains have exhibited great potential for revealing clues about the ecology and demography of past populations. One such example is the discovery of a strong male bias in the fossil record of large mammals, which suggests that behavioral differences between males and females can skew the sex ratio in mammalian remains. Rodents constitute the most diverse taxon of all mammals, are numerous in the fossil record, and are important biostratigraphic markers. Nevertheless, the sex ratio in rodent subfossils has so far not been investigated. In this study, we genetically sexed 515 individuals from five main genera of rodents; *Arvicola, Microtus, Lemmus, Dicrostonyx* and *Alexandromys,* as well as the extinct lineage *Lasiopodomys anglicus.* We compared the sex ratio between different genera, as well as investigated the sex ratio between cave sites, where rodent subfossils are often deposited by predators, and non-cave sites, where rodents are more likely to have occurred naturally. Despite sharing a similar social structure, we find distinct differences in the sex ratio between different genera of rodents, and explore how sex ratio in the fossil record of small mammals is influenced by ecology, social structure, variations in sex determination systems and predator preference.

Mid-Pleistocene ground squirrel palaeofeces shed light on North American mammoth migration

1. Wild animals and plants

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Abstract text: We extracted and analyzed DNA from a series of fecal pellets attributed to Arctic ground squirrels recovered from Late and Middle Pleistocene deposits in the Yukon, Canada, enriching mitochondrial DNA with the PalaeoChip Arctic bait set. Metagenomic screening revealed abundant ground squirrel DNA alongside a diverse range of animal and plant sequences. Six of these samples dating to between ~30 ka and ~700 ka contained mitochondrial DNA from mammoths. When further enriching these samples with proboscidean specific baits we found that three samples revealed mixtures of distinct mammoth mitochondrial clades, suggesting temporal or spatial overlap of divergent mammoth lineages within the region. One of the mixed samples included a lineage belonging to Clade F, typically associated with Columbian mammoths (*M. columbi*), indicating that members of this clade likely extended farther north than previously believed.

The oldest sample (~700 ka) contained DNA most similar to that of steppe mammoth–like individuals previously recovered from Siberia. This sample is temporally constrained by its association with the Gold Run tephra layer which provides one of the most securely dated occurrences of early *Mammuthus* DNA. This well-dated record offers a valuable calibration point for refining the molecular clock and evolutionary timeline of mammoth phylogeny.

Middle Pleistocene mystery bones provide insight into an ancient mammalian lineage in east Beringia

1. Wild animals and plants

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Abstract text: A horn, scapula, and molar from a large mammal were recovered from a Middle Pleistocene site near Dawson City, Yukon, Canada in 2023. The bones' size and in-situ proximity to one another suggested that they may originate from the same individual, however, morphological assessment of the bones were inconclusive and varied between *Rangifer*, *Ovibos*, *Bootherium*, *Ovis*, and the Bovidae family in general. We generated DNA sequencing data from the samples and assembled a mitochondrial genome each for the horn and molar. From a reference panel of a variety of North American megafauna, both of the samples mapped most highly to muskox (*Ovibos moschatus*). These results provide novel insights into the evolution of muskox populations in North America, in relation to past climatic changes throughout the Pleistocene.

Mitochondrial Genome Capture Reveals Evolutionary Relationships of Pleistocene Elephantidae and Cervidae in the Eastern Mediterranean

1. Wild animals and plants

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Abstract text: The Eastern Mediterranean served as a dynamic biogeographic region during the Pleistocene, hosting diverse faunal communities including endemic island dwarf megafauna. Understanding the genetic relationships and evolutionary history of these extinct populations requires ancient DNA data. We applied a mitochondrial DNA capture approach to bone and dental samples from a range of Pleistocene elephants and deer recovered across key sites in the region. Our capture results for several individuals, including specimens representing the dwarf forms, yielded full, near-full, or partial mitochondrial genomes. Phylogenetic analysis of the data offers insights into the mainland origins and inter-island dispersal patterns that shaped these island populations. Furthermore, we report the results from deep sequencing of two particular deer specimens, which yielded higher coverage and provided novel insights into their evolution and demography. This study significantly enhances our understanding of the deep-time genetic consequences of insularity in the Mediterranean.

Mitochondrial genomes of Stegodon orientalis provide new insights into the evolutionary history of proboscideans

1. Wild animals and plants

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Abstract text: As one of the world’s most iconic megafaunal lineages, the evolutionary history of proboscideans has attracted global scientific interest. While ancient DNA studies have resolved relationships among various extinct and extant proboscidean lineages, Stegodontidae remains the only family that survived into Pleistocene without genetic data and its taxonomic status and geographic origin are highly debated. Here, we recovered two nearly complete mitochondrial genomes of *Stegodon orientalis* (Stegodontidae) from Yumindong Cave in southern China, using targeted capture and iterative mapping. Mitochondrial phylogenetic analyses place *S. orientalis* as a sister lineage to Gomphotheriidae (represented by *Notiomastodon*) and Elephantidae, rejecting the hypotheses that Stegodontidae was a sister clade or direct ancestor of Elephantidae. Notably, it suggests that Stegodontidae evolved the Elephantidae-like dental morphologies independently through convergent evolution. The divergence time between Stegodontidae and its sister lineages is estimated to ~23.6 million years ago, predating the “Gomphotheriidae land bridge” (~19 million years ago) that allowed gomphotheres to disperse from Africa to Eurasia. Our results suggest that stegodontids or their ancestors migrated to Asia independently of gomphotheres, the lineage that gave rise to Elephantidae.

Molecular sexing of ancient faunal remains: methods, limits and prospects

1. Wild animals and plants

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Abstract text: High-resolution identification of biological sex from archaeological and palaeontological remains is central to reconstructing social structure, demography, and behaviour in past human and animal populations, yet traditional osteological sex-determination is often unreliable for fragmentary or weakly dimorphic specimens. The advent of ancient DNA and whole-genome sequencing (WGS) has provided a powerful alternative to accurately determine chromosomal sex from genomic data. While several WGS-based strategies have been implemented to infer sex karyotypes in XY systems from ancient DNA data (i.e. *Ry*, X-to-autosome, *Rx* and *karyo_RxRy* methods), there is not a clear consensus on the minimal sequencing data threshold needed to obtain reliable results using most of them. Here we evaluated the performance of these methods by subsampling >1x genomes across 27 samples from 9 vertebrate families to files harbouring different sequencing reads counts, representing ultra-low coverage levels, and assessed their sex karyotypes at each coverage level. Our results revealed the minimal sequencing reads needed to obtain >95% concordance sex determination estimates for each method. Our study shed light on the limits of sex determination using ancient DNA, which is of great relevance for researchers working with poorly preserved samples, often deriving from subtropical and tropical latitudes.

Natural or Neolithic? Re-evaluating the Origins of the Orkney Vole

1. Wild animals and plants

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Abstract text: The common vole (*Microtus arvalis*) has a broad native distribution across Eurasia but is restricted in the British Isles to the Orkney archipelago as the subspecies *M. a. orcadensis*. The prevailing hypothesis suggests an accidental Neolithic human introduction from coastal France or Belgium but lacks direct archaeological evidence.

Here we present new ancient mitochondrial and nuclear genomes for *M. arvalis* from two Orkney sites and several sites across England, Wales and Scotland. Low-coverage nuclear genomes confirm the taxonomic identity of 22 specimens spanning Late Pleistocene to Early Holocene contexts, demonstrating that the common vole inhabited mainland Britain before the Neolithic and contended a wide geographic range. Phylogenetic analyses of ancient mitochondrial genomes reveal affinities between southern British specimens and modern Orkney voles, suggesting a natural colonisation route through southern Britain before the postglacial submersion of Doggerland. Orkney voles form a distinct sublineage that diverged from the Western North lineage approximately 9.6 ka BP, predating Neolithic settlement.

This reinterpretation challenges the anthropogenic introduction hypothesis for the Orkney subspecies and reframes *M. arvalis* as an extirpated native of the British Isles. Ongoing radiocarbon dating and population modelling will refine the species' temporal and spatial range and improve understanding of island colonisation dynamics.

NEWINDS of Time: Decoding Past Environments Through ancient eDNA.

1. Wild animals and plants

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Abstract text: Animal dental calculus is increasingly recognised as a valuable source of ancient DNA, preserving biomolecular traces beyond the host organism. In Palaeolithic contexts, the calculus of hunted animals offers an unexpected archive of ecological information, including plant eDNA derived from diet, foraging environments and the host microbial diversity. In this study, we examined the potential of dental calculus from prey species to reconstruct past vegetation structure and human–environment interactions though the integration of this with other archaeological datasets. Using high-throughput sequencing and a metagenomic framework, we analysed plant taxa embedded within the calculus of deer and ibex recovered from an archaeological context in the Cantabrian region (northern Spain), spanning distinct climatic regimes, which were visible through the calculus data. By comparing plant eDNA profiles across species and stratigraphic layers, we assess whether prey animals function as "mobile samplers" of local vegetation and whether their calculus can capture fine-scale environmental patterns not accessible through paleopalynology or sedimentary eDNA alone. Our results demonstrate that animal calculus provides a unique, host-mediated perspective on landscapes faced by Palaeolithic groups, enriching reconstructions of past plant diversity, grazing ecologies and hunter–gatherer interactions with their environments.

Nuclear Genome Reconstruction of Megafaunal Xenarthrans for Phylogenetic and Physiological Elucidation

1. Wild animals and plants

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Abstract text: Xenarthrans are a clade of mammals hailing from the Americas, consisting of sloths, anteaters and armadillos, whose diversity has been diminished due to late-Pleistocene extinctions. Extinct megafaunal xenarthrans, such as ground sloths and glyptodonts, represent keystone species in Pleistocene ecosystems and serve as important models for anthropogenic-driven extinction. Despite their importance in understanding the world of the Pleistocene and its changes, there is a great deal unknown about their evolution and physiology, with most previous genomic analyses focusing on the mitochondrial genome. To enable us to answer these questions, we attempt to reconstruct the nuclear genomes for some iconic species, including Mylodon, Megalonyx and Megatherium, profiling a collection of bones, teeth and other samples for endogenous DNA with shotgun sequencing and targeted enrichment. A database of related references genomes (*i.e. Bradypus and Choloepus*) allows for genomic assembly as well as informed bait design to enhance capture enrichment. Assembled genomes will enable a comparison of previous mitochondrial and morphological-based phylogenies and allow characterization of key phenotypic markers, such as *ENAM*, potentially answering long-standing questions regarding diet, dentition and more. Furthermore, this work demonstrates how ancient DNA techniques have advanced, given the often tropical poorly preserving conditions for many species of xenarthrans.

Palaeogenomic insights into late Quaternary African faunas

1. Wild animals and plants

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Abstract text: Palaeogenomic data from African taxa are relatively scarce. This talk will present four case studies providing novel insights into extinct species, past distributions, and genetic shifts: From the highlands of Ethiopia: (i) We sequence the nuclear genome of a 42,000 year-old wildebeest molar (*Connochaetes* sp.), the oldest sub-Saharan African aDNA to-date, and identify it as a previously unknown, extinct lineage; (ii) Via palaeogenomic analysis of a ~40,000 year-old ibex tooth (*Capra* sp.), we identify the presence of its predator, the brown hyaena (*Parahyaena brunnea*), which today is found only in southern Africa. From South Africa: (iii) We sequence for the first time the DNA of a previously-described extinct African Pleistocene species, the long-horned buffalo (*Syncerus antiquus*), and explore its phylogenetic relationship with its closest extant relative, the African buffalo (*S. caffer*); and finally (iv) Using the first South African faunal population-level palaeogenetic dataset, we show that the Cape grysbok (*Raphicerus melanotis*) has lost unique mitochondrial diversity during the Holocene. We illustrate that in Africa, palaeogenomics can be used to study extinct Pleistocene taxa, and identify range contractions and temporal genetic dynamics of extant taxa. This improves our understanding of evolution and can guide conservation decisions in the present day.

Palaeogenomic Insights into Mammoth Herd Structure, the Anthropogenic Origins of Bone Accumulation Sites, and Late Pleistocene Hunting Strategies

1. Wild animals and plants

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Abstract text: Woolly mammoths are thought to have lived in social structures similar to modern elephants, with matriarchal herds of females and juveniles, and with solitary or small-groups of males. However, there has yet been little evidence to support this idea. Here we use mammoth ancient DNA data from diverse settings to study mammoth behavior and human hunting strategies. We generated genome-wide data for >50 mammoths from six bone accumulation sites thought to have been created through human exploitation (hunting, scavenging, butchery), as well as >300 mammoths from naturally-deposited contexts. Genetic sexing of individuals revealed >2x more females than males at accumulation sites. This contrasts with the sex distribution across naturally deposited remains, which show a significant (>2x) overrepresentation of males, likely linked to the greater vulnerability of solitary males to natural traps. Contextualized with archaeological evidence and elephant behavioral studies, our results provide strong support for the hypotheses that mammoth herds were female-dominated and that the bone accumulations are anthropogenic in origin. Our findings suggest that Late Pleistocene hunter-gatherer groups strategically targeted matriarchal herds, likely due to predictable seasonal movements. They further indicate coordinated, seasonal hunting practices of Ice Age hunter-gatherers shaped by social knowledge of mammoth behavior.

Paleogenomics Reveals Arctic Range and Aquatic Specialization in the American "cheetah", Miracinonyx trumani

1. Wild animals and plants

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Abstract text: The "American cheetah" (*Miracinonyx trumani*) was a key predator in North America's Ice Age ecosystems that went extinct at the end of the Pleistocene, yet its geographic range, ecological role, and evolutionary history remained poorly understood. Here, we generated paleogenomic data from three Yukon fossils originally identified as puma (*Puma concolor*) and radiocarbon dated to ~30,000 years ago, plus a 22X genome from a *M. trumani* specimen from Wyoming (23,522 calBP). Mitochondrial DNA analyses revealed that all three Yukon specimens were *M. trumani*, extending the species' known range into Arctic latitudes. Phylogenomic comparisons confirmed that *M. trumani* and puma were sister taxa that diverged ~2.6 million years ago. Paleogenomic analyses revealed shared demographic trajectories for both samples until their divergence 43,000 years ago with similarly low genome-wide diversity and small effective population sizes. Selection scans identified sensory perception genes under positive selection, likely reflecting adaptations for predation. Stable isotope analyses revealed striking dietary flexibility, with Arctic populations occupying higher trophic positions than their southern counterparts, suggesting exploitation of aquatic resources. These findings fundamentally expanded the known range and ecological diversity of *M. trumani*, demonstrating the power of paleogenomics and stable isotopes to reshape interpretations of Pleistocene megafaunal communities.

Parapatric speciation in extinct Late Pleistocene rhinos

1. Wild animals and plants

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Abstract text: Three species of rhinoceroses survived into the Eurasian Late Pleistocene: the woolly rhino (*Coelodonta antiquitatis*), a typical element of the glacial mammoth steppe, as well as the closely related Merck's (*Stephanorhinus kirchbergensis*) and narrow-nosed rhino (*S. hemitoechus*) that roamed forested and savannah-like habitats, respectively, and were more widespread during temperate interglacial phases. Here were show that all three species were present in the Upper Rhine Graben in southwestern Germany in close spatial and temporal proximity during the middle of the last glacial (38-48ka; i.e., MIS3). Good DNA preservation enabled us to reconstruct 12 new mitochondrial genomes as well four medium-coverage nuclear genomes (5-13X), thus representing the first paleogenomic data of rhinos outside Siberia and the first data for the narrow-nosed rhino. Phylogenetic analyses revealed only limited support for a close relationship or recent divergence of Merck's and narrow-nosed rhino but strong signal of gene flow among all three species analyzed here. However, introgression tracts are small and indicate that gene flow was ancient. The short time between successive splits, divergence with gene flow among all lineages and the ecological differentiation among species (steppe tundra, forest, temperate savannah) suggest that the three extinct rhinos represent a case of parapatric speciation.

Phylogenetic Relationships Between Ancient and Recent Representatives of the Genus Vulpes in Siberia

1. Wild animals and plants

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Abstract text: Currently, paleogenetic research largely focuses on the domestication of dogs and the wolves' phylogenetic history. However, the genus Vulpes remains understudied, both in terms of its recent population structure and past evolutionary events. In our study, we focus on representatives of the genus Vulpes from Siberian and European Russia to contribute to filling this gap.

The study includes 55 recent red foxes from the Omsk region, the Sakha Republic, the Novosibirsk region, the Primorsky Krai; 4 recent corsac foxes from the Novosibirsk Zoo; 6 ancient specimens of corsac foxes, arctic foxes, red foxes from Siberia and European Russia. We constructed Illumina libraries from the isolated DNA of ancient and recent specimens. Then, we enriched both sets of DNA with target sequences in two steps. Using complete and partial mitochondrial genomes as markers, we compared ancient and recent representatives of the genus Vulpes and constructed phylogenetic reconstructions. This study provides the most comprehensive for this moment review of the Siberian red foxes' phylogenetics. We identified a distinct subclade among Yakut foxes and obtained the first mitochondrial genome of an ancient Siberian corsac fox with 99.6% coverage and the first mitochondrial genome of an ancient Southern Siberian arctic fox with 99.98% coverage.

Quid paleogenomics: Reconstructing Wild Plant-Based Consumption in Ancient Mesoamerica

1. Wild animals and plants

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Abstract text: Archaebotanical quids—chewed plant remains often recovered from archaeological sites—offer a unique and underexplored source of information on past plant consumption and human-plant interactions, acting as a unique window into ancient plant use and dietary practices. Through the generation of palaeogenomic data from quids (n=25) from different archaeological sites (n=4) and historical periods throughout Mesoamerica, we are revealing them to be rich reservoirs of diverse genetic material. Combining shotgun ancient metagenomic sequencing and cpDNA whole genome capture, we perform a comprehensive taxonomic characterization, identifying both wild and cultivated plant species and microbial communities associated with the samples. Combining ethnobotanical and anthropological knowledge, this approach allows for the identification of plants used for food, medicine, and ritual practices, as well as insights into the ecological interactions that shaped human-plant relationships. Aiming to reconstruct plant-based consumption patterns, and explore the co-occurrence of plant and microbial taxa, this research contributes to a broader understanding of ancient diets and offers new perspectives on the biodiversity of past Mesoamerican cultures.

Reconstructing genetic diversity changes in alpine conifer species since the Lateglacial through ancient DNA

1. Wild animals and plants

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Abstract text: Future climate change is expected to lead to large-scale range shifts, resulting in intraspecific biodiversity loss and impacting a species' ability to survive. Changes in the genetic diversity of long-lived species, such as conifers, are especially challenging to study via neoecological or modern genetic studies due to their limited temporal range. Another approach is to analyse ancient DNA preserved in natural archives coupled with palaeoecological vegetation reconstructions. This study aims to investigate the long-term changes in intraspecific biodiversity of four alpine conifer species: A*bies alba, Larix decidua, Picea abies,* and *Pinus cembra,* in response to postglacial climate changes in the Western Alps. We analysed Lac de Siguret, in the Durance Valley (French Alps), for pollen and macrofossils to reconstruct local vegetation dynamics since the Lateglacial. We also used ancient DNA extracted from macrofossils and *sed*aDNA to infer population dynamics and changes in intraspecific diversity. By integrating palaeoecological and molecular data, this research aims to illustrate the effects of past climate events on conifer genetic diversity. Understanding these long-term patterns will improve predictions of species responses to ongoing warming and provide valuable insights to support future conservation strategies and climate adaptation policies

RECONSTRUCTING POPULATION DYNAMICS OF THE EUROPEAN SARDINE (SARDINA PILCHARDUS) USING PALAEOGENOMICS

1. Wild animals and plants

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Abstract text: Overfishing has affected numerous marine species, reducing their effective population sizes to a fraction of their historical levels. Yet, reliable catch records are often lacking, our understanding of how these pressures shaped species' evolutionary trajectories remains limited. One of the most impacted species is the European sardine (Sardina pilchardus), a key pelagic resource in Atlantic waters and of major economic importance, particularly in Southern Europe and Morocco, where it is the primary target of purse-seine fisheries and a critical source of income for coastal communities. The species ranges from the southern Celtic and North Seas to Mauritania and Senegal, including the Azores, Madeira, and the Canary Islands, and is also abundant throughout the Mediterranean. Current populations form three genetic clusters: one from the Azores and Madeira; a second encompassing Iberian populations; and a third containing Mediterranean and Canary Islands, with Iberian sardines showing signs of admixture. In this study, we apply ancient DNA approaches to specimens from before intensive fishing and compare their genetic profiles with those of modern, post-exploitation populations. This enables to examine genetic continuity over time and compare levels of genetic diversity before and after exploitation—providing essential baselines for stock delineation, and fisheries management across FAO areas.

Reconstructing the genomic history of Ice Age grey wolves

1. Wild animals and plants

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Abstract text: Grey wolves survived the widespread large mammal extinctions of the late Pleistocene while maintaining a vast range across different climates in Eurasia and North America, and gave rise to the first species to fully adapt to an anthropogenic niche through domestication. Strong and widespread gene flow is thought to have contributed to the resilience of grey wolves, yet this striking connectedness is poorly understood. Here we generate new genomes for 45 ancient grey wolves, for a combined dataset of 133 palaeogenomes. Using a mitochondrial phylogeny, we estimate the ages of undated samples and extend the temporal range of wolf palaeogenomes into the Middle Pleistocene. We find evidence for several rapid genomic ancestry transformations across Holarctic wolves in the past hundred thousand years. By time-stratifying our dataset, we investigate the extent and directionality of gene flow between regions, as well as the geographic and temporal origins of dog ancestry. We also use a deep time series in the Altai Mountains to compare continuity and genomic diversity in northern and southern Siberian grey wolves. Overall, grey wolf evolution during the Late Pleistocene is characterised by strong gene flow and ancestry turnovers, likely contributing to the adaptation of grey wolves to changing environments.

Small mammal DNA from Kalavan-2 an open-air Middle-Paleolithic site in Armenia

1. Wild animals and plants

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Abstract text: Kalavan-2, is a unique open-air Middle-Palaeolithic site located at 1640 m above sea level in northeastern Armenia. It spans MIS-3, characterized by rapid climatic fluctuations and shifting steppe woodland mosaics. Recent multidisciplinary study of the site's chronology and deposition provides a rare opportunity to examine small mammal dynamics within a well-constrained chronological framework.

This study uses ancient DNA from twenty-two *Mesocricetus* (hamsters) at Kalavan-2 to refine species-level identification and explore the potential of high-elevation sites in the Armenian Highlands to preserve genetic signals of Late Pleistocene populations. Two species were identified (*M. brandti* and *M. auratus*), both with different ranges and/or lineage affinities in the present.

While Kalavan-2 layers are dated 60-50 to 35 kBP, the radiocarbon ages recovered for the hamsters in this study range from about 41,200 cal BP to over 50,000 BP. Lack of correlation between hamster dates and depth of the layer they were from, or between damage patterns and layer depth, contrasted with the agreement of age and damage, indicating hamster burrowing at this locality.

This study showcases how molecular approaches enhance the interpretive power of micromammal assemblages and contribute to broader questions of species resilience and biogeographic structure in Pleistocene mountain-steppe ecosystems.

The Balkan Brown Bear Project (BaBBe): Integrating Ancient DNA, Isotopes, and Archaeology

1. Wild animals and plants

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Abstract text: The brown bear (*Ursus arctos*) is an iconic megafaunal species that survived Late Pleistocene extinctions. Once widespread across Europe, its range has been drastically reduced through intensive hunting and large-scale habitat loss. Today, European brown bears persist in ten fragmented populations, three of which occur in the Balkans, with potential historical contact zones in Serbia. This project investigates the evolutionary history of Balkan brown bears over the past 50,000 years by integrating (paleo)genomic analyses with isotope biochemistry. Preliminary results from Holocene specimens in Serbia reveal unexpectedly high mtDNA diversity, suggesting that past genetic variation greatly exceeded that of present-day bears. To explore this further, we will analyse osteological material spanning the Late Pleistocene and Holocene and combine these data with genomic information from modern populations. This interdisciplinary framework enables reconstruction of temporal and spatial patterns of demographic change, ancestry, admixture, and migration patterns. Stable isotope measurements of bone collagen will provide insights into diet and ecology, while direct radiocarbon dating will establish a robust chronological context. Together, we aim to clarify how brown bears persisted in the region and to generate knowledge essential for understanding long-term population dynamics.

The project is funded by the National Science Centre, Poland (2024/53/B/NZ8/02682).

The evolutionary history of species from the subgenus Terricola, reconstructed on the basis of modern and ancient nuclear and mitochondrial genomes

1. Wild animals and plants

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Abstract text: The Late Pleistocene was marked by rapid climatic oscillations, with repeated shifts between cold stadials and warmer interstadials. These fluctuations strongly affected species distributions and population sizes, including small mammals. Environmental change drove migrations, colonization of new habitats, and local extinctions, shaping population structure and genetic diversity. Voles are an excellent model for such research because they are numerous, have short generation times, exhibit narrow ecological tolerances, and respond rapidly to environmental shifts.

This study aims to reconstruct key elements of the evolutionary history of Terricola voles (genus Microtus) in Southern Europe, from the Late Pleistocene to the early Holocene, using DNA from both ancient and modern samples. Previous research on other small mammal species revealed major demographic changes linked to climate fluctuations over the last 50,000 years. Our goal is to determine whether similar processes occurred in Terricola populations in the southern part of the continent.

Preliminary mtDNA cytochrome *b* data from Late Pleistocene specimens indicate the presence of species currently restricted to Southern Europe, implying major range shifts. The next step will be to reconstruct demographic history using Pairwise Sequentially Markovian Coalescent analysis of nuclear genomes from modern individuals to assess whether demographic patterns mirror observed range shifts.

The first late Pleistocene whole-genome sequences of North American wild sheep (Ovis spp.)

1. Wild animals and plants

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Abstract text: Oftentimes, evolutionary relationships can be impacted by missing lineages, *i.e.*, ghost lineages, a gap potentially filled by ancient DNA (aDNA). Here, we used whole-genome sequences (WGS) to study the evolutionary history of North American bighorn (*O. canadensis*) and thinhorn (Dall: *O. dalli dalli*; Stone: *O. d. stonei*) sheep. Our dataset included the first WGS for late Pleistocene wild sheep from the Yukon Territory, CAN (N: 6; >51-14 14C ka BP) and Wyoming, USA (N: 1; 47-2314C ka BP) as well as contemporary individuals. These WGS were filtered, and we obtained approximately 47-91% endogenous DNA for the Yukon samples and 11% for the Wyoming specimen. We then estimated genetic similarities, which suggested that the Wyoming fossil may represent a hybrid lineage between the bighorn and thinhorn clades. Given this finding, we estimated hybridization patterns using different methods. Our best-fitting model proposed that at least two missing lineages could have contributed to the Wyoming and Yukon fossils and Dall sheep clades. Therefore, we not only demonstrated the importance of using aDNA to detect missing lineages but also showed that these specimens were survivors of the last glacial cycle, providing new insights into their evolutionary history.

The immigration history and extinction dynamics of the Scandinavian aurochs (Bos primigenius).

1. Wild animals and plants

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Abstract text: This study presents a comprehensive analysis of the immigration history and extinction dynamics of the Scandinavian aurochs (Bos primigenius) during the Early Holocene, highlighting the intricate interactions among environmental, genetic, and anthropogenic influences. Utilising phylogenetic and palaeogenetic data, we trace its post-glacial colonisation from a Western European refugium, delimit the period of connectivity with the main European population, prior to the severing of the land bridge by rising sea levels. Genetic analyses further point to inbreeding and genetic drift, exacerbated by population bottlenecks and geographical isolation, diminishing resilience over time. Population modelling indicates a classic boom-bust pattern correlated with intensified human settlement, hunting, and resource exploitation. Despite environmental conditions permitting refugial persistence amidst increasing forest cover, subsequent habitat loss and human pressures accelerated demographic decline. Our integrated approach indicates that the extinction resulted from a synergistic effect of habitat fragmentation and degradation, genetic depletion, and prolonged anthropogenic pressures. These findings highlight the complex, multifactorial processes underlying species extinction and emphasise the importance of cross-disciplinary methods in palaeoecological research.

The Japanese Archipelago Sheltered Cave Lions, not Tigers, during the Late Pleistocene

1. Wild animals and plants

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Abstract text: Lions and tigers, as dominant apex predators, likely overlapped and competed after lions expanded from Africa into Eurasia about 1 Mya, forming a lion–tiger transition belt from the Middle East to the Russian Far East. At the eastern edge of this zone, the Japanese Archipelago has been considered a Late Pleistocene tiger refugium, supported by large felid subfossils traditionally attributed to tigers, though their taxonomic identity has remained uncertain. To clarify the origin and biogeography of Japan's Pleistocene felids, we analyzed 26 ancient specimens previously regarded as tigers. Using mitochondrial and nuclear genome hybridization capture sequencing, paleoproteomic analyses, Bayesian molecular dating, and radiocarbon dating, we found that these Japanese *Panthera* remains represent cave lions (*P. spelaea*), not tigers (*P. tigris*). One specimen was radiocarbon dated at 31,060 ± 190 BP. These cave lions likely dispersed to the Japanese Archipelago between ~72.7 and 37.5 Kya, when a land bridge connected northern Japan to the mainland. Our findings challenge the long-held view that tigers once took refuge in Japan, revealing instead that cave lions were widespread in northeast Asia during this period and were the *Panthera* lineage that colonized Japan, reaching even its southwestern regions despite habitats previously thought to favor tigers.

The Lost Kingdom: Palaeogenomics of the cave lion

1. Wild animals and plants

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Abstract text: The Eurasian cave lion (*Panthera spelaea*) was once widespread across the Northern Hemisphere but vanished during the Late Pleistocene megafaunal extinctions. Using 12 genomes spanning over 100,000 years, we show that cave lions and modern lions (*Panthera leo*) were distinct evolutionary lineages with separate demographic histories and unique adaptive genetic variation. We present the first genomic evidence of ancient gene flow between them, likely originating from a now-extinct Southwest Asian modern lion population. This admixture, linked to glacial cycles, reached up to 4% in a Central East Asian cave lion ~20,000 years ago. Our findings shed new light on the population dynamics and ecological legacy of one of the Pleistocene's apex predators.

The past informs the future - the impact of climate change on Aotearoa New Zealand's bird fauna

1. Wild animals and plants

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Abstract text: The impact of global climate warming on the biodiversity of isolated island systems is controversial. For example, Aotearoa New Zealand (NZ) has been identified as one of three global hotspots of projected climate-driven biodiversity loss, according to a recent study published in *Science*. In contrast, the "extinction filter" hypothesis predicts that island taxa, which have survived *in situ* throughout the severe cold-warm oscillations of the Pleistocene (2.6 Mya – 11 Kya), are unlikely to be driven to extinction by climate change alone. By integrating (palaeo)genomic approaches and state-of-the-art ecological niche modelling (ENM), we are testing these competing predictions and develop the foundations of a climate extinction-risk atlas for the NZ vertebrate fauna**.** Our first results for the NZ bird fauna suggest that while past environmental change was a major driver of biodiversity change in NZ, climate warming alone is unlikely to cause major biodiversity loss. Local threats such as introduced predators and non-climate driven habitat loss appear to be stronger predictors of extinction risk. The results not only highlight the use of palaegenomic approaches for informing conservation management but also contribute to our understanding of the impact of climate warming on islands globally.

Titans of the skies: Accipitrid palaeogenomes provide insight into rapid island gigantism

1. Wild animals and plants

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Abstract text: Aotearoa New Zealand (NZ) was home to a great number of outsized bird species. Among the most impressive of these are two iconic now-extinct accipitrids: kērangi Eyles' harrier (*Circus teauteensis*), 4-6x heavier than their sister species; and the titanic pouākai Haast's eagle (*Aquila moorei*), >15x heavier than their closest relatives. These raptors are remarkable in that they diverged from much smaller ancestral Australian forms around the same time in the early Pleistocene ca. 2.5-2.2 Mya, but they are not closely related to one another. These lineages therefore represent independent yet concurrent examples of rapidly evolving island gigantism. Here we present reconstructed paleogenomes of both Haast's eagle and Eyles' harrier with a view to interrogating the molecular basis of this astonishing evolutionary pattern. We apply phylogenomic and comparative genomic approaches to identify signals of selection across the genome, including at previously identified loci involved in determining body size. We ask if selection acted in similar ways on the two species and compare these molecular signals with other examples of island giants in NZ. This study represents an important molecular assessment of rapid macroevolutionary change and is our first look at the genomes of NZ's apex terrestrial predators.

Tracing cave bear population turnovers and East–West expansion through ancient genomes

1. Wild animals and plants

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Abstract text: Cave bears are among the most well-known Pleistocene species. Knowledge of their population dynamics in Europe is, however, almost entirely based on mitochondrial DNA. We analysed nuclear genomes from 21 individuals sampled across Europe and the Urals. In contrast to the mitochondrial phylogeny, the autosomal tree shows that bears assigned to *spelaeus* and *ingressus* form a clade that is sister to the *kanivetz* lineage, with *eremus* basal to this group. Within the *spelaeus-ingressus* radiation, we identify three major clades, all of which include Romanian individuals: two clades are exclusively Romanian, while the third comprises Romania together with all western European populations. Moreover, Romanian individuals from each respective clade are non-overlapping in time. This suggests multiple population turnovers potentially driven by migration pulses from the east. These time-dependent processes dominate the population structure of European cave bears, which is relatively weakly associated with geography by comparison. In contrast, gene-flow analyses consistently reveal admixture between geographically and temporally adjacent populations, even those currently regarded as different species. Together, the results indicate complex population dynamics involving repeated lineage turnovers and persistent gene flow throughout the evolutionary history of European cave bears.

Tracing the Hidden Stories of Wild Animals and Plants through Ancient DNA

1. Wild animals and plants

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Abstract text: Title: Tracing the Hidden Stories of Wild Animals and Plants through Ancient DNA **Abstract**:Wild animals and plants carry hidden stories in their DNA, stories that reach far beyond living memory. Ancient DNA allows us to open this record and see how species survived, moved, and changed over thousands of years. This study explores genetic remains from animals and plants that lived during past climate shifts. By comparing ancient and modern DNA we see patterns of loss, survival, and adaptation. Some animals show how they moved to new lands when conditions became harsh. Some plants reveal how they kept genetic traits that helped them survive dry or cold periods. Together these findings show that ancient DNA does not only speak of the past but also teaches us about the future. Understanding how wild species adapted before can guide us in protecting them now at a time when nature faces great pressures from climate change and human activity. **Keywords**: Ancient DNA, wild animals, wild plants, evolution, climate change

Tracing Vaccinium uliginosum lineages through time and space using multiplexing PCR

1. Wild animals and plants

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Abstract text: Population level data has been challenging to obtain from sedimentary ancient DNA (*sed*aDNA) due to either a low taxonomic resolution of the method used, or by being limited in the reference material or template DNA. Multiplexing different markers together provides an efficient method for the recovery of population level genetic data from *sed*aDNA. *Vaccinium uliginosum* has a circumpolar distribution with several distinct populations and is frequently detected in *sed*aDNA studies. Here, we apply six multiplex markers targeting known intraspecific plastid regions to reconstruct the *V. uliginosum* population over time and space. A total of 129 sediment samples have been processed, from 31 locations, spread across Europe, with a strong focus on northern Scandinavia and the Alps. Up to five samples were selected per location, temporally spread across the Holocene in order to identify the populations present and potential changes. All markers could be successfully amplified. The majority of the samples had one dominant population present, but co-occurence of different populations could be observed in some samples. The multiplexing method enabled large-scale palaeo-phylogeographic reconstruction at a low cost and is a promising method for other taxa.

Unlocking paleogenomic insights from plant macrofossils preserved in ice caves

1. Wild animals and plants

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Abstract text: Ice caves act as natural traps for plant remains offering valuable but largely unexplored archives for paleogenomic research. Their frozen conditions can provide ideal settings for the preservation of plant macrofossils and their endogenous ancient DNA (aDNA). Analyses of aDNA from plant macrofossils can provide insights into the evolutionary history and the factors that have shaped their current genetic diversity.

This study analyzes aDNA from Holocene plant macrofossils recovered from ice caves across the central and southern European mountain ranges. Our aim is to assess whether past populations experienced shifts in genetic diversity and how these patterns relate to those of present-day populations. Extracted aDNA was incorporated into single-stranded DNA libraries and shotgun sequenced. Preliminary results show successful recovery of endogenous aDNA from two target species: *Dryas octopetala* yielded over 30% endogenous DNA with a mean nuclear genome coverage of ~2x, while *Pinus uncinata* yielded up to 15% endogenous DNA with a mean nuclear genome coverage of ~0.06x. The samples show damage patterns, supporting their suitability for subsequent paleogenomic analyses.

This research highlights the value of ice cave archives, which may vanish in a warming future, and underscores their potential to improve predictions of future ecosystem responses to environmental change.

Unraveling the Evolutionary History of Arctic Marine Mammals: From Prey to Top Predator

1. Wild animals and plants

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Abstract text: The Arctic is currently the fastest-warming region on Earth, with sea ice projected to decline by up to 94% by 2050. By losing their habitats, ice-associated marine mammals are highly vulnerable to changes in sea ice conditions. Historically, Arctic ecosystems have experienced dramatic shifts in sea ice cover and sea level during the Late Quaternary. Yet, how climate change has affected Arctic marine mammals on a long-term scale is still not well understood.

Covering from prey to top predators, we collected more than 100 ancient marine mammal specimens, including ringed seals (*Pusa hispida*), beluga whales (*Delphinapterus leucas*), bowhead whales (*Balaena mysticetus*), and polar bears (*Ursus maritimus*). Genomic data from museum samples collected across the circum-Arctic and dated from the late Pleistocene to the Holocene were recovered using whole-genome shotgun sequencing and mitochondrial capture, providing a broad temporal and geographic range.

By integrating stable isotope analyses, we aim to reconstruct changes in gene diversity and evolutionary dynamics across the last glacial-interglacial cycles. This work provides one of the few ancient studies of the Arctic marine mammals, and may provide valuable insights for understanding how global warming and diminishing Arctic sea ice might impact future marine mammal conservation efforts.

Where Did You Come From, Where Did You Go? The Origin of the Norwegian lemming

1. Wild animals and plants

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Abstract text: The Norwegian lemming (*Lemmus lemmus*) is a small rodent endemic to the Fennoscandian tundra. The species likely evolved during the Late Pleistocene, although its exact origins remain unclear. Interestingly, previous research based on short mitochondrial markers has suggested that the species may have survived the Last Glacial Maximum in a local, ice-free refugium within Fennoscandia, from which it subsequently expanded. In this study, we generated eight high coverage whole genomes as well as 15 additional mitogenomes from Late Pleistocene and Early Holocene lemmings of the genus *Lemmus*. These samples were analysed together with modern whole genomes from *L. lemmus*, *L. sibiricus*, *L. paulus*, *L. amurensis*, and *L. trimucronatus*. We use a combination of phylogenetic and population genomic methods to investigate the evolutionary history of the Norwegian lemming, and to test the hypothesis of a local survival of the species during the last ice age. Furthermore, we identify species-specific genomic differences between *L. lemmus* and its sister species *L. sibiricus*, to determine highly evolved genes and genes under positive selection in the Norwegian lemming.

Wild vs domesticates: A Paleogenomics Perspective on the evolution of the Bovina

1. Wild animals and plants

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Abstract text: The aurochs occupied a prominent and long-standing place in the imaginary of hunter-gatherers, as seen in cave and wall paintings as well as sculptures from the Paleolithic to the Neolithic. It was a dangerous hunting target that led to its particular role in Paleolithic and early Neolithic societies. It was gradually domesticated during the early Neolithic in South West Asia, leading to a diversification of the resources it contributed to humans. The Neolithic migrations into Europe reconfigured the population structure of both humans and the species they domesticated. We have reconstituted the population dynamics of aurochs and its non-domesticated sister species, the bison, around the Mediterranean over the last 50,000 years using paleogenomic analyses of hundreds of archaeological bones. We identified the impact of environmental and climatic fluctuations on wild bovine populations at the onset of domestication that blurred the genetic consequences of the domestication process. We will discuss our results as well as the impact of the gene flow between the wild and early domesticate populations, which seems to have been a prominent evolutionary driver during the Neolithic.

Yak X: an archaic bovine from Denisova Cave

1. Wild animals and plants

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Abstract text: An extinct and previously unknown bovine mitochondrial lineage was recently identified at Denisova Cave and in the broader mid-latitude Asia (Gilardet & Oppenheimer, 2025). Although this new clade X fell sister to all known modern yak (*Bos mutus*) diversity, bovine species are characterized by complex evolutionary histories involving incomplete lineage sorting and/or ancient admixtures. Now, analysis of nuclear paleogenomes has confirmed that both the yak X mitochondrial and nuclear lineages fall sister to the modern yak. Similarly, molecular dating based on both mitochondrial and nuclear data has shown a deep split between yak X and its modern yak relatives, at around 675,000 years ago. Preliminary gene flow analysis has suggested that the yak X was its own evolutionary unit over around 200,000 years. Demographic reconstructions have pointed at a possible bottleneck around the Eemian interglacial, although only a slight loss of heterozygosity was observed between genomes pre- and post-Eemian. Taken together, these results suggest the discovery of a new extinct megafaunal species, which might correspond to the Baikal yak, a species only described morphologically in the archeological record.

2. Humans

A fine-grained assessment of migration into Ireland from the Early Bronze Age onwards

2. Humans

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Abstract text: The end of the Neolithic in western Europe was marked by major demographic change and the introduction of Indo-European languages. In the Rhine region, the emergence of Bell Beaker culture is associated with a large influx of steppe-related ancestry, likely derived from Corded Ware populations further east. The spread of Bell Beaker culture into Britain is estimated to have led to a long-term 90% population replacement, with further migratory influxes to the island identified across the Bronze and Iron Age, providing candidate windows for Celtic language entry. However, little is known of how the neighbouring island of Ireland absorbed steppe-related ancestry and Indo-European languages through time, with only three Bronze Age genomes from the northeast published thus far. Here we present over 50 new shotgun sequenced genomes from the Early Bronze Age onwards. Through haplotype-based admixture modelling, we characterise ancestry contributions from Britain and the continent through time, as well as the earlier Neolithic population. This reveals Ireland to have its own unique trajectory after the initiation of the Bronze Age, including long-term survival of local Neolithic ancestry. Using IBD segments, we further uncover fine-grained mobility networks between archaeological sites in Ireland, Britain and the continent.

A genetic bridge over the Gulf of Finland: tracing the origin of genetic connectedness between Finns and Estonians

2. Humans

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Abstract text: The Finnish population is a unique example of a genetic isolate affected by a recent founder event. Previous studies have suggested that the ancestors of Finnic-speaking Finns and Estonians reached the circum-Baltic region by the 1st millennium BCE. However, high linguistic similarity points to a more recent split of their languages. We set out to study genetic connectedness between Finns and Estonians directly.

In a study published in 2021, we searched for long shared allele intervals (LSAIs; similar to identity-by-descent segments) in unphased data for >143,000 present-day Estonians, 99 Finns, and 14 imputed ancient genomes from Estonia. We found unexpectedly high levels of individual connectedness between Estonians and Finns for the last eight centuries, contrasting their clear differentiation by allele frequencies.

Here, to shed more light on the origins of the connectedness between Estonians and Finns, we extracted and sequenced ancient DNA from 16 additional prehistoric individuals from Estonia dating to 1,400 BCE to 700 CE, including the first genomes from 300–700 CE. We show that already the 300–700 CE individuals had higher levels of individual connectedness with modern Estonians and Finns than individuals from earlier time periods, including preceding individuals from 600–100 BCE.

A paleogenomic history of Colombia's eastern highlands

2. Humans

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Abstract text: The Sabana de Bogotá in Colombia's eastern Andes has a rich archaeological record spanning from late Pleistocene hunter-gatherers to Muisca chiefdoms. We generated genome-wide data from 209 early–middle (10,000–7,000 BP), middle (7,000–4,000 BP), and initial late Holocene (4,000–2,500 BP) hunter-gatherers and agriculturalists from the Herrera (2,200–1,300 BP) and Muisca (1,200–500 BP) Periods, co-analyzed with 21 previously-published individuals. We document genetic continuity among hunter-gatherers over five millennia with structure reflecting drift in small populations without detectable external gene flow. A ~2,800 BP individual has ancestry consistent with earlier hunter-gatherers but a C_4-based isotopic signature, providing evidence that tropical crop agriculture – mainly maize – was adopted by local groups prior to a demographic turnover whose timing could not previously be identified due to a 4000-year sampling gap. We show that the emergence of Herrera culture corresponds to a sharp genetic break reflecting migration into the Sabana de Bogotá that largely replaced earlier populations. The incoming population descended from a mixture ~4,000 years ago between groups related to lower Central American Chibchan speakers and populations from the Amazonian–Andean interface. During Herrera and Muisca periods, we detect north–south genetic substructure consistent with cultural differentiation between regions.

A Seven-Generation Lineage Reveals Zhao-Mu system and Commoner Social Organization in Ming–Qing Northern China

2. Humans

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Abstract text: As the foundation of ancient social organization, kinship shaped the layout of cemeteries and the conduct of funerary practices. The spatial arrangement of individuals reflected not only biological relatedness but also their social roles and hierarchical positions. Reconstructing kinship among ancient individuals provides essential insight into past social organization. Here, we present an interdisciplinary study of the Lizui family cemetery, located on the Grand Canal in northern China and dating to the Ming–Qing period (14th–18th centuries CE). Ancient genomic data from 79 individuals reveal a seven-generation pedigree organized along patrilineal lines, representing the largest and most complete East Asian lineage reconstructed from ancient DNA. The Lizui lineage exhibits clear patterns of patrilocal residence and female exogamy. Integration of mortuary patterns with genomic evidence highlights axial layouts, generational distinctions, and the hierarchical placement of male kin and female spouses, reflecting ritual norms and mechanisms reinforcing lineage continuity, inheritance, and hierarchy. These findings reconstruct a rural clan genealogy, providing genetic corroboration of the hierarchical structure of the clan (the Zhao-Mu system) recorded in historical sources. Our study further illuminates the social organization of canal-side villages, showing how kinship, marriage, and ritual practices maintained cohesion within families and the wider community.

Ancient DNA from birch tar artefacts: insights into population structure and gendered practices in Neolithic Alpine Europe

2. Humans

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Abstract text: Birch tar is emerging as an alternative source of ancient DNA, particularly in archaeological contexts where human remains are scarce or absent. As part of the *AlpGen* project, we have screened over 100 birch tar artefacts from Neolithic Alpine lake settlements to assess their potential for biomolecular analysis. In a region where skeletal material is largely lacking, birch tar provides a unique archive through which ancestry, population structure, and genetic relationships between communities can be explored. Many artefacts contain enough ancient human DNA for genetic sex determination, enabling new approaches to studying gendered practices in the production and use of birch tar. The recovered DNA also allows us to investigate ancestry and population structure among lake-dwelling groups, shedding light on the genetic makeup of Neolithic Alpine communities. The presence of oral microbial DNA helps identify chewed tar and supports the reconstruction of oral microbiome composition and past oral health, offering a potential alternative to dental calculus. In this paper, we present initial findings from *AlpGen,* showing that birch tar can preserve ancient biomolecules at a scale suitable for population-level research. These results underscore its value as a biomolecular archive for understanding the genetic and cultural landscapes of prehistoric Europe.

Ancient DNA from Jamestown Settlement Reveals Early European Migration Dynamics in the Colonization of North America

2. Humans

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Abstract text: The Jamestown settlement in Virginia (USA) represents the first permanent English settlement in North America. We analyze ancient DNA from 19 individuals from the 1607 Burial Ground to understand migration structure and population history at the nexus of European colonization of North America. To investigate ways of increasing genomic coverage and variant calling rates for these poorly preserved archaeological individuals, we implemented a multimethod enrichment strategy, dividing each library for either shotgun sequencing, whole genome enrichment, and 1240K enrichment. This combined approach improved data recovery rates relative to shotgun sequencing or single-enrichment methods. After filtering for contamination and damage patterns, we generated seven low coverage genomes (0.08-3.12X) and one mitogenome (1.27X). We impute genotypes for higher coverage samples to inform population affinity within Europe. All individuals were male and affiliated with contemporary European populations. Uniparental mtDNA and Y-chromosome analyses showed distinct lineages that are also found in contemporary European populations. We identified second degree relatedness between two sets of burials, suggesting that distant kin networks may have impacted migrant recruitment in England. Our analysis places the ancestry of these settlers in the context of regional British Isles variation and samples from later waves of English migration to the Chesapeake region.

Ancient DNA reveals Iron-Age gene flow from Eastern Baltic and long-standing East–West genetic structure in Finland

2. Humans

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Abstract text: The population of present-day Finland has unique characteristics within the European genetic landscape: both Finns and Saami carry signatures of small population sizes and Siberian-related ancestry. Additionally, Finns show a pronounced East-West substructure. However, ancient DNA research in Finland and nearby regions has been challenging due to poor skeletal preservation, with the oldest uncremated human remains dating only to the turn of the Common Era.

Here, we present genome-wide data from 140 ancient individuals from regions of present-day Finland, Karelia, and Ingria, spanning the last two millennia. We find evidence of gene flow from the Eastern Baltic to Finland in the first centuries of the Common Era, followed by admixture with a genetically Saami-like population. Furthermore, our data suggest that Saami-like ancestry was present along Finland’s western coast, at least sporadically, until the Late Iron Age. Overall, the western coastal region experienced repeated genetic shifts throughout the Common Era, likely reflecting migration events to, and within, Finland. In contrast, the central and eastern regions show evidence of long-term population continuity. Finally, we demonstrate that the East–West genetic division characteristic of present-day Finns was already established in the early medieval period across the permanent settlement zone of southern Finland.

Ancient Genomes from the Western Zhou Dynasty Illuminate Millennia of Population Dynamics in the Yellow River Basin

2. Humans

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Abstract text: The Yellow River basin, a core region in the formation of early Chinese civilization, underwent profound sociopolitical and demographic transformations from the Late Neolithic through the Bronze Age. Yet the genetic impact of these processes, particularly under early state institutions, remains insufficiently understood. Here we generate genome-wide data from 32 individuals from the Western Zhou–period Dong'an site in Zouping, Shandong. The data reveal a patrilineally organized cemetery, within which practices including polygyny or remarriage after spousal loss occurred. Close-kin unions were rare, consistent with historical prohibitions against marriage between individuals sharing the same surname. Population genetic analyses show that the Dong'an individuals primarily inherited their ancestry from local Late Neolithic groups, who themselves had incorporated southern gene flow beginning in the Middle Neolithic. This ancestry profile persisted into the historical period, with limited subsequent gene flow. During the Western Zhou, genetic heterogeneity both between and within the middle and lower Yellow River regions suggests that the political geography of enfeoffment territories intersected with patterns of population structure. More broadly, interactions among regional populations were longstanding and accompanied by a trend toward increasing genetic homogenization, which intensified during the Middle to Late Neolithic and broadly coincided with periods of climatic fluctuation.

Ancient Genomes Reveal the Diverse Regional Origins of the Mary Rose Crew

2. Humans

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Abstract text:
The English warship *Mary Rose*, Henry VIII's flagship, represents a period when England was expanding and strengthening its naval power. During a battle defending the realm against a French invasion, she capsized and sank near the Isle of Wight in 1545, with a crew of around 500. The wreck was discovered in the Solent in the 1960s and subsequently excavated. Despite extensive historical and archaeological research, the regional origins of her crew, important for understanding Tudor naval recruitment, have remained unresolved.

To address this, we investigated the geographic origins and genetic composition of the crew using archaeogenomic analysis. We generated genomic data for 19 crew members recovered from the wreck and applied state-of-the-art methods, including genotype imputation and Identical-by-Descent (IBD) analysis.

Our results show that the *Mary Rose* crew originated from diverse regions across England. Fine-scale ancestry profiles, supported by IBD segments shared with present-day counties within the British Isles, demonstrate that we can pinpoint the crew's regional origins with high precision. Isotope analyses further corroborate the genetic evidence for their diverse backgrounds.

This study highlights the unprecedented genomic resolution achievable for the *Mary Rose* crew and provides new insights into naval organisation, mobility, and recruitment practices in Tudor England.

Ancient genomes uncover the spatiotemporal dynamics of adaptive evolution in Neolithic East Asia

2. Humans

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Abstract text: Farming introduced a host of selection pressures related to diet and pathogen exposure. At least two origins of agriculture stemming from rice and millet have occurred in East Asia, yet previous studies of selection have focused primarily on ancient genomes from Europe. Thus, we assembled a large dataset of published ancient and present-day genomes from East Eurasia (N=1771) to reconstruct the evolutionary histories of adaptive loci. We detected new selection candidates in our logistic regression-based selection scan, including *TMEM229B* which is involved in macrophage activation ($P=2.03 \times 10^{-6}$). Our analysis resolved longstanding questions about the timing of selection at known loci. Selection on the *FADS1*/*FADS2* derived haplotype involved in fatty acid metabolism began prior to the Neolithic (15,982 yBP), in contrast to hypotheses that suggested selection driven by agriculture. For the strongest signal of selection, a missense variant of *ADH1B* that accelerates ethanol oxidation, selection started at 5,652 yBP, considerably after the beginning of rice domestication in China (11 kyBP). Furthermore, we reconstructed the allele frequency spread of the *ADH1B* adaptive allele based on a spatiotemporal diffusion model and found support for the hypothesis that the source of this spread was concentrated around the lower Yangtze River where rice farming began.

Ancient human epigenetics: a deep time approach to aging and osteoporosis

2. Humans

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Abstract text: Bioarchaological research typically focuses on analyses of the skeletal remains, but ancient DNA (aDNA) has occupied an increasing role in exploring questions about the past. Recently, aDNA research has begun to include studies of ancient epigenetics, considering that modifications such as DNA methylation can contain key information about the life course. Modern forensic studies are already using methylation-based methods to estimate key information like age-at-death, supporting the necessity of exploring new techniques for age estimation specifically and the overall strength of this approach for postmortem populations. This project aims to demonstrate the bioarchaeological utility of methylation patterns and provide additional evidence for the feasibility of bisulfite sequencing. To accomplish this, samples from the Maxwell Museum Documented Collection were treated using an optimized bisulfite sequencing method and then enriched for loci associated with aging and osteoporosis risk - two areas where bioarchaeological methods struggle. Preliminary results from enrichment will be presented, demonstrating an approach for direct measurement of specific CpG sites with bisulfite sequencing while minimizing strand breakage and loss of data. Future directions will be discussed, including generating a chronological age estimation algorithm from methylation data with improved precision compared to current osteological methods.

Archaeogenetic analysis sheds light on genomic substructure and kinship practices of Xianbei nobles from the Yihe Nur site

2. Humans

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Abstract text: The Xianbei confederation was the most powerful among the many historically documented nomadic groups. It played a pivotal role in the political, military, and historical landscape of ancient and even the broader Eurasian region. Recent studies on the Xianbei have shed light on Xianbei commoners' origins and migration patterns. However, the genetic structure of Xianbei nobles and their kinship relationships remain insufficiently understood. This represents the first recovery of ancient genomic data from the Xianbei nobles. New genomic data were also retrieved from an individual associated with the Liao Dynasty, excavated at the same site. We found that the Xianbei nobles generally carried ancestry components associated with early Xianbei populations. However, one female noble exhibited a predominant genetic profile derived from Central Plains populations, with a minor contribution from early Xianbei ancestry, suggesting potential population interactions and genetic influences between Xianbei nobles and other East Asian groups. We also identified a parent-child relationship among the Xianbei nobles, who were buried in close proximity, implying that genetic kinship may have played a role in shaping Xianbei funerary practices. An individual from the Liao Dynasty exhibited significant genetic affinity with agricultural populations during the period from the Xianbei to Liao Dynasty.

Archaeogenetic data reveals genetic diversity and social dynamics in the Greek colony of Empúries (northeast Iberia)

2. Humans

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Abstract text: Empúries (Girona, Spain), in northeast Iberia, marks the western edge of Greek colonial expansion in the Mediterranean and later became one of the main entry points of Rome into the Iberian Peninsula. This dual historical role makes it a key enclave for investigating Greek and Roman colonial and imperial dynamics in Iberia. While over a century of archaeological research has clarified its urban development and funerary landscapes, only recently have genomic data begun to refine our understanding of population composition, mobility patterns, and kinship, which are crucial for reconstructing the social dynamics and everyday life of the settlement. Here, we assembled genome-wide data from 64 individuals from Empúries dated from Late Archaic to the Roman periods and including three main sub-urban necropolises and a few intra-mural burials. Preliminary results show a high diversity of ancestral origins since the earliest period, with indigenous Iberians as the major group inhabiting the city, but with significant contributions of Greek, Gallic, Italic and North African ancestries. The identification of close familial relationships spanning distinct ancestral backgrounds provides an unprecedented window into social dynamics and reveals processes of mixing between Greek settlers and local Iberian communities, who adopted imported cultural elements while preserving long-standing traditions.

Archaic Introgression in ancient Eurasians

2. Humans

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Abstract text: Archaic introgression, the DNA inherited from archaic humans, has been an important source of variation for the adaptation of modern humans outside sub-Saharan Africa. Despite its significance, most of our knowledge comes from analyses of genomes belonging to present-day individuals, while only limited insights have been obtained from the large datasets of ancient genomes available so far.
When, and through how many events, modern humans encountered and admixed with Neanderthals and Denisovans remains an open chapter in our evolutionary history. Equally unresolved is how archaic introgression influenced past human adaptation and how these inherited regions evolved within modern genomes.
Imputation using a panel of present-day individuals is known to be a valuable way to improve ancient DNA quality. It has recently been shown to be highly effective at recovering genotypes within archaic introgression regions, thereby improving our ability to identify introgressed segments in the genomes of ancient individuals. We applied this approach to investigate a dataset of nearly two thousand ancient individuals from Eurasia. Our preliminary analyses reveal spatial and temporal patterns of archaic introgression across the continents and highlight genomic regions of archaic origin that appear to be over-represented in specific ancient populations.

Archaic introgression in pre-European contact Americas

2. Humans

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Abstract text: When the North American ice sheets melted around 17 ka, small groups of humans emerging from Beringia dispersed rapidly across the Americas, reaching South America in a remarkably short time. These founding populations, adapted to the extreme Arctic environment for thousands of years, were suddenly exposed to a wide range of novel environmental conditions. How they adapted to these new environments in such a short time remains unclear.

One potential source of genetic variation that may have facilitated their rapid adaptation is archaic introgression, the genomic regions inherited from Neanderthals and Denisovans during earlier admixture events outside Africa. Understanding how much archaic ancestry was carried into the Americas, and whether these regions contributed to adaptation during the peopling of the continents, remains an open question.

To address these questions, we reconstructed archaic introgression patterns by directly analysing ancient genomes belonging to pre-European-contact individuals. We built a dataset of available shotgun genomes and imputed their genotypes. After assessing imputation accuracy on high-coverage ancient genomes, we inferred global and local archaic ancestry across time and space in both North and South America. Our results reveal patterns of archaic ancestry in the Americas before European colonisation and lay the groundwork for future investigations.

Assessing biases in local ancestry inference of imputed ancient DNA

2. Humans

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Abstract text: Local ancestry inference is used to study demographic history and selection in admixed populations. The growing availability and quality of ancient DNA now allows these approaches to be applied to ancient populations. We benchmarked six local ancestry inference methods on 176 imputed genomes from European Neolithic farmers – an admixed population of hunter-gatherers and migrating Anatolian farmers. All methods systematically overestimate hunter-gatherer ancestry (0.33–0.44 vs qpAdm 0.20), though individual-level estimates are highly correlated (R>0.85). Methods differ in sensitivity to sample size, unlike analyses of present-day data, where proportions are robust. Inferred local ancestry tract lengths vary across methods, leading to differing admixture time estimates (TRACTS: 5-50 generations). Of all methods tested, only RFMix produces a plausible tract length distribution (11 generations). Because the correlation between the location of ancestry tracts across methods is low, we combined calls across methods to identify four genomic regions with consistent ancestry deviations (Z>3) and replicated in an independent dataset. These include increased hunter-gatherer ancestry at the HLA and increased farmer ancestry at *FADS1* and *SLC24A5*. Our results demonstrate that choice of local ancestry inference method substantially affects inferred ancestry patterns and demographic interpretations, highlighting potential and limitations of these approaches for ancient DNA analyses.

Beachy Head Woman: clarifying her origins using a multiproxy anthropological and biomolecular approach

2. Humans

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Abstract text: The skeletal remains of an individual colloquially referred to as Beachy Head Woman (BHW) were re-discovered in the Eastbourne Town Hall collection in 2012, and have remained the subject of significant public interest since. Radiocarbon dating yielded a calibrated date of between 129 and 311 calCE indicates that she lived during the period of the Roman occupation of Britain and, over more than a decade, there have been several attempts to unravel her geographical origins and ancestry. Initial osteological analyses indicated possible sub-Saharan origin, with BHW thus presented as one of the earliest British-Africans. However, her story was complicated by subsequent suggestions that she had recent European ancestry. Here we present high quality ancient DNA data indicate that Beachy Head Woman has a strong genetic affinity to individuals from rural Britain during the Roman occupation and modern day Britons. We find no signals of admixture that would suggest recent sub-Saharan ancestry. Phenotypic predictions suggest she had blue eyes, intermediate (between pale and dark) skin pigmentation and light hair. Combined, our multiproxy approach indicates that Beachy Head Woman was of local British ancestry.

Bio-Archives of the Early Islamic Site of Nahal Omer: Recovering Ancient Human DNA from Stained Desert Textiles

2. Humans

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Abstract text: This research presents the first results of human ancient DNA extraction and sequencing from stained archaeological textiles. A recently discovered assemblage of worn, cut, and stained textiles (cotton, linen, wool) was found in-situ in a refuse mound at the early Islamic desert site of Nahal Omer (c. 7th–10th centuries CE). Located along a lesser-known artery of the Silk Roads in the Arava, these items provide a powerful entry point for investigating the nomadic or semi-nomadic individuals who interacted with the material and left remnants of their actions embedded in the threads. Testing the stain itself offers a rare opportunity to begin addressing innovative questions related to intimate aspects of daily life and identity in desert communities. This study further establishes stained archaeological textiles as valuable bio-archives, demonstrating both the feasibility and the interpretive potential of recovering ancient DNA from organic materials preserved in an arid desert environment.

Conflict and Convergence: The Archaeogenetic Legacy of Medieval Islamic Iberia

2. Humans

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Abstract text: During the medieval period, the Iberian Peninsula was a melting pot of diverse cultures, religions, and ethnicities, shaped by the Islamic conquest in the 8th century and the subsequent establishment of Al-Andalus. This era saw the arrival of Arab, Berber, and other North African populations alongside existing Hispano-Roman, Visigoth, and Jewish communities, fostering significant scientific, artistic, and intellectual advancements. The fragmentation of the Umayyad Caliphate in the 11th century led to the rise of smaller Taifas, and as Christian kingdoms expanded southward during the Reconquista, the region's demographic and cultural landscape evolved. Today, traces of North African ancestry persist in modern Iberian populations, reflecting centuries of interaction and migration.

We investigate the genetic patterns of medieval Iberia, focusing on the interactions between the Islamic and Christian realms. By combining ancient genomic data with historical and archaeological evidence, the research will explore population mixing, migration, and the genetic impact of the Islamic conquest. The interdisciplinary approach integrates genomics with historical and archaeological data to provide deeper insights into the demographic and genetic processes that shaped the region's past and present.

Contact with Archaic humans and Paleolithic origins of East Asians

2. Humans

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Abstract text: Multiple diverse human lineages coexisted in East Asia by ~10,000 years ago. However, the exact origins of East Asians in the Upper Paleolithic remain largely unclear, due to the limited number of genomes sequenced to date during this time period. This period also marks the contacts between East Asians and Denisovans, a deeply diverged homo lineage that used to be widespread across Asia, while this contact history remains obscure.

We performed local ancestry inferences at the haplotype level using more than 100 ancient genomes, representing diverse basal East Asian lineages spanning the last 40,000 years, along with 4000 present-day genomes as a worldwide comparison panel. We find that a modern human group had met at least two different Denisovan groups when they arrived in Northeast Asia by 40,000 years ago. We demonstrate that some lineages in East Asia derived elevated levels of Denisovan ancestry compared to most others, indicating a complex contact history with Denisovans. In contrast, a lineage that the present-day Japanese partially derived from almost missed those contact events. We then jointly model archaic introgression and population admixture, providing insights into human dispersals to and within East Asia during the Paleolithic.

Crossing the Sea: a paleogenomic perspective on the main Italian islands

2. Humans

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Abstract text: The Mediterranean and its largest islands have always played a key role in the peopling processes and cultural shifts that have shaped Europe over the centuries and millennia. However, their contribution to the genetic history of this area still requires further investigation. This is the context for the PRIN2020 "Crossing the Sea" project, which is mainly aimed at reconstructing the genetic history of the main Mediterranean italian islands from the Upper Palaeolithic onwards, through the analysis of ancient and modern genomic data using a multidisciplinary approach.
The paleogenomic analyses involved more than 260 ancient individuals from Sicily and Sardinia so far, of whom 56 were selected, based on their molecular preservation, and yielded whole genome data with a mean coverage between 0.1x and 5.3x.
Starting from Sicily, different computational approaches such as pseudohaploid genotyping and genotype imputation methods were applied according to the genome coverage. Subsequent analyses including principal component, admixture, IBD and genotype likelihood based demographic modelling were performed or are in progress.
The results so far produced made it possible to outline the genetic history of Sicily and to compare the evidence obtained with what happened in the past in the Italian peninsula as well as in Europe.

Detecting DNA methylation changes separating humans from nonhuman African apes

2. Humans

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Abstract text: Human lineages, including anatomically modern and archaic humans such as Neanderthals and Denisovans, exhibit notable morphological and behavioral differences from nonhuman African apes like chimpanzees and gorillas. As regulatory changes are thought to be a major driver of phenotypic divergence, we sought to identify such regulatory changes along the lineage leading to humans since the split from chimpanzees. Given that DNA methylation serves as the best proxy for gene expression in ancient samples, we compared methylation maps across modern humans and nonhuman African great apes, alongside DNA methylation reconstructed from ancient DNA of anatomically modern humans (AMHs) and archaic humans.

We experimentally generated whole-genome DNA methylation maps from bones of a gorilla, two chimpanzees, and six present-day humans, supplemented by reconstructed methylation profiles from a Neanderthal, a Denisovan, and 28 high-coverage AMH samples. Applying stringent and conservative filtering criteria, we identified over 350 differentially methylated regions (DMRs) distinguishing humans from nonhuman African apes. These DMRs are most significantly enriched in pathways related to heart formation and function, as well as bone remodelling.

Diversity of uniparental markers provide insights into sex biased admixture in colonial Mexico

2. Humans

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Abstract text: The colonisation of the Americas, 500 years ago, was one of the last major population clashes resulting in a significant demographic and cultural change. The recent quincentenary in today´s Mexico highlighted the need to reevaluate how colonial history has been narrated. The process of mestizaje (admixture) assumes a simplistic narrative of a mix of European men and indigenous women, ignoring the contribution of African populations. Here, we focus on the impact of this event in Mexico City, formerly the City of Tenochtitlán, ruled by the Mexica Empire. We present mitochondrial and Y chromosome data from 94 and 43 individuals, respectively, spanning Prehispanic and colonial populations from the Basin of Mexico to estimate diversity of uniparental markers and to get insights into sex biased admixture. Our results show an increase of European Y chromosome lineages in the XVIIIth century, with little presence in the early colonial period, proposing that the admixture was, potentially, not as immediate as previously suggested.

From Grave to Genome: Archaeogenomic Perspectives on the Post-Byzantine Population of Poros, Heraklion, Crete

2. Humans

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Abstract text: Due to its strategic location in the Mediterranean, Crete has diachronically served as a crossroads of populations. This study presents the first archaeogenomic data from the post-Byzantine cemeteries in Poros (Heraklion) and Doliani (Ioannina). Its aims are to investigate the social dynamics reflected in the Poros burial assemblage and to explore the genetic affinities of both groups with other populations across time and space, using published archaeogenomic data. The analysis revealed no close genetic kinship among Poros individuals, nor shared mitochondrial or Y-chromosomal haplogroups, indicating a high degree of heterogeneity in both maternal and paternal lineages. This pattern suggests that the cemetery served as a communal burial ground rather than reflecting family-based interments, although socially constructed kinship cannot be excluded. Population genetic comparisons placed Poros individuals in continuity with Aegean and Eastern Mediterranean populations from Bronze Age through the Roman period, showing stronger affinities with Anatolian groups from the Roman and Byzantine eras and with Roman populations from Italy. Doliani individuals were genetically distinct from Poros and exhibited stronger affinities with MBA Mainland Greek populations and with medieval, post-medieval Balkan groups. These findings underscore genetic diversity and long-term interactions across the Eastern Mediterranean, highlighting the need for expanded archaeogenomic research.

Gene-culture coevolution in the European Upper Palaeolithic

2. Humans

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Abstract text: Human palaeogenomic studies have traditionally been focused on biological relatedness and demography. Many of the the resulting papers have been criticised for underplaying the complexity of the archaeological record and how it articulates, or contradicts, the genetic interpretations. Studies that analyse palaeogenomic and archaeological data in true parallel are lacking. Here, we focus on the European Late Ice Age (~22,000 – 11,000 years BP) as a case where a steadily increasing size of palaeogenomes can be articulated with a rich archaeological record, all set against an environmental canvas of dramatic climatic changes. Drawing on high-quality, publicly available data, we present a methodology for directly linking palaeogenomes with archaeological material, and to query these for patterns of gene-culture coevolution, migration, and changing population sizes. Our results suggest overall concordance between genetic and cultural phylogenies, pointing to a linked evolution of these inheritance systems at this time. Nevertheless, some differences in the coevolutionary histories of these systems can be observed. We interpret these patterns considering the most likely practices of kinship and social transmission of knowledge, which together determined how cultural and genetic information circulated. Grounded in well-established gene-culture coevolutionary theory, our approach contributes to a more robust integration of archaeology and palaeogenomics.

Genetic ancestry and kinship patterns in coastal and inland communities of Medieval Northeastern Estonia

2. Humans

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Abstract text: In this study, we investigate the genetic history and kinship patterns of individuals from two late 12th - 13th-century burial sites in northeastern Estonia: the coastal site of Kukruse and the inland site of Jõuga. Although the sites are in proximity to each other (ca. 26 km), archaeological records indicate significant cultural differences between the two groups, which raises the question of whether this is also reflected genetically. We extracted DNA from 19 and 12 individuals in Kukruse and Jõuga, respectively, and imputed the genomes (coverage: 0.08X-0.4X, mapped to GRCh38) using QUILT2 with the enriched reference (eRef) panel (manuscript in preparation). The principal component analyses with imputed ancient genomes and Estonian Biobank individuals place the Kukruse individuals mostly with the northern modern Estonians, while the Jõuga individuals are shifted somewhat southward, suggesting different genetic backgrounds. We estimated the kinship for each site using the imputed genotypes with READv2 software. Reconstructed pedigrees indicate distinct kinship patterns in the two communities, with closer familial ties at Jõuga (up to third-degree relatives) and only second- and third-degree relationships at Kukruse. Next, we will utilize segments identical-by-descent and runs of homozygosity to explore the deeper kinship and genetic patterns among individuals from the two sites.

Genetic Insights into Late Bronze and Early Iron Age Central European Populations: First Results from Uniparental Marker Analysis

2. Humans

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Abstract text: The widespread cremation practices of the Urnfield phenomenon have created significant gaps in understanding the genetic history of Late Bronze and Early Iron Age Central European populations, particularly the Lusatian, Knovíz-Štítary, and Hallstatt cultures. To address this, we assembled a unique collection of skeletal remains from biritual sites with predominant inhumations in Upper Silesia (Poland), Moravia, and Bohemia (Czech Republic).

We aim to elucidate the genetic backgrounds of these populations and investigate their origins, relationships, and migration patterns by assessing whether genetic patterns align with cultural differences observed in Urnfield-related phenomena. Kinship analysis from densely sampled sites, including common and multiple burial pits, will reveal marriage patterns, social structures, and inheritance practices. Our multidisciplinary approach integrates ancient DNA analysis, radiocarbon dating, and isotopic measurements. We plan to analyze more than 160 individuals for aDNA and more than 70 individuals for isotopic analyses (^{14}C, $\delta^{15}N$, $^{87}Sr/^{86}Sr$, $\delta^{18}O$, $\delta^{13}C$).

Here, we present the first results from Y-chromosome and mitochondrial DNA analyses, tracing paternal and maternal lineages to reveal sex-specific migration patterns, population continuity, and social influences on genetic transmission. Haplogroup distributions enable reconstruction of demographic processes, gene flow assessment, and insights into kinship's role in shaping these ancient communities' genetic landscape.

Genomes of late Neandertals

2. Humans

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Abstract text: Despite genome-wide data being recovered from close to 20,000 ancient humans to date, genomic data from Neandertals, our closest evolutionary relatives, are still comparatively sparse. Thus far, nuclear genetic data have been recovered from 35 Neandertals from 17 archaeological sites, spanning large parts of their history and geographical range. These data have offered a broad overview of Neandertal populations, indicating the existence of multiple distinct groups, as well repeated population turnovers. Archaeological and genetic evidence suggests that Neandertals lived in small groups, however, it is still unclear whether these groups were part of isolated communities or belonged to larger, well-connected populations.

To reconstruct a more fine-scale view of Neandertal populations, we used minimally destructive sampling of 36 skeletal remains which were radiocarbon dated to between ~52 and ~36 kya from ten archaeological sites in Belgium and France. Out of those, 27 contained enough endogenous DNA to generate autosomal, mitochondrial and Y-chromosomal data, including a new high-coverage genome

from an ~45,000-year-old (i.e., ~45 kya old) Neandertal from Goyet. We found that late Neandertals from west Eurasia had much higher genetic diversity than the Neandertals from the Altai mountains, which lived between ~130 and 60 kya, suggesting that they lived in larger or better-connected groups. These Neandertals also had fewer long tracts of homozygosity, comparable to those found in the Upper Palaeolithic humans present in Europe around the same time. Although our Neandertals overlapped temporally with early modern humans, we find no evidence of recent gene-flow from humans in their genomes. Moreover, we find no evidence for the accumulation of the deleterious mutations in the genomes of late Neandertals and no increase in genetic load over time, arguing against genetic deterioration as a driver of Neandertal extinction.

Genomic ancestry and kinship of Iron Age individuals from the Czech Republic

2. Humans

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Abstract text: Our research project focuses on a transition from Bronze Age to Iron Age in Central Europe. We have assembled a unique collection of more than 200 human skeletal samples from the archaeological sites located in Upper Silesia (Poland), and Moravia and Bohemia regions (Czech Republic). Several tens of Iron Age individuals from the Czech archaeological sites of Rousínov, Kralice na Hané, Vyškov and Zápy, belonging primarily to the Iron Age La Tène horizon and covering both Bohemia and Moravia regions have been sampled and sequenced. In our poster, we would like to present the preliminary results of those samples‘ genomic data, supported by radiocarbon (^{14}C) dating. We will concentrate on their genomic ancestry, searching for source populations as well as the question of local and regional (dis)continuity between Bronze Age and Iron Age settlements. Most of the sampled individuals are males, and their kinship analysis will offer further insights into marriage patterns, social structures, and inheritance practices of Iron Age Central European populations.

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Genomic Continuity at a Key Cosmopolitan Roman Site in the Southern Levant

2. Humans

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Abstract text: The Roman era was a period of profound transformation, shaped by imperial expansion and cultural exchange across the Mediterranean. Yet the genetic landscape of communities living in Roman-period Judea remains largely unexplored. Our study addresses this gap by generating the first genomes from Judea, recovered from Herodium – one of the most significant archaeological landmarks of the early Roman southern Levant.

Built by Herod the Great around 30 BCE, Herodium served as a fortified palace, administrative center, and symbolic seat of power for two centuries. Throughout its history, it hosted a diverse population, including Hasmonean and Roman elites, and later Jewish rebels during the Jewish revolts. It is also widely regarded as the burial site of King Herod.

We analyzed ancient DNA from four individuals excavated from the mausoleum and the palace-fortress. Kinship reconstruction revealed no close familial ties among the mausoleum individuals. Population modeling further showed that all individuals cluster genetically with Late Bronze Age Levantine (Canaanite) groups, reflecting strong continuity with earlier local populations despite the site's cosmopolitan history.

These genomes provide the first genetic insight into Roman-period Judea and serve as a valuable reference for future archaeological and population-genetic research in the region.

Genomic history and selection in Roman and early medieval Britain

2. Humans

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Abstract text: Understanding the processes contributing to present-day population structure not only bears historical interest but can also be a key contributor for studies reconstructing different aspects of genome biology and their impact on health and disease processes.

We shotgun sequenced 1039 ancient genomes from Britain (median coverage of 1.38x), with a main focus on the 1st millennium CE, covering the Roman and early medieval periods (*n*=829), known as times of societal change and potential influx of ancestries. We performed imputation using the UK Biobank reference panel, and employed a range of haplotype- and genealogy-based approaches for a high-resolution view of ancestry in Britain through time, combining patterns of relatedness at different scales with a Twigstats-boosted *f*-statistics framework.

We detect increased mobility into Britain during the Roman period – evidencing the integration into wider Roman networks – but widespread continuity in ancestry, despite disruption of Iron Age kinship practices, and uncover previously uncharacterised genetic heterogeneity in the post-Roman period. In addition, we identify signals consistent with natural selection in regulatory elements near key immunity genes in pre-medieval Britain, possibly driven by evolutionary pressures on innate immunity response to a changing infectious disease landscape.

Genomic insights into the Iron Age Lusatian culture in Central-Eastern Europe

2. Humans

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Abstract text: The Iron Age was a period of significant transformations across Europe. In Central-Eastern Europe, particularly in present-day Poland, many of these changes are only indirectly reflected in historical sources. Ancient DNA provides a valuable tool to investigate population movements and interactions, offering new insights into the region's genetic history.

Our research aimed to assess genetic diversity, including kinship patterns, and to explore the origins of populations associated with the Lusatian culture during the first millennium BCE. Analyses were conducted in a sterile laboratory at the Adam Mickiewicz University in Poznań. DNA was extracted from the petrous part of temporal bones or from teeth, and genomic libraries were subjected to shotgun sequencing on an Illumina NovaSeq X platform.

Genome-wide data from over 130 individuals revealed genetic continuity in southern Poland from the Middle Bronze Age to the Hallstatt period, with minor contributions of new genetic components likely originating south of the Carpathians. At the largest Lusatian culture site in Przeczyce (southwestern Poland), we detected numerous close and distant kinship connections and evidence for a patrilocal social structure.

These results highlight the potential of ancient genomics to illuminate population dynamics and social organization in prehistoric Central-Eastern Europe.

Insights into Prehistoric Communities of the Qatari Peninsula.

2. Humans

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Abstract text: Background. The Arabian Peninsula holds substantial archaeological potential, yet the prehistoric communities of the region remain partially understood. This study aims to contribute new data on early groups inhabiting Qatar.

Methods. We examined burials excavated across the Qatari Peninsula and combined them with material from earlier campaigns, resulting in a dataset of the remains from 67 individuals. Each individual underwent morphological analysis and samples were processed for bioapatite dating and Sr, C, and O stable isotope measurements. Additionally, twenty petrous bone and tooth were selected for ancient DNA analysis through deep sequencing and enrichment. Further genomic results should be available by the time of the conference.

Results. The remains span the Neolithic to the Late Pre-Islamic period (6.5–1.5 kya). Many individuals showed important pathological manifestation: enthesopathies, dental pathologies, periostitis and Schmörl's nodes. All human and faunal samples exhibited $^{87}Sr/^{86}Sr$ ratios within local geological ranges, suggesting limited mobility. Stable isotope results point to diets with C4/CAM plant input. Initial shotgun sequencing and capture assays revealed badly ancient DNA preservation, and evaluation of the available data is ongoing.

Conclusion. These findings provide initial archaeological, bioarchaeological, and molecular insights into prehistoric populations in Qatar and lay the groundwork for improved paleogenomic resolution.

Insights into the Genetic Diversity of Early Bronze Age Individuals from a Cave in the Apuseni Mountains

2. Humans

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Abstract text: For millennia, caves have served as enduring points of contact between people and their landscapes. Toplița de Vida Cave in northwestern Romania exemplifies this deep relationship, preserving a nearly continuous record of human presence from the Mesolithic to the Early Bronze Age (9000–4300 cal BP). This study provides an initial analysis of eight individuals recovered from the site by examining their maternal lineages and placing them within the wider framework of European prehistory. Ancient DNA extracted from teeth and petrous bones reveals a high diversity of mitochondrial haplogroups. Haplogroup H2a constitutes a major component of this variation and, together with T2a, likely reflects a local Neolithic substrate. Furthermore, the presence of haplogroups U4b and U5a signals genetic contributions from Eurasian steppe populations. This combination of maternal lineages highlights the complex population dynamics that characterised the Late Neolithic–Early Bronze Age transition. It suggests that communities in this region were shaped by an interplay of long-established local groups and wider population movements unfolding across Europe.

Integrating Genetics and Paleopathology to Investigate Tuberculosis and Matrilineal Relationships in an Ancient Andean Community

2. Humans

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Abstract text: Infectious diseases have played a decisive role in human history, shaping social dynamics, mobility patterns, demographic structure, and mortality rates. Their impact is most notably displayed in the osteoarchaeological record, where direct evidence of infectious processes can be identified. For some chronic infections such as tuberculosis, certain paleopathological manifestations may also be preserved in bone tissue.

The Colombian archaeological site of Tibanica, corresponding to the Late Muisca period (950–350 BP) represents an ideal context to explore these dynamics. This pre-Hispanic cemetery has revealed abundant osteological material associated with a complex agricultural society in which infectious diseases played a significant role in health and mortality.

The combination of paleopathological and genomic analyses, particularly through the recovery of mitochondrial DNA, allows for the assessment of matrilineal biological relationships among affected individuals. By comparing the presence of lesions compatible with tuberculosis with genetic profiles, we can ascertain whether specific family groups show greater exposure and transmission. It also reveals how social relationships were structured around the disease and offers a privileged window into the epidemiological and social dynamics of Muisca populations. These insights enable the reconstruction of patterns of kinship, mobility, and biological vulnerability to tuberculosis.

Into ancient North-African societies: ancient DNA reveals complex funerary traditions in the Canarian necropolis of El Agujero

2. Humans

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Abstract text: The tumular necropolis of El Agujero–La Guancha (Canary Islands) provides a lens into the funerary practices and social structures of ancient North African communities. This collective burial site consists of several tumuli containing the remains of adult individuals. The main tumulus is composed of a central tower surrounded by cists and pit graves in concentric rings, containing 43 individuals. Additionally, the burial site includes five smaller tumuli that were used to bury one to three individuals. Our study aims to use paleogenomic techniques to explore the genetic composition, kinship patterns and cultural dynamics underlying this burial expression.

Sampled individuals exhibited diverse maternal and paternal lineages, consistent with other indigenous Canarian populations. Despite hypotheses suggesting close genetic ties within the necropolis, our analyses revealed only one second-degree relationship, emphasizing the influence of cultural and social factors over strict familial relationships. High genomic diversity and low levels of consanguinity suggest that the population was regionally integrated and maintained exogamous practices. However, maternal haplogroup sharing within tumuli hints at a matrilocal component in burial organization. Yet, the predominance of male burials and the hierarchical arrangement of tumuli point to a possible male-dominated social structure, as previously suggested.

Isolation and migration in two similar but different Iron Age populations from central and northern Poland.

2. Humans

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Abstract text: The genetic landscape of Iron Age Europe around the turn of the Common Era is challenging to reconstruct. In this presentation, we aim to shed some light on it by examining two neighboring populations from central and northern Poland that appear to reflect different social structures, as suggested by their genetic profiles. Our study generated genomic and isotopic data for 135 newly analyzed individuals from these two groups.

Obtained results show that the Gothic tribes—represented by individuals associated with the Wielbark and Oksywie archaeological cultures from northern and central Poland, form a relatively isolated genetic cluster. We also observe numerous close genetic connections both within and between most of the analyzed sites, as indicated by high levels of shared IBD fragments.

In contrast, the contemporaneous population associated with the Przeworsk archaeological culture from the Kuyavia region in central Poland appears to be much more genetically diverse. Although, at first glance, many Przeworsk individuals occupy a similar position to the Gothic group on the PCA plot, we identified multiple genetic outliers and only few direct genetic connections within and between the analyzed sites, despite them being roughly contemporary and within 10 km radius from each other.

Kinship and Female Social Roles in a Bronze Age Collective Burial: Paleogenomic Insights from Montanisell Cave

2. Humans

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Abstract text: Traditionally, the Bronze Age has been portrayed as a male-dominated world, with long-distance exchange networks. However, recent evidence highlights the role of female mobility in cultural transmission. Grave goods associated with women, such as those documented in Montanisell Cave, suggest their social significance. The Montanisell Cave burial, located in the Catalan Pyrenees (Spain), contained eight individuals: one adult woman richly adorned with exceptional grave goods, placed in the centre of the cave; one young adult woman (19 years); one adult man; one adolescent (14 years); and five children under 12 years of age. Previous bioanthropological analysis suggested patrilocality and female exogamy based on high mitochondrial diversity and demographic structure, though genetic resolution was insufficient to confirm biological kinship. We now present paleogenomic data from all individuals, revealing a structured kinship network: two minors (IDs 9 and 11) are full siblings, and both share second-degree relatedness with infant ID5. Additionally, infant ID2 and the adult male exhibit second-degree kinship. Altogether, indicating a multi-generational family cluster. The central figure of the burial complex, the adult woman (ID 1), shows no genetic relatedness up to second degree nor shared mtDNA haplogroup, suggesting her prominent role was social rather than familial.

Kinship practice and Sacrifice rituals: Ancient Genomic Insights into the Neolithic Shimao city

2. Humans

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Abstract text: The discovery of Shimao city (ca. 2,300–1,800 BCE), a premier state-level Neolithic fortified settlement in Shaanxi, China, played an important role in helping us understand the emergence of socially stratified urban societies. However, key questions remain regarding how ancestry and kinship shaped the hierarchy of this class-based society characterized by human sacrifice. The origin of the founding populations of Shimao and other Loess Plateau settlements, and their interactions within the broader ancestral landscape, have yet to be determined. By sequencing 144 ancient genomes from Shimao city and its satellites, we present pedigrees among tomb owners spanning up to four generations. Our findings reveal a predominantly patrilineal descent structure across Shimao communities and sex-specific sacrificial rituals. We also characterize the population history, revealing that Shimao culture-related populations originated mostly from a Yangshao culture-related population present at least one thousand years earlier in the local region, and the lasting inflow of Yumin-related population from Inner Mongolia did not interrupt regional genetic continuity. Broader genetic influence from southern mainland ancestry over Shimao culture-related populations supports evidence of rice farming expanding further north than previously expected. Taken together, these results uncover fine details of the regional peopling and social structure of early state establishment.

Kinship system of the Western Zhou Dynasty in China: A case from Liulihe Site

2. Humans

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Abstract text: Kinship system of the Western Zhou Dynasty in China: A case from Liulihe Site

Supported by both historical records and archaeological evidence, the Western Zhou Dynasty (ca. 1046-771 BCE) was known as the earliest enfeoffment polity with elaborate ritual and musical systems during Chinese history. However, our knowledge of the kinship system and mortuary practices within the non-elite populations is still limited. Here we analysed ancient DNA from 31 individuals in Chengbei cemetery at the Liulihe site, the capital of Yan State located in Beijing. We reconstructed one extended pedigree spanning up to four generations and encompassing approximately 22 individuals. Our findings demonstrated a patrilineal social framework characterized by patrilocal burial practices and female exogamy among commoners in Western Zhou society. The existence of consanguinity may suggest that close-kin marriage was not strictly forbidden for non-elite people. Moreover, the spatial correspondence between genetic kinship and burial position of most individuals supports the presence of a lineage-based organization in the Chengbei cemetery. Together, these findings not only provide new insights into the kinship structure and cemetery organization of the Western Zhou Dynasty, but also shed light on the complex social systems that characterized the formation of these early polities in China.

Lepenski Vir revisited. Exploring site-level interactions between farmers and foragers

2. Humans

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Abstract text: Lepenski Vir in the Danube's Iron Gates (c. 6,200-5,900 BC) is widely hailed as one of Europe's most remarkable prehistoric sites, owing to its trapezoidal houses, fish statues, and unusual burial record. For decades archaeologists have described it as a Mesolithic fishing village that resisted the arrival of Neolithic agriculture in the Central Balkans. Recent genetic evidence has upended this narrative. Sixteen human genomes, in addition to stable isotopes and other biomolecular proxies, now offer an unprecedented snapshot of population changes at the site. The reanalysis undertaken here aimed to contextualize new genomes across the different occupation layers at Lepenski Vir. Ancient DNA results not only reveal recent admixture (two to three generations in the past) between incoming Aegean farmers and Iron Gates hunter-gatherers, but also challenge the notion that Lepenski Vir was an established Mesolithic community that welcomed a few Neolithic women. Entire immigrant families, including newborns, appear to have resettled at the site. Analysis of kinship and shared IBD segments provide additional clues as to what might have happened at Lepenski Vir. This project illustrates how the integration of high-resolution archaeological and genomic data can uncover unexpected facets of our ancient past.

Local Hunter-Gatherer Legacies in Neolithic Iberian Genomes (4300–1700 years before the Common Era)

2. Humans

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Abstract text: Late Prehistoric Iberia was a pivotal meeting ground between incoming early farmers and long-established hunter-gatherer groups.
To investigate this interaction, we analyse a comprehensive genome-wide dataset of 92 individuals from 29 sites spanning western, northern and southern Iberia, dated to 4300–1700 BCE.
While all individuals derive most of their ancestry from early European farmers, the majority retain a dual hunter-gatherer signal composed of Western Hunter-Gatherer ancestry and a Magdalenian-related component rooted in Iberia since the Last Glacial Maximum.
Two Mesolithic groups provide plausible local sources for this Magdalenian-related ancestry. Among them, spatial patterns point to a southwestern origin, with this ancestry declining with increasing distance across Iberia.
Despite this structured input, Neolithic populations across Iberia exhibit a broadly consistent three-way ancestry profile across regions, sites and mortuary contexts.
These findings demonstrate that admixture with locally rooted hunter-gatherers shaped Iberian genetic landscapes, leaving a persistent legacy within otherwise stable farming populations.
By integrating fine-scale spatial and temporal data, this study highlights the enduring imprint of hunter-gatherer communities on Neolithic societies and advances our understanding of population dynamics in southwestern Europe.

Paleogenomic analysis of the temporal evolution of the human population of Gran Canaria

2. Humans

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Abstract text: Multidisciplinary studies of the indigenous population of the Canary Islands have concluded that the settlement of the archipelago occurred around the 3rd century CE and that its inhabitants originated from North Africa. However, whether these populations remained isolated until the European conquest in the 15th century remains unclear.

A paleogenomic study published in 2023, determined that the indigenous population of Gran Canaria exhibited the highest genomic diversity across the entire archipelago. Furthermore, its genetic composition, along with Fuerteventura and Lanzarote, differed from that of the western islands. While these findings may be attributed to asymmetric migrations within the archipelago, as proposed based on archaeological evidence, paleogenomic data analyzed thus far indicates no evidence of a significant gene flow in Gran Canaria.

A limitation of previous studies lies in the small sample size, particularly during the early and middle periods of indigenous settlement. To address this, we propose a detailed temporal analysis of the human population of Gran Canaria, spanning from the onset of indigenous colonization to the establishment of the colonial society. This study will examine remains from 20 new archaeological sites and 117 individuals, enabling a comprehensive reconstruction of demographic and genetic changes.

Paleogenomic and Functional Insights into Human Adaptation to Toxic Metals in the Andes

2. Humans

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Abstract text: Inorganic arsenic (iAs) and mercury (Hg) are among the most toxic elements affecting human health both today and historically. Due to persistent volcanic and geological activity, populations in the central Andes, from central Peru to northern Chile, have experienced chronic exposure to these metals for millennia. Here, we investigate the genetic basis of tolerance to iAs and Hg using ancient and modern genomic datasets from Andean populations. In Peru, preliminary analyses focus on ancient individuals from Hacienda Pucará (Junín), a colonial-era mining region where silver extraction relied on mercury amalgamation. In northern Chile, we generated 12 high-coverage ancient genomes spanning the last 7,000 years and combined these with genomic data from modern Indigenous (n=24) and admixed (n=896) populations to reconstruct their genetic history and identify signals of selection. We identified regulatory variants in the *AS3MT* gene associated with arsenic metabolism, traced their temporal dynamics across regional cultural periods, and validated their enhancer activity in human liver cells exposed to arsenic. Our ongoing analyses are expanding to assess genetic variation in other metal-related pathways, including ABC transporters, glutathione metabolism, and aquaporins. Overall, this project highlights how long-term environmental toxicity has shaped human evolutionary history and continues to influence present-day health.

Pedigree-based Inference of Ancestry from low-depth samples in pedigrees

2. Humans

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Abstract text: Dense population samples, for instance from cemeteries, often contain closely related individuals connected by one or several pedigrees. These familial relationships introduce dependencies into the genomic data that violate the assumption of independence, an assumption that is central to many population genomic analyses. A common workaround is to analyze each sample separately, which ignores the rich information that can be gained from related samples.

Here, we introduce *filia*, a collection of three methods for pedigree-aware inference of ancestry. The first two methods exploit (complex) familial relationships to improve ancestry estimates obtained with either D-statistics or admixture-like models, respectively. By explicitly modeling dependencies among related samples, *filia* propagates information between samples and also to unsampled relatives, thereby resulting in more robust and accurate estimates of ancestry than conventional approaches that assume independent samples, particularly in low-depth or sparsely sequenced datasets. The third method extends these former methods by using genotype likelihoods to jointly infer individual ancestry proportions and individual genotypes, thereby effectively imputing genotype information in pedigrees. As we show with both simulations and downsampling experiments, pedigree-aware inference often leads to much more accurate ancestry inference than existing methods and in particular much less often infers spurious ancestry components.

Population Genomics of Etruscans in the Po Valley: Local Persistence and Celtic-related Gene Flow

2. Humans

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Abstract text: The Etruscan civilization was an influential culture of Iron Age Italy, known for its sophisticated art,
engineering, and religious traditions. Archaeological and genetic research supports an autochthonous origin, tracing Etruscans to Villanovan communities in Central Italy during the Bronze Age. Nevertheless, direct genomic evidence for this continuity is still missing due to the predominance of cremation practices in Villanovan communities. Moreover, genetic data from Etruscan necropolises are currently available for central Etruria (Tuscany and Lazio), whereas regions such as the Po Valley, a region in Northern Italy with major Etruscan centers, remain largely unexplored.
To investigate the genetic development of Etruscan communities, we generate genome-wide data for 104 individuals from necropolises in Emilia-Romagna, spanning from Villanovan phases to the Imperial period (10th–3rd centuries BCE), and performed population genetic analyses including PCA, ADMIXTURE, F-statistics, qpAdm modeling, and IBD analysis.
Our results show that Villanovan and Etruscan communities of the Po Valley exhibit a predominantly local genetic profile, in continuity with Central Italian Bronze and Iron Age populations, and closely related to central Etruria groups. Approximately 20% of individuals display Central-European genetic affinities, indicating cultural and genetic Etruscan-Celtic interactions in the Po Valley starting at least by the 8 th century BCE.

Population Size Dynamics through the European Later Stone Age

2. Humans

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Abstract text: Through most of the Later Stone Age (45-6kya), Europe was inhabited by hunter-gatherer societies, whose demography is still poorly understood relative to later food-producers. Of particular interest is the impact of climate on rates of population growth and decline, as foragers at high latitudes may be particularly vulnerable to environmental perturbations. Here, we present a holistic appraisal of population size change throughout this period by leveraging IBD segments and recently published HapNe-IBD software. We compare trajectories for different regional populations, including Ireland, for which we present four new Mesolithic genomes. We observe relative stability before the Last Glacial Maximum (LGM), followed by decline in the Oldest Dryas. The Bølling–Allerød Interstadial brings a period of growth, with most Holocene populations showing sustained exponential increase. The new Irish Holocene data however shows a unique trajectory, with an extreme bottleneck coinciding with the 8.2kBP cooling event, followed by rapid growth. This extreme fluctuation likely reflects the population's vulnerability on an isolated island at the northwestern edge of Europe. We further find little evidence of sex-biased demography across hunter-gatherer Europe, in keeping with ethnographic datasets. These new population histories give important insights into how climate shapes the spatial ecology and social organisation of hunter-gatherers.

Population structure revealed by ancient DNA: comparison of rural and urban communities of Medieval Estonia

2. Humans

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Abstract text: The Middle Ages reached the territories of the Eastern Baltic much later than Central Europe, in the 13th century AD, bringing major cultural and social changes to the historical regions of Livonia. To understand the extent to which these events medieted by the Northern Crusaders altered the genetic structure of the local population, we analyzed the ancient DNA of 176 medieval individuals from Estonia. The study sample consisted of human remains from three towns and rural cemeteries distributed across present-day territory of Estonia. Individuals from towns could be classified into different social groups based on their archaeological context. We compared these groups by genetic ancestry and dietary isotopes and found that the medieval population of Estonia consisted of commoners of local origin buried in rural and parish cemeteries, and an elite of predominantly Western European origin buried mainly in towns. This is consistent with historical evidence of Germans arriving in Livonia during Christianization and via the establishment of the Hanseatic League trade networks. Daily lives of these social groups differed significantly, as shown by historical records, isotope data, and osteological studies. Our study highlights the importance of an interdisciplinary approach in exploring the human past.

Residence patterns in the earliest sedentary societies

2. Humans

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Abstract text: The ethnographic record demonstrates a diversity of postmarital residence patterns among traditional human societies. Certain trends can also be seen in this data, such as sedentary food-producing societies more frequently following patrilocal practices than foraging societies. To date, the majority of archaeogenomic studies on prehistoric agricultural societies from Europe has indicated patrilocal-like practices. However, the emerging evidence from Anatolia point to bilocal or matrilocal patterns in Neolithic communities, which had existed millennia earlier than their descendants in Europe. I will describe published evidence from the Anatolian site of Çatalhöyük as well as unpublished data from our team in Ankara, describing social dynamics from earlier and later settlements from Southwest Asia. I will also present alternative methodological approaches to most effectively capture sex-biased residence patterns, and discuss what these results imply about factors shaping human social organisation and practices.

Similarities and Differences in the Social Organization of Two Steppe-Derived Populations in the Migration-Period Carpathian Basin

2. Humans

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Abstract text: This study presents a comparative archaeogenomic analysis of two eastern nomadic groups in the Carpathian Basin: the Avars (6th–8th c.) and the Early Medieval Magyars (the early Hungarians, 9th–10th c.). Drawing on genome-wide ancient DNA from multiple, completely sampled key cemeteries from these periods, we examine kinship structures, sex-biased mobility, and reproductive patterns within and between these communities. Using ~90 new whole genomic data, we reconstruct fine-scale biological relatedness and assess the extent of connectivity within early Magyar cemeteries.

By integrating genetic data with archaeological context and spatial burial patterns, we compare how these groups were organized into social units and whether they followed patri- or matrilinear burial practices. Only a 150–200-year gap was between the Avar and Early Medieval Magyar groups, yet a high contrast in their social organisation became visible. Avar communities appear to have maintained large, relatively closed social structures, whereas early Hungarian-period groups show indications of more open forms of interaction and integration with surrounding populations. These distinctions underscore shifting sociopolitical dynamics within the Carpathian Basin.

Social structure in an ancient Oceanian population

2. Humans

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Abstract text: Near Oceania, the region extending to the Solomon Islands, was first settled over 50,000 BP by people carrying Papuan-related ancestries. In contrast, the settlement of the rest of Oceania began only ~3,000 BP with the Austronesian expansion, which reached western Polynesia and introduced East Asian-related ancestries. Later movements, including westward dispersals of Polynesian-speaking groups (Polynesian Outliers), further shaped the cultural and genetic diversity of Oceanians. Nevertheless, how these processes influenced social organization in island communities remains largely unexplored.

We analyse genomic data from 111 ancient individuals from the Namu burial site on Taumako (eastern Solomon Islands), a community with strong Polynesian cultural influences. Radiocarbon dates of 400–40 BP indicate that the site is younger than previously assumed, but genetically distinct from present-day Polynesian Outlier communities. The Taumako population shows homogeneous genetic ancestry (~50% Papuan-related, ~50% East Asian-related) and extremely dense networks of genetic relatedness. We reconstruct multi-generation pedigrees and identify patterns indicative of female exogamy, likely mediated by mobility to nearby islands. Analysing archaeological wealth indicators, we identify a sibling pair with the highest wealth scores and evidence of parental first-cousin relatedness. Together, we provide new insights into the genetic history and social organization and a past Oceanian community.

The dynastic ties of the early Scythian-Siberian elite in the "Valley of the Kings" of Tuva

2. Humans

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Abstract text: In the first millennium BC, numerous population groups belonging to Scythian-type nomadic cultures inhabited the Eurasian steppes and influenced the surrounding world. Archaeological evidence indicates the origin of their economy and lifestyle in the East, primarily in the territory of the present-day Republic of Tuva, Russia. Scythian-type large-scale 'kurgans' of the IX-VII centuries BC have been studied in a valley holding burials of tribal leaders surrounded by the graves of their supposed family members or associates.

The crucial issue of the peoples' origin remains unclear, along with the kinship of those buried in the high-status sites and the 'ordinary' nomadic graves around them. Solving these issues can shed light on the ancestries of the earliest nomadic societies, their dynastic rules and social relationships.

We analyzed ancient DNA of individuals unearthed from the recently excavated sites known as Arzhan 2, Chinge-Tey I, and Tunnug 1. We compared genome-wide data of these individuals with those of Bronze and Early Iron Age population groups in Asia. We then conducted kinship analysis of all high-status individuals and compared their genomic data with that of the other inhabitants of the region.

The Earliest South American Multiple Burial Indicates a Failed Migration Wave into Patagonia

2. Humans

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Abstract text: Patagonia in southernmost South America was one of the last regions of the world to be settled by humans about 14,000 years ago. The limited archaeological and genetic record makes the identification of the timing and understanding of the early migrating waves challenging. One of the critical questions still not clearly answered is how many and which were the initial settling attempts. The site of Baño Nuevo 1 (Aysén, Central Patagonia) offers a privileged location to answer these questions. The cave produced a sequence spanning the last 16,000 years and includes the skeletal remains of 11 individuals dated to 10,200 BP, most likely representing a single community. Here we present genomic analyses of all individuals, supported by exceptionally well-preserved DNA. Our results identify a distinct genetic lineage not previously sampled in South America. This ancestry doesn't notably contribute to later Holocene Patagonian populations, suggesting an early migration wave that ultimately left no lasting genetic legacy in the region. These findings raise new questions about the diversity of early settlement attempts, the social structure of pioneering groups, and the strategies that enabled, or limited, their survival in harsh environments. We integrate these genetic insights with archaeological data at a continental scale.

The genetic structure of the Basin of Mexico across prehispanic and colonial periods

2. Humans

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Abstract text: In 1521, the Hispanic Monarchy conquered the Mexica Empire and imposed a colonial rule that transformed the lives of millions of people and reshaped the demographic dynamics of Mesoamerica. Our project investigates the genetic imprint of colonization in archaeological samples from the Basin of Mexico by analyzing the population structure before and after the conquest.

We analyzed a total of 170 individuals and compared the genomes of prehispanic and colonial populations from 10 sites. We find evidence of strong genetic continuity across the Basin of Mexico, extending from the prehispanic site of Huipulco (600-900 CE) through to the colonial chapel of Los Olmos (1533–1570 CE), located on the northeast coast of the former Lake Texcoco. Although 16th-century samples from Tenochtitlan Island (Mexico City) already present admixture, all 41 individuals from Los Olmos show exclusively Mesoamerican ancestry, despite being buried according to Catholic rites. Moreover, we observe a notable absence of genetic relatedness in Los Olmos, consistent with historical records describing the chapel as a refuge for dislocated individuals fleeing outbreaks during the mid-16th-century cocoliztli epidemics.

These results challenge narratives that equate cultural identity with genetic ancestry and underscore the need for multifaceted approaches to understand the impact of Hispanic colonization.

The impact of isolation on ancient North African islanders

2. Humans

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Abstract text: Isolated environments, particularly oceanic islands, present extreme examples of limited resources pushing populations to the limits of survival. El Hierro, the smallest, youngest, and remotest island of the Canary Islands, a volcanic archipelago located off the coast of the Sahara, serves as a unique example of this extreme isolation. In this study, we present genome-wide data from 86 individuals of the island's ancient population, spanning from the 4th to the 14th century CE. Genomic evidence shows extensive runs of homozygosity, bottleneck events, and intense genetic drift, all of which shaped the population's genetic landscape over time. The diversity observed in early individuals steadily declined, reaching the lowest values in the archipelago by the last centuries. This high background relatedness likely led to the manifestation of homozygous recessive diseases, including osteological abnormalities such as double temporal bones found in the archaeological record. Overall, this study sheds light on the complex demographic history of the ancient population from El Hierro, illustrating the profound effects of over 1,000 years of isolation in a resource-poor environment but also highlighting the population's remarkable resilience in adapting to these harsh conditions.

The making of Italy: Archaeogenetic insights from the post-Roman period

2. Humans

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Abstract text: At the end of the Western Roman Empire, Italy underwent profound political, social, and economic transformations, further intensified by the Late Antique Little Ice Age and the Justinianic plague.

In this context, Central Italy acted as a hinge between the northern regions, which increasingly gravitated toward continental Europe, and the southern regions, whose centre of gravity was located within the Mediterranean world, becoming a crossroads of encounters, conflicts, and exchanges between two spheres that were politically, culturally, religiously, and genetically distinct.

This project investigates the role of Central Italy in the social and demographic dynamics of the period through an archaeogenetic approach, analysing a dataset of over 100 individuals from sites with distinct political and economic contexts: Pesaro and Senigallia (6th–7th cc.), two cosmopolitan Byzantine urban centres; Castel Trosino (6th–8th cc.), a Longobard cemetery at the Byzantine frontier; Fossombrone (5th–7th cc.), a stronghold contested by Romans, Goths, Byzantines, and Longobards; and La Selvicciola and Fara Sabina (4th–8th cc.), rural settlements between Longobard and Papal territories.

The genetic analyses of these sites - soon expanded with additional contexts and samples - will provide unprecedented insights into the mobility, kinship networks, ancestry and health of people who made the modern Italian population.

The Neolithisation of the Northwest: New insights from genealogy

2. Humans

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Abstract text: The northwestern fringe of Europe was one of the final regions reached by Neolithic farmers, who spread across the continent from Anatolia following Danubian and Mediterranean routes of expansion. These migratory arms of the Neolithic met in Northern France *c.* 5000-4500 BC, where complex admixture events took place with local hunter-gatherer groups. Following a prolonged pause, agriculture subsequently spread rapidly across the islands of Britain and Ireland, starting *c.* 4000 BC. While this led to a long-term population replacement, the process by which the Neolithic spread across the islands is still poorly understood from a genetic standpoint. Specifically, the routes of migration across the islands are unclear and the source population(s) in France remain unidentified. Here, we address these questions using a dataset of approximately 600 Neolithic and Mesolithic individuals from across Europe, including 30 newly imputed genomes from Ireland. We leverage identical-by-descent (IBD) segments binned into different length categories to establish recent and deep origins of the islands' Neolithic populations. We further characterise patterns of genealogical relatedness within and between megalithic tombs to explore social organisation, including new data from the great passage tomb at Knowth.

The unique genomics of ancient southern Africans

2. Humans

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Abstract text: *Homo sapiens* evolved hundreds of thousands of years ago in Africa, later spreading across the globe, but the early evolutionary process is debated. A few studies have recently sequenced complete genomes of ancient southern Africans, dating back to 10,000 years ago, revealing long-term isolation of ancient southern Africans, and a genetic make-up outside the range of genetic variation in modern-day humans (including southern African indigenous Khoe-San, although they retain ~80% ancient southern African ancestry). This isolation is manifesting in a large fraction of '*sapiens*-specific' variants unique to ancient southern Africans. *Sapiens*-specific variants at amino-acid-altering sites fixed for all humans – likely to have evolved rapidly on the *sapiens* branch – were enriched for genes associated with kidney-function, likely impacting water-retention, and possibly linked to the human-unique trait of endurance and temperature-control via sweating. The ancient southern Africans show little spatiotemporal stratification for 9,000 years, consistent with a large, stable Holocene population transcending archaeological phases. Whilst southern Africa served as a long-standing geographic refugium, there is outward gene-flow >8,000 years ago, however, inward gene-flow only manifests after ~1,400 years ago. Ancient southern African genomes are key to the evolution of *H. sapiens*, and important for advancing our understanding of human genomic variation.

They’re the same picture. Ancestry composition inference under minimum differentiation of source populations – a case of Iron Age Europe humans.

2. Humans

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Abstract text: Population genomic methods have been widely applied to investigate the levels of introgression between populations and to test hypotheses about genetic continuity within particular regions. Such approach brought many spectacular findings such as confirmation of a demic nature of Europe’s neolithization or the spread of Steppe ancestry throughout Europe connected to the appearance of Indo-European languages and the Corded Ware phenomenon. Yet, when applied to investigate the interactions of distinct but genetically similar populations, the conventional tools of population genomics fail to reconstruct ancestry composition robustly.

The very limited resolution of methods such as standard *F*-statistics has been shown previously for Late Iron Age and Early Medieval Central and Northern European populations (see: Speidel et al. 2025, *Nature* and Gretzinger et al. 2025, *Nature*). In my talk, I will showcase how the low resolution to differentiate the ancestry sources could be and, indeed, has been misinterpreted as support for genetic continuity within the region. I will provide an overview of alternative approaches that have been and can further be applied to disentangle ancestry composition using the case study of the new data we obtained from a longitudinal genomic transect for the (pre-)historic inhabitants of the Oder and Vistula basins region.

Uncovering a Medieval Pogrom: Genetic History of Jewish People

2. Humans

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Abstract text: The Black Death pandemic, combined with the deeply antisemitic climate of 14th-century Europe, led to widespread violence against Jewish communities, including numerous pogroms such as the one in 1348 in Tàrrega (Catalonia, Spain). In the Roquetes necropolis of Tàrrega, six communal graves containing at least sixty-nine individuals, with signs of violence, have been dated to 1348. Based on the hypothesis that Spanish medieval Jewish communities preserve genetic similarities to other Jewish ancient and modern communities, our study seeks to determine whether these remains belong to victims of the Tàrrega pogrom.

We sequenced DNA from sixteen individuals from Roquetes necropolis using Twist ancient DNA enrichment capture. Several analyses were conducted to determine their population origins. PCA and Admixture analyses reveal genetic affinities with ancient and modern Jewish populations. Uniparental markers, which show significant diversity, align with typical Jewish community patterns. Relatedness assessments show no close kinship, while RHO analyses indicate a certain level of endogamy and a small, isolated population. Finally, one-way qpAdm modeling suggests that the ancestry of these individuals can be better explained by Jewish populations than by coetaneous Iberian non-Jewish groups.

These findings strongly support the hypothesis that the Roquetes graves contain victims of the 1348 Tàrrega pogrom.

Uncovering the Role of Regulatory Variants in Human Evolution

2. Humans

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Abstract text: Changes in gene regulation are key drivers of human evolution. However, how these changes shaped human adaptations remains largely unknown. Here, we employed massively parallel reporter assays in skeletal and neural cells to uncover the functional role of all 71,443 variants distinguishing Neanderthals and Denisovans from modern humans. This extensive atlas revealed thousands of substitutions that altered human gene expression. To link these variants to their targets, we generated human-chimp hybrid cells, a powerful system for detecting expression differences driven by nearby variants. Synergizing these approaches uncovered three systems that experienced unique selective pressures: the face, vocal tract, and cerebellum. Interestingly, we detected many instances of convergent functional evolution between modern and archaic humans, including in tumor suppressor genes. Finally, we identified an archaic substitution in *PPM1E* that markedly increased its activity. Introducing the archaic substitution into neural progenitors using CRISPR/Cas9 confirmed that it significantly increases *PPM1E* expression. Phenotypic assays identified that higher *PPM1E* RNA levels likely reduced neuronal mushroom spines, roots, and neurites in Neanderthals and Denisovans. Together, our findings provide the first functional atlas of variants that separate archaic from modern humans, illuminating the molecular changes that shaped their neural and skeletal traits.

Urban Kinship and Genetic Diversity in Thessaloniki: A Genomic Perspective

2. Humans

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Abstract text: Urbanization has long fostered interaction among individuals beyond close kin. Yet, we still know little about how familial, religious, and economic networks shaped everyday life in Roman and post-Roman urban centers. This study employs ancient DNA analysis to investigate such dynamics in the city of Thessaloniki, a major urban and cultural hub throughout European history. Our dataset spans the entire Byzantine period (324–1453 CE), with a particular emphasis on the Late Byzantine period (1204–1453 CE). We explore how the formation of social, religious, and neighborhood-based subgroups may have encouraged endogamy, reducing genetic diversity within subgroups. We applied standard ancestry inference approaches and population genetic metrics including inbreeding coefficients (F), Wright's FST and nucleotide diversity estimates (π and θ) to assess genetic structure and heterogeneity. We integrated these genomic findings with historical and archaeological sources to understand how cultural norms and social organization influenced patterns of diversity in the city. Our results indicate clear signs of population structure especially in Byzantine Thessaloniki, which we interpret as a probable reflection of localized family systems and broader socio-cultural frameworks. This research is part of the ERC-Consolidator Grant CityLife: A bioarchaeological study of 1,800 years of resilience and adaptation to urbanity (Project: 101126337).

3. Pathogens/Microbiomes

Amylase-binding proteins as indicators of dietary adaptation in the human oral microbiome

3. Pathogens/Microbiomes

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Abstract text: Bacterial populations evolve and fix genetic changes much more rapidly than humans, and consequently the evolutionary patterns of bacteria within the human microbiome have the potential to serve as a proxy for tracing human behavioral and dietary changes over time. One such shift, the adoption of starch-rich diets, is reflected in humans by copy number expansion of the salivary amylase gene (*AMY1*). Certain *Streptococcus* species in the human oral microbiome produce amylase-binding proteins (ABPs) that interact with human salivary amylase, suggesting co-evolution of these microbes along with humans. This project investigates how the diversity and evolution of ABP genes reflect host dietary adaptation. We examine the distribution and phylogenetic relationships of ABP genes across a wide range of ancient and modern comparative datasets, including industrial and non-industrial human dental plaque, non-human primate and mammalian dental calculus, soil metagenomes, and human gut microbiomes. By establishing a comprehensive overview of modern ABP diversity and host associations, against which we contrast ancient human diversity, this study provides a framework for identifying evolutionary patterns linked to starch consumption. These findings inform future analyses of ancient microbiomes and contribute to understanding the coevolutionary relationship between human diet, host genetics, and commensal microbial adaptation.

Ancient genomes illuminate the evolutionary history of Merkel cell polyomavirus

3. Pathogens/Microbiomes

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Abstract text: Merkel cell polyomavirus (MCPyV) is a common human DNA virus believed to be the causative agent in the majority of Merkel cell carcinomas, a rare but incurable skin cancer. In this study, we expand the virus' phylogenetic analysis by sequencing ancient MCPyV genomes from various human remains. These include soft tissue, teeth and petrous bones from individuals of the Chachapoya culture in Peru (800–1470 CE), and of a tar-burning grave in Finland (~1800 CE), as well as a Yamnaya individual from present-day Bulgaria (~2700 BCE). The last one represents the oldest sequenced genome of a human cancer-causing virus (oncovirus) to date. These findings provide new insights into the temporal and geographical distribution of MCPyV in human populations and its evolution.

Ancient host-associated microbes obtained from mammoth remains

3. Pathogens/Microbiomes

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Abstract text: Ancient genomic studies have extensively explored human-microbial interactions, yet research on non-human animals remains limited. Here, we analyzed ancient microbial DNA in 488 mammoth samples, of which 359 are newly sequenced, spanning a time transect from the Holocene to over a million years ago. After accounting for contamination and conducting phylogenetic analyses, we identified six bacterial clades related to modern commensal or putative pathogenic species. These include *Streptococcus* from woolly mammoth teeth on Wrangel Island, *Erysipelothrix* from a 1.1-million-year-old steppe mammoth, and *Pasteurella*-related bacteria that have previously been linked to African elephant deaths. Although additional complete genomes are required to fully evaluate the gene content of the ancient mammoth bacteria, the identification of potential virulence genes suggests that some microbes could have played a pathogenic role. Collectively, these findings demonstrate that mammoth remains can serve as microbial archives, opening up new avenues to explore the health, ecology and co-evolution of extinct megafauna through ancient DNA.

Selected references

Translator

Translator

Ancient oral microbiomes from present-day France reveal an expanding picture of past health and lifestyles during 17,000 years of prehistory

3. Pathogens/Microbiomes

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Abstract text: The metagenomic study of ancient dental calculus provides insight into the evolution of oral microbiomes and host health in response to the biocultural shifts endured throughout human history. In particular, the Neolithic and Bronze Age transitions had profound effects on diet, lifestyle, demography, and health. While these periods are well-documented by archaeological and palaeogenomic research, metagenomic studies remain limited. Notably, present-day France remains uninvestigated, despite its rich archaeological record and palaeogenomic data attesting to divergent regional migration dynamics during both the Neolithic and Bronze Age. Here, we present the first study of oral microbiome evolution in present-day France within the context of these two transitions. We report the taxonomic composition, functional profiles, and phylogenetic history of 42 high-quality metagenomes and 28 bacterial genomes from shotgun-sequenced dental calculus (18,000-1,000 BCE). Our results trace the emergence of widespread disease-associated microbiomes to the arrival of food-producers, while regional differences mirror local settlement patterns and subsistence strategies. Furthermore, we consider the contributions of host ecology and genotype, highlighting a correlation between the genetic diversity introduced by Neolithic migrations and microbiome composition. Overall, this study contributes to the documentation of ancient microbiome variability and underscores the value of metagenomic studies in understanding past lives.

Ancient Pathogens in British Fauna: Towards a Better Understanding of Zoonotic Disease Emergence

3. Pathogens/Microbiomes

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Abstract text: Understanding diseases in the past is essential for contextualising modern observations, determining whether newly emerging diseases are truly newly emerging, and informing control efforts. Although there are now many examples of human pathogen DNA retrieval from archaeological and museum material, the number retrieved from animals remains limited, especially wild animals.

Part of the “OneZoo” doctoral programme, this project aims to better understand the prevalence and diversity of zoonotic diseases through history, with a focus on British fauna. Specific objectives include, 1. Developing new protocols for non-destructive sampling of fluid-preserved museum specimens for helminth DNA, 2. Investigating links between skeletal pathologies and infection in the archaeological record, 3. Investigating the origins of bovine tuberculosis in British animals, and its transmission between species . I will present preliminary results, and discuss how ancient genetic data can help us to better understand the risks of zoonotic diseases.

Ancient Treponema pallidum genomes reveal phylogenetic diversity and lineage persistence through time in South American populations

3. Pathogens/Microbiomes

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Abstract text: *Treonema pallidum* is a pathogen responsible for several pathologies in humans around the globe. Its origin and spread have been subject to debate for centuries. Recently, the retrieval of ancient genomes has greatly deepened our understanding of *T. pallidum* evolution and global spread. Here, we expand on this framework by reporting additional ancient *T. pallidum* genomes from Peru obtained using a targeted pathogen DNA enrichment approach. These genomes span a broad time period and encompass various cultures, including the Moche and the Inca civilizations. Our results reveal a high phylogenetic diversity of *T. pallidum* in prehispanic Peru, lending support to previous research conducted in several South American regions. Additionally, we increase the coverage of a previously reported ~5.500 years-old highly divergent genome from the Northern Andes by almost 10-fold, allowing for a deeper investigation of its genomic features and a more accurate estimation of its divergence from present-day subspecies. We demonstrate that this lineage survived up until the first centuries CE in Peru, suggesting a multi-millennial presence in South American populations. These results set the ground for a better understanding of the spread and persistence of this disease in South American populations through the millennia.

Archaeogentic Analysis reveals a devastating Black Death outbreak in Northern Norway

3. Pathogens/Microbiomes

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Abstract text: The Black Death (1346-1353 CE) is one of the most infamous historical pandemics, with estimated mortality rates as high as 50%. This pandemic has been recorded across Eurasia and North Africa, but detailed knowledge of its impact remains limited to regions with extensive historical records. Here, we apply ancient DNA analysis to 50 individuals buried in multiple mass graves, showing the devastating impact of the Black Death (caused by the plague pathogen *Yersinia pestis*) on the small island of Sanna, in Nordland, Northern Norway. Excellent preservation enabled an exceptionally high pathogen DNA recovery rate, suggesting that nearly all of these individuals died from plague infections. The plague genomes place at the Black Death polytomy of the *Y. pestis* phylogeny, suggesting that this represents a contemporaneous outbreak to those in London and Barcelona, emphasising the speed at which this pandemic reached even the northern extremities of Europe. We reconstructed high-quality human and plague genomes, showing that this represents a single community, with family units being buried across different graves. This community was surprisingly diverse, with low levels of background relatedness and high uniparental haplotype diversity. This study offers a high-resolution picture of both pathogen and human diversity in mid-fourteenth century Nordland.

Archaeological Metagenomics Unveils Subsistence Strategies and Ecological Context in Harappan Civilization Remains

3. Pathogens/Microbiomes

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Abstract text: Metagenomics sequencing of archaeological specimens enables comprehensive characterization of preserved biological materials, elucidating specimen provenance, ecological context, and anthropogenic activities complementing traditional archaeological interpretations. We employed aMETA pipeline, utilizing probabilistic taxonomic assignment algorithms integrating k-mer based classification with phylogenetic placement methods to enhance taxonomic resolution in ancient metagenomics datasets, investigating distinct specimens from Dholavira, Gujarat: bone specimen (DB) and artefact pottery material (DA). High-depth Illumina sequencing with approximately 25 GB data per specimen ensured exhaustive coverage, capturing rare taxa and minimizing taxonomic underrepresentation. Taxonomic profiling revealed striking compositional disparities with differential unclassified sequence ratios. DB demonstrated halophilic bacterial dominance—Gammaproteobacteria (83%), predominantly Vibrionaceae (60%), overwhelmingly *Vibrio harveyi* complex (*V. alginolyticus*, *V. owensii*)—indicating post-depositional halotolerant saprophytic colonization and osseous matrix biodegradation. Conversely, DA revealed terrestrial paedogenic communities: balanced Alphaproteobacteria (46%) with diverse actinobacterial genera (Streptomyces, Burkholderia, Mycobacterium), reflecting soil-mediated diagenesis. aMETA analysis also identified few dominant eukaryotic signatures—*Cyprinus carpio* (common carp), *Mytilus galloprovincialis* (Mediterranean mussel), *Apis mellifera* (honeybee), *Bombyx mori* (silkworm) providing molecular signatures on possible Harappan dietary, storage and trading practices. This metagenomics approach establishes transformative methodologies in archaeological interpretation, integrating molecular biology with traditional archaeological frameworks to reconstruct ancient socioeconomic systems and environmental contexts.

Are humans driving widespread invasions of intragenomic parasites in insects?

3. Pathogens/Microbiomes

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Abstract text: When we compared the genomes of 200-year-old fruit flies (*Drosophila melanogaster*) from museum collections and recently captured wild flies we were surprised to find that large parts of the fruit fly genome were missing from the old specimens. About 1 million base pairs, roughly 1% of the genome, were absent from the old flies. The missing parts largely consist of transposable elements (TEs) - parasitic DNA that replicates in genomes. Based on genomic time-series data, including the genomes of museum specimens, we show that 12 different TEs invaded worldwide fruit fly populations during the last 200 years. These invasions were triggered by horizontal transfer from different species. Such a high rate of genomic invasions is likely not normal and may have a substantial impact on the evolution of the genome and phenotype of the flies. We propose that the rate of invasions has increased recently due to human activity. To test this hypothesis we are currently sequencing museum specimens from diverse taxa.

Beyond Morphology: Metagenomic Authentication of Ancient Fish Remains Through Ichthyopathogenic Signatures

3. Pathogens/Microbiomes

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Abstract text: Ichthyoarchaeological investigations in South Asia's Indus Civilization have predominantly relied on morphological assessments, lacking molecular validation frameworks to authenticate taxonomic assignments and establish specimen biological provenance. This methodological gap has limited robust reconstruction of aquatic resource exploitation patterns compared to terrestrial faunal assemblages. This study employed integrated morphometric-molecular authentication of skeletal material from Dholavira, Gujarat, analyzing a single specimen through comparative osteological examination against modern reference databases, suggesting *Cyprinidae* family assignment. To provide independent molecular validation through preserved host-associated microbiota, metagenomic DNA was extracted using GENECLEAN® ancient DNA protocols and subjected to high-depth Illumina sequencing to ensure comprehensive taxonomic coverage of microbial communities without detection bias., with taxonomic profiling via Kraken and Centrifuge classifiers. Metagenomic analysis revealed fish-associated pathogenic bacterial assemblages including *Aeromonas hydrophila*, *Aeromonas salmonicida*, *Lactococcus garvieae*, *Pseudomonas fluorescens*, and *Mycobacterium marinum*—obligate ichthyopathogens serving as molecular authentication markers confirming fish origin. Recovery of these fish-specific microbial communities provides independent molecular corroboration of morphological identification, establishing ichthyological exploitation as a deliberate subsistence component during Harappan occupation. This integrative approach demonstrates metagenomic pathogen profiling as a robust molecular validation tool for ichthyoarchaeological specimens, expanding methodological frameworks for reconstructing aquatic resource utilization in South Asian contexts.

Characterization of the ancient human oral microbiota recovered from teeth

3. Pathogens/Microbiomes

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Abstract text: Metagenomic sequencing of ancient DNA extracted from dental calculus has yielded important insights into the composition and functional diversity of the human oral microbiota in the past. Ancient human teeth have been sampled widely for studies of human host DNA, however their characteristics as potential sources for ancient human oral microbiota have yet to be determined.

Here, we present a comprehensive characterization of the microbiota retrieved from 1,313 ancient humans ranging from the Upper Paleolithic to historic times. Analyzing species abundance profiles derived against a modified version of Genome Taxonomy DataBase (GTDB), we demonstrate that oral microbiota are frequently recovered from ancient human teeth samples. We further characterize the composition of the teeth microbiota of 217 high abundance samples against large-scale reference dataset including publicly available modern and ancient oral microbiomes.

Our study demonstrates that ancient metagenomic data extracted from ancient human teeth can provide a hitherto under-exploited resource to study human oral microbiome evolution.

Clade-specific evolutionary rates and regional diversity in Mycobacterium lepromatosis across regions and times

3. Pathogens/Microbiomes

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Abstract text: The recent identification of *Mycobacterium lepromatosis* in pre-contact Americas has raised key questions about its evolutionary history, such as the timing and mechanisms of its long-term persistence and inter-regional transmission. Reliable molecular dating is crucial yet hampered by limited samples and rate heterogeneity. Here, we broaden and reanalyze data from ancient and modern *M. lepromatosis* genomes. To resolve its timeline, we implement a local clock approach, enabling independent rate estimation across ancient Canadian and Southern Cone samples, modern divergent North American strains, predominant present-day clades, and red squirrel–associated lineages. Our model uses phylogenetic priors to address deep branching and sparse sampling. Ancient South American genomes (4,000–1,000 years BP) form a monophyletic lineage, confirming deep temporal continuity. Ancient Chilean and deep-branching modern North American strains evolved tenfold faster than ancient Argentinian, Canadian, or animal clades, revealing marked heterogeneity. Clade-specific rate differences among Argentinian and Chilean lineages highlight regional variation in evolutionary dynamics. Red squirrel strains from the British Isles form a highly similar clade, confirming clonal expansion from a single introduction. Our findings improve leprosy's timeline and suggest that regional rate variation may indicate overlooked reservoirs or transmissions, underscoring the value of local clocks for infectious disease paleogenomics.

Co-infection of Yersinia pestis and other zoonoses during Italian prehistory

3. Pathogens/Microbiomes

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Abstract text: The infection of humans by the causal agent of Plague, *Yersinia pestis*, has been attested as far back as 5500 BP. Although the specific aetiology of the disease caused by these prehistoric genomes remains unclear, the bacterium swiftly spread westwards towards Europe, likely reaching the continent during the Late Neolithic to Bronze Age (LNBA). In this study, we analysed 9 genomic samples originating from 8 different human individuals dating to around 4920 cal BP from the site of *Grotta della Spinosa*, Tuscany, Italy. Metagenomic screening of these samples reveals one individual (GSP013) to be co-infected by *Yersinia pestis, Erysipelothrix rhusiopathiae*, and Hepatitis B virus (HBV). At least three further individuals from the site were infected with HBV. The phylogenetic placement of *Y. pestis* in GSP013 shows that this strain is closely related to the earliest LNBA Caucasus genomes of the bacterium, basal to later European diversity. This represents the earliest evidence of *Y. pestis* in the Italian peninsula (and Southern Europe more widely) to date, predating previously discovered genomes by at least 200 years. This contributes to

our understanding of *Y. pestis* transmission in prehistoric Europe, and offers insights into disease dynamics in communities during the 3rd millennium BCE.

Current insights and future aDNA research perspectives on Africa's disease landscape

3. Pathogens/Microbiomes

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Abstract text: Africa's biodiversity, rapid ecological change and intense human–wildlife contact make it a critical hotspot for emerging infectious diseases. Ancient DNA studies outside Africa have generated high-resolution genomes of ancient pathogens, transforming our understanding of past epidemics. In Africa, however, ancient pathogen research remains in its infancy, lacking a systematic survey of sub-Saharan contexts, with research efforts concentrated on Egyptian mummies. To date, only one study has directly analysed metagenomes from sub-Saharan human remains, identifying *Rickettsia felis* in a 2,000-year-old child from Ballito Bay, South Africa. This sparse genomic record contrasts with Africa's long history of infectious disease, reflected in burdens of typhoid, tuberculosis, cholera, malaria and schistosomiasis, and in genomic evidence pointing to an African origin of the MTBC ancestor. Written sources suggest African roots for the Justinian plague, and the continent continues to experience the highest global incidence of plague, with Madagascar as a hotspot. Yet evidence for how these pathogens shaped past African populations, influenced outbreaks and drove host adaptation remains limited. With expanding archaeological access, advances in biomolecular methods and increasing interest in Africa's disease history, the coming years are likely to transform our understanding of ancient pathogens and their impacts on African populations.

De novo assembly of ancient metagenomic data from dental calculus to disentangle the Neolithic transition in Southern Europe

3. Pathogens/Microbiomes

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Abstract text: The interest in ancient metagenomics is increasing with over 1.700 ancient microbial genomes, partial genomes, and metagenomes characterized. However, most studies focused on aligning sequences to modern reference genomes, limiting discoveries to known taxa and introducing a reference bias, as ancient and modern genomes differ genetically. A way to overcome this is through *de novo* assembly, which reconstructs genomes of all species present in a sample. We evaluated multiple *de novo* assembly pipelines using simulated ancient metagenomes and identified the optimal pipeline for reconstructing ancient metagenome-assembled genomes.

We applied this approach to ancient metagenomes covering the Neolithic transition, a major cultural and demographic event in Europe that affected both human evolution and the oral microbiome. We collected published metagenomic data from different regions in Europe ranging from the Palaeolithic to the Bronze Age, along with newly sequenced samples from Italy. We focus on reconstructing the ancient genome of *Anaerolineaceae oral taxon 439*, a bacterium found at higher abundance in the oral microbiome of Neolithic farmers. Through genome reconstruction, we investigated its genetic variability and perform functional annotation to identify genes that may have been lost/gained and can have an impact in the metabolization of food/medicines.

Deep-time Leptospira and Borrelia in Eurasian water voles revealed by ancient metagenomics

3. Pathogens/Microbiomes

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Abstract text: Leptospirosis is the most widespread bacterial zoonosis and is primarily maintained in rodent reservoirs, yet its deep evolutionary history and that of other rodent-borne infections such as Lyme disease remain largely unexplored in ancient DNA. Here, to reconstruct long-term rodent-pathogen associations, we use metagenomic screening of around 300 water vole (*Arvicola* spp.) specimens spanning 500,000 years across Eurasia. We detect multiple understudied *Leptospira* species from diverse time periods and locations, all within a clade comprising pathogenic *Leptospira*, including the first ancient signal of *L. kirschneri*. We also find low-level signals for *L. borgpetersenii* and *L. kirschneri* in earlier contexts including the early Holocene and the late Pleistocene (c. 29–11.7 ka), suggesting a long-standing association of *Leptospira* with *Arvicola*. Finally, we identify the first ancient DNA evidence for *Borrelia afzelii* in a Holocene specimen, potentially extending the temporal depth at which Lyme disease-associated pathogens interacted with water voles. To deepen the resolution of these lineages, we are now applying targeted hybridisation capture using custom bait sets. Together, these findings provide the first spatiotemporal framework for infectious organisms in ancient water voles and will lay the groundwork for reconstructing long-term rodent-pathogen evolutionary dynamics.

Genomic reconstruction of pathogens from modern and historical Chimpanzees of Gombe, Tanzania

3. Pathogens/Microbiomes

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Abstract text: Infectious diseases pose an ongoing threat to the conservation of non-human primates, particularly in populations already affected by habitat loss and human expansion, such as those at Gombe, Tanzania. To investigate pathogen presence across time, we generated shotgun sequencing data from 26 *Pan troglodytes schweinfurthii* individuals in the Gombe Skeletal Collection (1966–2010), using dentine and/or dental calculus. We also analyzed fecal samples from living chimpanzees at Gombe. From the historical dental samples, we identified DNA from oral pathogens, including *Tannerella forsythia*, demonstrating the long-term persistence of oral disease–associated bacteria in wild chimpanzees. Remarkably, samples from two individuals contained 5,000–7,000 reads mapping to *Mycobacterium leprae*, and one living individual showed ~6,000 reads aligning to the same pathogen. These findings represent the first evidence of *M. leprae* circulating among wild chimpanzees at Gombe. Ongoing capture-enrichment of *M. leprae* from these samples will increase genomic coverage and enable phylogenetic comparisons with published genomes from humans, chimpanzees, and other animal hosts. Together, this work expands our understanding of pathogen diversity in wildlife and provides new insight into how infectious agents circulate and adapt within chimpanzee populations over time.

Genotype 2 human parvovirus B19 from early modern warships bridges a gap of nearly a millennium in the European record

3. Pathogens/Microbiomes

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Abstract text: Early modern warships were floating societies in confined quarters that favoured pathogen transmission. We screened calcified tissues from 31 sailors (19 from the *Mary Rose*, 12 from *Kronan*) using shotgun metagenomics. Human parvovirus B19 (B19V), a common childhood virus that causes fifth disease, colloquially called slapped cheek syndrome, and can lead to severe anaemia and foetal complications, was detected in 21 individuals (14 of 19 from the *Mary Rose* and 7 of 12 from *Kronan*). We reconstructed two complete and one partial B19V genomes, all genotype 2, a lineage historically widespread in Europe but now largely replaced by genotype 1. Ancient origin is supported for 11 individuals by deamination patterns, fragment length distributions and enrichment of coverage in the inverted terminal repeats. Phylogenetic placement shows that these genomes bridge a gap of nearly a millennium between early medieval European sequences (around 950 CE) and twentieth-century European clinical material and indicate continued genotype 2 circulation, with within-ship diversity pointing to pre-embarkation infections and long-term tissue persistence rather than onboard transmission. Our results also demonstrate that DNA viruses can be recovered and authenticated from human remains that lay submerged in marine sediments for centuries, highlighting shipwrecks as informative archives for pathogen evolution.

Historical Genomes Reveal a Centuries-Long Competition–Colonization Trade-off in Pseudomonas

3. Pathogens/Microbiomes

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Abstract text: Microbial competition drives rapid adaptation, often forcing organisms to specialize in new ecological niches. Adaptations that improve competitive ability can reduce performance in other environments, creating evolutionary trade-offs. Whether such trade-offs persist in nature, or are eroded as lineages adapt through compensatory changes, remains largely unknown. Here we show that a trade-off between competitive ability and host colonization has been stably maintained in natural *Pseudomonas* populations for centuries. Wild plant-pathogenic *Pseudomonas* compete using tailocins—phage-derived molecular weapons that bind to specific cell-surface receptors. Genomic surveys and functional assays reveal that the most broadly lethal tailocins remain rare. While tailocin production increases competitive killing, it also compromises plant colonization. Crucially, herbarium-derived historical genomes spanning two centuries demonstrate that the underlying polymorphisms are not transient. These time-resolved data reveal that the competition–colonization trade-off has persisted for at least 10^5–10^6 generations, providing direct evidence that this constraint is evolutionarily stable rather than transient. Together, these results show that in natural populations, a trade-off between competition and colonization is fundamental and not easily overcome. This stability suggests that tailocin resistance may come with predictable fitness costs, highlighting tailocins as a promising therapeutic avenue where resistance could weaken pathogens in natural or clinical settings.

Insights into retroviral evolution through paleovirology

3. Pathogens/Microbiomes

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Abstract text: *Retroviridae* is an important viral family that contains many mammalian pathogens and has a long history of co-evolution with vertebrates. The obligate integration of retroviruses into host DNA during infection leads to endogenous retroviruses (ERVs), which can be passed on to progeny if integrated in a germline cell. These elements act as molecular "fossils", providing insights into evolutionary trends over millions of years.
We created a pipeline to detect ERVs based on sequence similarity to retroviral proteins, reconstruct the ancestral proteins and classify them with custom HMMs. We then use MMSeqs2 to cluster the POL proteins of each ERV into viral lineages. We identify LTRs and use their divergence to estimate the age of each ERV within a species.

Collecting data from 4,155 vertebrate genomes, we identify discrepancies in the types and rate of retroviral integration in different host orders, indicating the differential burdens that retroviral infections have on species over time. We also identify ERVs from recently circulating retroviruses to understand the transmission dynamics influencing the modern global retrovirome, and possible zoonotic reservoirs for vertebrate pathogens. Finally, we explore the origins of retroviral genera, expanding our understanding of the evolutionary patterns that shape this viral family.

Leveraging ancient metagenome-assembled genomes to understand pathogenicity evolution in microbiome species

3. Pathogens/Microbiomes

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Abstract text: Advances in ancient microbial genome reconstruction through *de novo* assembly paved the way for identification of previously unrecognized oral microbial species. Genomic variability of both extant and seemingly extinct oral microbial species and strains indicates substantial genetic diversity with a high potential for biotechnological exploration. We observe high conservation of clinically relevant antibiotic resistance gene clusters across diverse taxonomic groups extending far back in time, preceding pharmaceutical antibiotic exposure. Individual gene clusters are part of unique networks of gene transfer that sustain and spread antibiotic resistance in oral microbes. Evolutionary relationships within resistance gene clusters provide evidence of horizontal gene transfer between unexpected taxa including previously unknown organisms. Comparison of gene distributions in ancient and modern oral microbiomes demonstrates both shifts and continuity in reservoirs of resistance over time. Tetracycline resistance, while one of the most prevalently detected mechanisms in modern oral microbiomes, is rare in ancient microbial genomes, and instead vancomycin resistance is nearly ubiquitous. These findings shape how we understand the purpose of antibiotic resistance genes in microbial communities, and provide insights into the molecular mechanisms by which host-associated microbial species evolve to evade antibiotics.

Metagenomic reconstruction of ancient oral microbiota from dental calculus: Preliminary results from 13th century Niceae dental calculus samples

3. Pathogens/Microbiomes

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Abstract text: Ancient dental calculus preserves microbial and eukaryotic DNA that can depict historical human oral microbiome, health, dietary habits and cultural practices. However, recovering this biomolecular information requires integration of several taxonomic, and functional metagenomics pipelines.

In this study we focused on medieval İznik (Nicaea), a culturally diverse city inhabited by Crusaders, local Muslims, and local Christians. Our workflow combines k-mer and alignment methods to classify and authenticate ancient bacterial reads. Furthermore we utilized metagenome assembly and binning strategies to reconstruct metagenome-assembled genomes and prediction of virulence factors.

Preliminary analyses from a subset of the Crusader individuals revealed authentic oral bacteria such as Streptococcus and Neisseria, along with opportunistic periodontal pathogens. Metagenome assembly produced 620 metagenome bins, at least 5 of them assigned to a taxonomy using marker genes. One particular bin was classified as Neisseriaceae and contains virulence factors that help bacteria to evade the immune system. Moreover, DNA fragments from dietary sources including sheep and pig were detected.

We are currently sequencing additional individuals from local Christians and Muslims. Together with the new dataset, our study will provide insights on the complex interaction of culture, oral microbiome, health and diet of the people from medieval İznik.

Microbial Time Capsules: Investigating Past Human Mobility and Interactions through Phylogenomics of Ancient Commensal Microbes.

3. Pathogens/Microbiomes

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Abstract text: Dental calculus, the calcified plaque that accumulates on tooth surfaces, exceptionally preserves the genetic record of the oral microbiome for millennia; one of the most stable and conserved human microbial communities across populations. Most knowledge surrounding the oral microbiome originates from modern samples, and little is known about these human-microbe associations across time and space, or how informative these microbes are about their host and host population history. We hypothesized that since oral microbial communities show similar taxonomic composition across populations and are primarily transmitted through close contact, they may be maintained within human populations over large spatiotemporal scales, and that their strain lineages could track human movements over time. To test this, we analyzed over ~2,700 ancient oral metagenomic samples from >70 countries spanning >100,000 years, applying strain-resolved phylogenomic approaches to oral microbial species recovered across diverse spatiotemporal contexts. Combined with archaeological information, these analyses reveal strong, reproducible biogeographic structure for several taxa, with clear signatures of dispersal coinciding with major episodes of human mobility and contact. Together, our results demonstrate that ancient dental calculus offers a robust, complementary archive to ancient human DNA for reconstructing past demography and mobility, while illuminating the evolution and ecology of host-associated microbes.

Paleomicrobiome based MAGs from a Harappan Site: Reconstructing Taphonomic and Cultural Relevance

3. Pathogens/Microbiomes

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Abstract text: Paleomicrobiome preserve signatures of prehistoric diagenetic processes, yet read-based taxonomic profiling lacks genomic resolution for robust phylogenetic inference. We analysed Metagenome Assembled Genomes (MAG) using nf-core/mag—one of few standardized pipelines for ancient DNA metagenomics—integrating MEGAHIT/SPAdes assembly, MetaBAT2/CONCOCT/MaxBin2 binning exploiting tetranucleotide frequency and coverage covariance, QUAST metrics, BUSCO completeness, GUNC filtering, and GTDB-Tk phylogenomic classification, investigating Dholavira specimens: osteological material (DB) and archaeological assemblage (DA). We performed high-depth sequencing spanning fragment lengths 25-1500 bp ensuring comprehensive coverage with 40.88 GB (DB) and 22.02 GB (DA) generated data. Consensus binning yielded 357 bins (346 post-QC, 110 GUNC-validated). Major MAGs identified using GTDB-Tk revealed DB-associated *Acinetobacter baumannii*, *Aeromonas veronii*, *Vibrio owensii*, *Shewanella algae*, *Cutibacterium acnes*, and *Bombiscardovia polysaccharolytica*, collectively mediating collagenase-dependent proteolysis, extracellular enzymatic degradation, halotolerant saprophytic metabolism, hydroxyapatite dissolution, and mammalian gut microbiome signatures. DA analysis revealed Gemmatimonadota (25%), archaeal *Nitrososphaeria* and *Nitrospirota* establishing syntrophic ammonia-nitrite oxidation pathways, alongside obligate *Apis mellifera* symbionts *Gilliamella apicola* and *Bombilactobacillus mellis* mediating nectar carbohydrate metabolism and pollen fermentation, constituting genomic signatures of Harappan apicultural systems. This pilot investigation establishes foundational MAG-based datasets; their deamination profile to distinguish ancient from modern genomes, further facilitating reconstruction of diagenetic pathways and socioeconomic practices through genome-resolved paleomicrobiome analysis.

Past population structure and indicators of gene flow in a malaria parasite, Plasmodium falciparum

3. Pathogens/Microbiomes

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Abstract text: Understanding the long-term dynamics of *Plasmodium falciparum* is essential for contextualizing modern malaria epidemiology and its current population structure. Historical genomic data from pre-eradication Western Eurasia remain extremely limited, leaving its genetic history largely unknown.

Here, we present ancient *Plasmodium* infections in a 230-year-old individual from Aknashen, Armenia. We show that the individual carried a co-infection of three of the major human-infecting Plasmodium parasites, *P. falciparum*, *P. vivax and P. malariae*, demonstrating their presence in the southern Caucasus regions before their eradication.

Using in-solution hybridization capture combined with shotgun metagenomic sequencing, we recovered genome-wide *P. falciparum* nuclear data at 0.13X average read depth, as well as a 3.5X mitochondrial genome. Joint analyses with published ancient genomes and modern population data shows that the ancient Armenian P falciparum has close genetic affinities with pre-eradication strains from southern Europe represented by a previously published sample from Spain, suggesting connectivity and a distinct Western Eurasian genetic cluster. Building on this, we construct admixture graphs and test alternative demographic scenarios for *P. falciparum*, providing new insights into its historical population structure and dispersal in Europe.

Plague before History: Reconstructing the Emergence and Spread of Yersinia pestis in Prehistoric Eurasia through a Historical Science Framework

3. Pathogens/Microbiomes

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Abstract text: Today, we witness the insurmountable challenges posed by emerging and re-emerging pathogens. No case reflects this more than the recent advent of the SARS-CoV-2 virus. Unfortunately, we are not yet able to fully understand the relationship between the natural and human forces that drive disease outbreaks. To overcome this knowledge impasse, we need an innovative methodological approach that coalesces insights from history, archaeology, and palaeoscience to obtain a richer appreciation of past disease outbreaks. This paper inaugurates such an approach by outlining the foundations of a "historical science" methodology that bridges these disciplines.

Plague research provides an excellent testing ground for this framework. In recent years, ancient pathogen genomics has uncovered plague's deep past, revealing that the plague pathogen (*Yersinia pestis*) infected prehistoric populations long before the first historically recorded pandemic, rendering the traditional three-pandemic narrative obsolete. Using case studies from the field of prehistoric plague, this paper demonstrates how historical science can reveal patterns in pathogen evolution and spread. Plague's long evolutionary history, shaped by the interplay between biological, environmental, and human interactions, offers a rare opportunity to investigate how infectious diseases emerge, persist, and infect humans over centuries or millennia.

Reconstructing 3,500 Years of Sheeppox Virus Evolution Using archaeological and codicological genomes

3. Pathogens/Microbiomes

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Abstract text: Sheeppox virus (SPPV) is a major pathogen of small ruminants, with descriptions of the disease dating back to Roman antiquity. We report the recovery of ancient SPPV genomes spanning the Bronze Age to the pre-modern period across the Eurasian steppes and Western Europe (n = 24). Our dataset includes multiple genomes obtained from medieval parchment manuscripts, highlighting animal-skin documents as an under-recognized source for reconstructing ancient livestock pathogen genomes. Notably, SPPV sequences recovered from parchment derive from a range of different host species. Phylogenomic analyses reveal that medieval SPPV strains were widespread and diverse during the Middle Ages, forming a now-extinct sister clade. Using this expanded temporal framework, we refine the evolutionary history of the Capripoxvirus genus and estimate that major lineages diverged ~5,000 years BP, with SPPV representing the earliest split from the lineage leading to goatpox and lumpy skin disease viruses. These results also highlight convergent gene-inactivation events between sheeppox and goatpox viruses.

Studying disease amidst the expansion of Medieval and Early modern Plague networks in Anatolia

3. Pathogens/Microbiomes

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Abstract text: *Yersinia pestis*, the causative bacterium of the Plague, killed ~30-50% of Europe's population during the Black Death (1348-1353), the initial epidemic wave of the second Plague pandemic (1346-1840). This devastating disease persisted in cyclical outbreaks across Afro-Eurasia for 500 years, and its descendants established global reservoirs, which continue to cause outbreaks today. Genomic studies of ancient *Y. pestis* recovered from archaeological remains have attempted to trace the bacterium's origins, locate reservoirs, and understand these patterns of persistence and reintroduction. One significant region currently lacking genomic evidence of *Y. pestis* is the Ottoman Empire. Situated between Asia and Europe, Eurocentric narratives continuously paint the Empire as an importer of Plague into Europe. Here, we screen 289 human and animal remains from across the Empire for evidence of *Y. pestis* and its reservoirs. We recover two ancient *Y. pestis* genomes from early outbreaks of the pandemic at the historically significant site of Nicaea and place them on an updated second pandemic phylogeny. We then explore the life histories of these two individuals using stable isotopes. Simultaneously, with our team of researchers from across the global North and South, we grapple with topics in ancient DNA ethics and their application within our work.

Studying the evolution of the oral microbiome of wild mammals using dental calculus metagenomics

3. Pathogens/Microbiomes

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Abstract text: Despite growing interest, wild animal microbiomes remain poorly characterized, particularly for body sites beyond the gut. A central question is whether host-associated microbiomes are shaped primarily by ecological traits, such as diet, or by host phylogeny. Progress has been limited by challenges in sampling wild species. Here, we use dental calculus preserved on museum specimens to investigate the evolution of the oral microbiome across wild mammals. Although dental calculus is widespread among mammals, it has been studied mainly in humans and other primates. We analyse dental metagenomes from 32 mammalian species (most newly sequenced) spanning broad phylogenetic, dietary, and ecological diversity. We find that both host diet and digestive physiology influence the taxonomic composition and metabolic potential of the oral microbiome. Mammal species typically harbour distinct microbial communities, but their diversification does not consistently track host phylogeny. Nonetheless, we identify specific microbial clades, including taxa commonly associated with the oral cavity or rumen, that show evidence of co-diversification with their hosts. Overall, the oral microbiome is shaped predominantly by environmental filtering imposed by conditions in the oral cavity, which are driven by diet, physiology and other uncharacterised species-specific traits, while finer-scale phylogenetic signal persists in particular microbial lineages.

Temporal metagenomics of population decline in Swedish brown bears

3. Pathogens/Microbiomes

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Abstract text: Population decline is exacerbated by numerous factors, including environmental perturbation and decreasing genetic diversity. Symbiotic microbiomes are intrinsically linked to host health, where community composition is mediated by host genetics. This relationship is especially relevant to wild systems in the face of climate change and rapid population declines. It is thus crucial to understand how long-term changes in genetic diversity of wild populations impact host-microbiome interactions. To this end, we utilised dental calculus, the calcified oral microbiome, from museum-preserved specimens of Scandinavian brown bears that experienced a dramatic bottleneck during the last 200 years. The population demonstrated high prevalence of oral disease where affected teeth had significantly perturbed microbiomes dominated by mutans-complex Streptococcus species that cause caries in humans. We compared phylogenies and virulence factor repertoires for metagenome-assembled genomes of brown bear *Streptococcus* to caries-associated *Streptococcus* genomes from ancient and modern human calculus metagenomes. We then characterised temporal diversity and function of oral microbiomes in healthy and diseased brown bears during population decline and recovery. Understanding the interplay between microbiomes and host genetic diversity is necessary for predicting the impact of population decline from a holistic perspective, encompassing the consequences of altered microbiome composition and function on overall host health.

The World's Highest Ritual Sacrifice: A Long Journey and Severe Health Stress Revealed Through Non-Invasive Mummy Sampling.

3. Pathogens/Microbiomes

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Abstract text: Discovered in 1999 atop the Llullaillaco volcano in the Argentinian Andes, the "Children of Llullaillaco" are among the best-preserved mummified human remains ever found. Sacrificed as part of the Inca *Capacocha* ritual around 1480 CE, they offer a rare opportunity to investigate the biological and cultural dimensions of high-altitude ceremonies. Using fully non-invasive sampling, we generated a comprehensive multi-omic dataset encompassing ancestry, diet, microbiomes, and pathogenic load during their final months. This integrative framework reveals the individuals' geographic origins with unprecedented precision and provides evidence from multiple pathogens suggesting potentially severe health stress before death. Multi-omic signals from both dietary remains and authentic microbiomes indicate that the children received a distinct final diet, as well as revealing undocumented variation. Moreover, our analyses suggest that the three individuals may not have been strictly contemporaneous, challenging long-held assumptions. By integrating genomic data with historical accounts and archaeological context, we further explore possible motivations behind their selection and ritual sacrifice. This study represents one of the most extensive genomic investigations of archaeological individuals to date and illustrates the transformative potential of non-invasive, multi-omic approaches for researching exceptionally preserved human remains.

Part of the multi-omic dataset created here was the recovery of RNA from surface swabs, yielding a low coverage transcriptome. The majority of mapped reads falls into exons, and we observe a high

degree of reads with signatures of splicing, and the most abundant gene products reflect the sampled body parts.

Tracing the evolutionary history of Epstein-Barr Virus using modern and ancient genomes

3. Pathogens/Microbiomes

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Abstract text: Epstein–Barr Virus (EBV) is a ubiquitous human pathogen with two main genotypes (type 1 and type 2), exhibiting distinct geographic distributions and disease associations.The long-term evolutionary dynamics of EBV remain poorly understood due to the lack of ancient EBV genomes. Here, we report the oldest ancient EBV genomes sequenced to date, recovered from pieces of chewed birch tar from Mesolithic and Neolithic European contexts. We demonstrate that both types of EBV circulated in prehistoric Europe. Phylogenetic analyses reveal that ancient type 1 EBV strains fall basally with contemporary Asian lineages, suggesting a deeper shared ancestry and supporting the hypothesis that EBV diversified accompanied with early human dispersal out of Africa. We next investigated coding variation to assess their potential roles in viral pathogenesis. One ancient strain carried two out of three high-risk variants within *BALF2* associated with nasopharyngeal carcinoma. Besides, we identified E201Q mutation in glycoprotein 350 under positive selection, associated with immune escape. These mutations may reflect early adaptations influencing viral infectivity and oncogenic potential.

Tracing the pre-antibiotic osteomyelitis pathogens behind today's hospital superbug epidemics

3. Pathogens/Microbiomes

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Abstract text: Osteomyelitis is a potentially life-threatening infection of the bone marrow, historically associated with high mortality prior to the introduction of antibiotics. Despite advances in treatment, it remains a significant healthcare burden today, with an incidence of ~17 per 100,000 in Germany. The condition can be caused by a wide range of pathogens, most notably *Staphylococcus aureus* and other members of the "ESKAPEE" group. Several of these taxa are of particular concern, due to their rapid acquisition of multidrug resistance. Despite their clear clinical importance, the evolutionary history of these pathogens remains unexplored. To address this, we analysed seven autopsy specimens from adults who suffered from osteomyelitis between the mid-1800s and 1920s in Germany. Using an untargeted pathogen screening approach, we identified virulent strains of *Acinetobacter baumannii, Staphylococcus aureus* and *Streptococcus pyogenes*. Phylogenetic analyses revealed links between these historical strains and modern pandemic lineages. Furthermore, all three strains harboured genes for adhesion, biofilm formation, cytotoxicity and immune evasion, suggesting these traits are crucial for establishing bone infections. We also demonstrated that the historical *S. aureus* strain was methicillin susceptible, while *A. baumannii* exhibited early multidrug resistance potential. Our findings provide novel insights for understanding the past and present of nosocomial infections.

Treponemal infection during the Ottoman Period in the Southern Levant: A paleogenomic–paleoproteomics approach toward reconstructing pathogen history

3. Pathogens/Microbiomes

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Abstract text: Treponemal infections particularly *Treponema pallidum* subsp. *endemicum*, the causative agent of endemic treponematosis (bejel) have long been considered part of the disease landscape of the Southern Levant. Yet, despite osteological suggestions of its presence, the epidemiology and evolutionary history of bejel in ancient Levantine populations remain largely unresolved, as no authenticated ancient genomes from the region have been recovered. This gap limits our ability to assess its antiquity, geographic spread, and lineage diversity in past communities. A pilot investigation on 2 individuals dated to the Ottoman period, whose skeletal remains exhibit lesions consistent with bejel.In this study, 2 teeth were sampled from each individual. DNA was extracted and converted to single-stranded DNA libraries before shotgun sequencing on an Illumina NextSeq platform. Treponemal genomic screening was complemented by paleoproteomics analysis on dentine, to reinforce pathogen authentication across independent biomolecular systems. Our preliminary results suggest that *T. pallidum* subsp. *endemicum* can be detected even in hot-climate archaeological settings. These results require further analysis; if confirmed, they would provide the first biomolecular indication of treponemal disease in the S. Levant and serve as a starting point for a broader, multi-individual study aimed at clarifying this long-standing gap in the region’s infectious disease history.

Unraveling the Impact of Vaccination on Morbillivirus Evolution

3. Pathogens/Microbiomes

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Abstract text: Despite the availability of highly effective vaccines, RNA viruses in the *Morbillivirus* genus continue to cause significant mortality in humans and other animals. Measles virus resurges whenever vaccination coverage declines, yet we still understand little about how these pathogens evolve over long timescales in response to control efforts. The eradication of rinderpest virus in 2011, the closest known relative of measles and the only RNA virus ever eliminated, offers a rare chance to ask a fundamental question: what allows a pathogen to disappear rather than persist?

This ongoing project reconstructs morbillivirus evolution with a focus on rinderpest and its relationship to measles by integrating modern and ancient genomic data. Newly generated genomes from nineteenth-century European specimens are paired with twentieth-century sequences from Africa and Asia, capturing viral dynamics before, during, and after major vaccination campaigns. Using advanced phylodynamic models that incorporate time-dependent rates and lineage-specific heterogeneity, we aim to quantify how interventions such as quarantine, culling, and vaccination reshaped rinderpest diversity, reduced its effective population size, and contributed to its disappearance. Taken together, this work aims to reveal the conditions that enabled rinderpest eradication and to generate insights that can strengthen control strategies for measles and other vaccine-preventable viruses.

Selected references

Translator

4. Sedimentary ancient DNA

Not One Story: Divergent Phytoplankton Responses Through 7,000 Years of the Baltic Sea

4. Sedimentary ancient DNA

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Abstract text: The Baltic Sea is characterised by high instability, making it vulnerable to the effects of climate change. Its semi-enclosed, shallow and brackish nature creates a highly dynamic environment. This is combined with repeated cold and warm periods over the last millennia, making the Baltic Sea an ideal system to study past climate impacts on biodiversity. As the basis of marine food webs, phytoplankton play a key role in oxygen and biomass production. This key but also diverse taxonomic group is frequently used to study the impacts of climate change. Here, we investigated the community dynamics of cyanobacteria, diatoms, and dinoflagellates independently to understand the Holocene dynamics of Baltic phytoplankton diversity. We focused on sedaDNA metabarcoding for community reconstruction and biomarkers for environmental reconstruction, spanning the last 7,000 years. Our analysis reveals three major community transitions (~6,000, 3,500, and 1,000 cal yr BP), each detected by only a subset of the investigated taxa rather than all three groups. These transitions align with the well-known Baltic Sea stages and Holocene climate fluctuations. Our study highlights that studying multiple taxa independently provides complementary insights, making these studies essential for the holistic analysis of climate responses.

100 metagenomes link stabilisation of the marine environment to a bloom in prehistoric forager societies in Aarhus Bay

4. Sedimentary ancient DNA

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Abstract text: Reconstructing marine ecosystems across the Holocene is critical for understanding long-term biodiversity dynamics and human adaptation to changing coastal environments. Hundreds of archaeological shell middens across Denmark, including coastal sites now submerged, show that hunter-gatherer-fisher communities (~ 7,500 yr BP) relied intensively on marine resources, with continuity across the transition to agriculture (~5,900 yr BP). However, knowledge of past marine biodiversity remains primarily dependent on the selective preservation of faunal remains from coastal shell middens. Sedimentary ancient DNA (*seda*DNA) has emerged as a powerful tool to reconstruct long-term ecosystem dynamics. Here, we analyse 100 metagenomic samples from three sediment archives from Aarhus Bay (Denmark) spanning the last 9,200 years to assess ecosystem changes in relation to human exploitation and cultural transitions. We observe a transformation from terrestrial to brackish and fully marine environments, with a rapid shift in eelgrass (*Zostera marina*), plankton, and benthic communities corresponding to Holocene sea-level rise events. We detect no clear anthropogenic impacts on biodiversity; instead, our findings, integrated with C14 age-depth models, archaeological site distributions, climatic and environmental proxies, suggest that rapid sea-level stabilisation in Aarhus Bay was a major factor enabling the flourishing of early hunter-gatherer-fisher communities in the region.

A fully harmonized global plant DNA metabarcoding datasets to track potential plant extinction

4. Sedimentary ancient DNA

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Abstract text: Plant extinction risk is increasing globally, but past plant extinctions remain unclear. Compared with pollen and plant macrofossil archives, sedaDNA records local plant communities at a high taxonomic resolution, making it well suited for tracking plant taxon loss through geological time. Here, we compile all available sedaDNA plant metabarcoding records worldwide generated with the chloroplast *trn*L (UAA) P6 loop, the most commonly used metabarcode for plants. In total, we obtained sedaDNA data from 76 cores generated by our research group and 74 cores sourced from published studies. To improve taxonomic assignment specificity, we used OBITools4 and 16 customized region-specific reference databases, which integrate GBIF taxon-occurrence data with sequences from existing genetic databases (arctborbryo, PhyloNorway, PhyloAlps, and EMBL). This results a harmonized dataset at the level of Amplicon Sequence Variants (ASVs), with database ASVs assigned at 100% match and non-database ASVs at ≥90% similarity, thereby enabling the detection of candidate extinct taxa. Further plant extinction analyses are underway and will be finalized and presented at ICP 2026. All data contributors will be acknowledged in the conference presentation.

A Sequence of Southern Sweden: Sedimentary Ancient DNA Analysis of Environmental Change on the Kullen Peninsula

4. Sedimentary ancient DNA

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Abstract text: The Kullen Peninsula in southern Sweden was amongst the first areas in the country to become ice free following the most recent deglaciation (~18,000 cal. BP). Previous investigations of Kullatorpssjön, a small lake on the peninsula, show that sedimentation began 17,000-18,000 cal. BP into what was then a brackish lagoon before isostatic rebound resulted in the isolation of the lake from the neighbouring Kattegat Sea 1000-1500 years later. Owing to its unique geographical position and its dynamic transition from a glaciated to marine to terrestrial environment, Kullatorpssjön offers an exceptional data point to refine our understanding of the timing and composition of postglacial colonising floral and faunal communities. Here, we present sedimentary ancient DNA (sedaDNA) shotgun metagenomic and metabarcoding results from ~100 samples spanning four meters of sediment cores collected from the lake in 2024, to investigate the critical shifts in the coastal environment of the Kullen peninsula ca. 18,000-7,500 cal. BP. Preliminary metabarcoding analyses indicate rapid colonisation and diversification of forbs, graminoids, and aquatic macrophytes. This research contributes to the broader discussion of post-deglaciation dynamics in a region of Fennoscandia not yet described using sedaDNA approaches.

Advancing detection of rare vertebrate lineages in Southern Ocean sedaDNA through integrated bioinformatic frameworks

4. Sedimentary ancient DNA

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Abstract text: Sedimentary ancient DNA (sedaDNA) provides a powerful tool for reconstructing past marine biodiversity, yet detecting low-abundance vertebrate taxa in complex shotgun datasets remains challenging. Additionally, scarce and highly fragmented sequences, combined with incomplete reference databases for Southern Ocean organisms, often limit taxonomic resolution to higher ranks rather than the species level. We undertook bioinformatic benchmarking to determine minimum target species input sequence thresholds at various taxonomic levels (family, genus) using a stringent ancient metagenomic workflow. Our results indicate that reliable identification of Southern Ocean vertebrates requires at least 250 sequence fragments at the family level. Building on these findings, we are developing a novel data processing framework that integrates established ancient DNA tools, reference sequence database building and validation, and the exploration of pangenome-based mapping using *soibean-Harvest*, a pipeline designed to make the soibean approach from Vogel et al. (2024) more widely applicable to both less diverse and highly diverse ancient environmental datasets beyond species-level prediction. The latter will be a key stepping stone toward improved detection of rare vertebrate lineages in sedaDNA and toward assessing their temporal persistence in Southern Ocean ecosystems.

Ancient DNA from Holocene sediments on Wrangel Island

4. Sedimentary ancient DNA

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Abstract text:

Wrangel Island, northeastern Siberia, is known for the late survival of its woolly mammoths into the Late Holocene (~4 ka). This late survival has produced conflicting and inconclusive explanations for the population's final demise. Sedimentary ancient DNA (sedaDNA) offers a way to investigate ecological changes through time at high taxonomic resolution. Using sediment samples from Wrangel Island, preliminary analyses show woolly mammoth DNA in the deepest sections but absent in the uppermost layers. Our age-depth model confirms continuous sediment deposition, providing confidence in reconstructing the timing of mammoth extinction. Analysis of the middle section, dated between 4848 and 3137 cal BP, has been hindered by inhibition currently preventing sedaDNA recovery. This section spans the projected extinction window and may provide clues to the mammoths' disappearance. In this project, we will identify and remove inhibitors, generate shotgun metagenomic data, and conduct plant and animal metabarcoding across the transect. These new sedaDNA data will allow testing whether plant community composition shifted around or just before mammoth extinction and whether sedaDNA-based extinction timing aligns with or extends beyond current fossil evidence. This work will provide a more detailed ecological and chronological context for the final Wrangel Island mammoth population.

Ancient DNA insights into pre-alpine pile-dwelling lake sediments

4. Sedimentary ancient DNA

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Abstract text: In the middle Holocene, pile-dwelling sites emerged on the marshy shores of pre-alpine lakes. Due to rising water levels, these sites were later waterlogged resulting in rich archaeological deposits. These deposits offer exceptional preservation of plant material, food remains, organic artifacts and fecal matter. Zooarcheological studies of pile-dwelling sites indicate both wild and domestic animal food sources. In order to gain a better understanding of animal usage at pile-dwelling sites, we analysed ancient DNA from archeological deposits and lake sediments to determine the source of mammalian DNA deposited. A total of 43 samples were taken from three sites: Mooswinkel on the Mondsee (A, 3800-3400 BCE), Zug-Riedmatt on the Zugersee (CH, 3200-3050 BCE) and Nidau-Seewassernutzung on the Bielersee (CH, around 2900 BCE). To allow for archeological contextualization, a microcontextual sampling approach was chosen by drilling specific contexts from resin impregnated microstratigraphic blocks. Samples were shotgun sequenced and analyzed for mammalian DNA. We uncovered ancient hominid, canid and suid DNA from 13 samples from Zug-Riedmatt and Mooswinkel, indicating that both dogs and pigs were kept at these sites. Combined with microcontextual information, these results further shed light on mammalian DNA deposition and into methodological aspects of sedaDNA in archaeological and lake sediments.

Ancient environmental DNA from peat bogs - a tale of caution

4. Sedimentary ancient DNA

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Abstract text: Ancient environmental DNA (eDNA) provides a complementary approach to plant macrofossils and microfossils proxies to study past biodiversity dynamics from a broad range of materials. Among them, peat records are often overlooked in palaeogenomic research, despite their importance for interpreting past environments. Moreover, metagenomic approaches have not yet been applied to detect ancient biotic communities from these archives.

In our study we explored the potential of ombrotrophic peat bogs in sub-arctic regions to reveal ancient ecosystems through the analysis of ancient eDNA. Both shotgun and target capture strategy targeting plants, insects, mammals, birds and fish were applied, since we sought to authenticate the ancient origin of the retrieved DNA molecules and compare this to existing proxy data from the site.

Numerous plant sequences were retrieved with both capture and shotgun metagenomics, although no ancient DNA specific damage patterns were obtained. There was an absence of vertebrate and invertebrate taxa, even in capture data. All results suggest that the eDNA record is dominated by a highly fragmented modern flora, characteristic of bog assemblages found at the sites.

Our study suggests caution when analyzing presumably ancient eDNA from ombrotrophic bogs, with DNA detection methods which lack direct authentication of ancient origin.

Ancient Environmental DNA reveals local environmental shifts during the Ålesund and Austnes Interstadials

4. Sedimentary ancient DNA

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Abstract text: Understanding the existence and ecology of refugia in glaciated Norway remains debated. Although several lines of evidence suggest that isolated ice-free areas may have persisted during the Last Glacial Maximum (LGM), interpretations of species composition and local environmental conditions before and during the LGM are limited by sparse geological archives and fossil preservation, hindering reconstructions of past biogeography, highlighting the need for alternative proxies. Here, we apply ancient metagenomics to investigate late Pleistocene environments using sedimentary deposits from two Norwegian cave sites (Skjonghelleren and Hamnsundhelleren). Our data spans the Austnes and Ålesund Interstadials (~41–34.5 ka BP) and complements existing fossils and geological archives. In Skjonghelleren, deposits attributed to the Austnes Interstadial yield a predominantly marine signature, including fish, mussels, and sea urchins; the presence of *Mytilus* indicates temperatures warm enough to sustain this species. During the Ålesund Interstadial (38.2–34.5 ka BP), the record shifts from marine taxa in the lower layer to terrestrial species in the upper layer, paralleling a transition from sand to clay. Hamnsundhelleren similarly shows terrestrial taxa throughout the Ålesund Interstadial and aquatic taxa in the oldest layer (Austnes). Together, these records demonstrate the value of aeDNA for assessing interstadial environments and potential refugia in glaciated Norway.

Ancient stickleback genomes reveal the temporal dynamics of parallel adaptation

4. Sedimentary ancient DNA

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Abstract text: Parallel evolution provides strong evidence of repeated selection on traits; however, studies of the parallel chronology of adaptive genetic changes remain scarce. The threespine stickleback is a model system for studying parallel evolution from marine ancestors to derived freshwater populations. Here we present genomic data from bulk (>20g) sediments from layers dated to back to the Late Pleistocene and spanning the ecological transition from marine to freshwater habitat. We find that freshwater ancestry initially accumulates at a subset of loci, rather than throughout the known marine–freshwater divergent regions of the genome. These include regions of chromosome IV containing the greatest genetic differentiation between marine and freshwater stickleback ecotypes and among the highest density of quantitative trait loci. For example, at the *Ectodysplasin* (*EDA*) locus, a large-effect pleiotropic locus associated with defensive armour and variation in neurosensory and behavioural traits. Freshwater ancestry is also consistently found at inversions and the X-chromosome early in the adaptive process. Our findings add to emerging evidence that freshwater adaptation in threespine stickleback could have a staggered but predictable temporal dynamic. Furthermore, they highlight the potential for sedaDNA time series to shed new light on the chronology and tempo of adaptation to past climate change.

Applying sedimentary ancient DNA to reconstruct Southern Ocean paleoenvironments

4. Sedimentary ancient DNA

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Abstract text: Sea ice in the Southern Ocean plays a critical role in global climate regulation, ocean circulation, and marine ecosystems, yet its past variability remains poorly constrained. Investigating past sea ice variability is essential to place current change in context and to improve predictions of future trends. Sedimentary ancient DNA (sedaDNA) is increasingly used in marine paleoecology to reconstruct past ecosystems to unprecedented detail beyond conventional proxies. Furthermore, sedaDNA holds great potential as proxy for sea ice reconstructions by tracking communities associated with sea ice environments through time. This presents a valuable addition to the existing sea ice proxies, which are few and have limitations to their application.

In this study, we use sedaDNA to reconstruct the paleoceanography, sea ice and ecosystem changes during the Late Quaternary in the Southern Ocean. Building on a modern metabarcoding baseline which demonstrates that eukaryotic surface sediment communities reflect modern sea ice condition in the Southern Ocean, we apply sedaDNA analyses to downcore sediment samples. We present preliminary data from a ~ 160,000-year sediment record from the Weddell Sea and compare these to other paleoceanographic proxies.

Arctic defaunation initiated a cascade of mammal–plant interaction shifts through dispersal dynamics

4. Sedimentary ancient DNA

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Abstract text: Amid accelerating defaunation, it remains unclear whether the loss of large mammals can trigger ecosystem collapse and through which functional pathways. Using sedimentary ancient metagenomics, we reveal the overlooked role of large mammal defaunation in driving the collapse of the glacial mammoth-steppe. Network analyses identified rewiring of mammal interactions during the late glacial triggering cascading effects. Crucially, megafaunal-mediated long-distance seed dispersal buffered vegetation turnover during periods of rapid climate warming but weakened with consecutive losses of vital dispersal interactions leading to the steppe–tundra's transition to open woodland in the early Holocene. Trophic interactions could not prevent turnover and became more dominant afterwards with the more stable climate. We identified resilient interactions that may support recovery, demonstrating the potential of rewilding to restore Arctic ecosystems.

Arctic ecosystem responses to climate change and permafrost thaw in the coastal Beaufort Sea, Canada

4. Sedimentary ancient DNA

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Abstract text: The Arctic climate is changing at unprecedented rates. In the Canadian Arctic, the thawing of its extensive permafrost is closely connected to alterations of landscapes and biodiversity shifts. Melting ground-ice leads to coastline destabilization, increased riverine discharge, and re-emergence of formerly buried material. Here we explore the genetic biodiversity preserved in coastal marine sediments from the Mackenzie Delta region of the Beaufort Sea, Canada, to assess ecosystem responses to regional and global climate change as well as impacts on the ancient DNA record.

We performed animal and plant metabarcoding, at multi-decadal resolution, of a sediment core from the Tuktoyaktuk harbor, Northwest Territories, Canada. Preliminary results reveal 4000 years of marine and terrestrial communities and the detection of extinct megafaunal taxa in surface sediments. We hypothesize that accelerated permafrost thaw in response to recent warming is reworking DNA from mainland permafrost into coastal sediments. To differentiate biological signals reflecting time-of-deposition from reworked components, we present DNA damage patterns of target sequences derived from shotgun metagenomic data.

Our study offers new perspectives on Arctic ecosystem sensitivity to climate change over the past four millennia, and a framework for the interpretation of sedimentary ancient DNA in a rapidly warming Arctic landscape.

Capture probe, metabarcoding, or shotgun sequencing: which reflects local vegetation best?

4. Sedimentary ancient DNA

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Abstract text: Any method's ability to detect and correctly identify plant taxa varies with DNA preservation, DNA reference library and the diversity of the local flora, making it difficult to compare results from different environments. Here we compare metabarcoding, shotgun sequencing, and capture probes using lake surface-sediments from Northern Fennoscandia with the comprehensive PhyloNorway genome skim reference library. We also undertook vegetation surveys from around the lakes to estimate the true positive detection rate, identify false positive detections, and provide optimal filtering cut-off thresholds for the three methods. Applying these thresholds, the rate of false positives was too high for reliable identification at species-level based on shotgun (49%) and capture probes (62%), whereas it was low for metabarcoding (5-12%). Our results show that metabarcoding on average detects 2.1 times as many true positive taxa as shotgun sequencing, and 6.4 times as many taxa as capture probes. The proportion of a taxon’s sequenced reads for the metabarcoding and shotgun methods was significantly related to the taxon’s abundance category from the vegetation surveys, but this was not the case for capture probe data. At present, metabarcoding provides the highest detectability and taxonomic resolution for correct identification and quantification of vascular plants.

Central Beringian critters: Late Pleistocene faunal communities of the Bering land bridge

4. Sedimentary ancient DNA

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Abstract text: Now submerged under the Bering Sea, the Bering land bridge (BLB) was an Ice Age conduit of migration between Eurasia and North America. While genetic studies have shed insight into patterns of migration across the land bridge and paleoecological research on Bering Sea islands have resolved details of these upland habitats, the faunal community residing on low-lying regions of the land bridge has not been evaluated. Additionally, whether the habitats of the BLB were mostly composed of mesic shrub tundra or arid steppe tundra is still uncertain. Here, we use sedimentary ancient DNA to reconstruct faunal communities from three BLB cores. "Basinito," "Deep Blue Sea," and "Cat's Ear" were collected during expedition SKQ202311S and contain both marine and terrestrial/lacustrine sediments dating to the late Pleistocene, offering an opportunity to investigate the terrestrial communities of the BLB. Using target capture, we reconstruct faunal communities containing mammoth steppe species such as woolly mammoth, bison, and ptarmigan, as well as wetland species such as waterfowl and beaver. While some species were present at all sites, species composition varied between sites, indicating that the BLB supported a mosaic of shrub and steppe tundra habitats and was not as homogeneous as previously believed.

Century-scale ecosystem change along the Western Antarctic Peninsula

4. Sedimentary ancient DNA

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Abstract text: The Southern Ocean is perceived as a pristine wilderness. However, southern seas have been subject to intense sealing and whaling over several centuries. Moreover, the region is on the frontline of human-induced climate change and is among the fastest warming marine ecosystems on the planet. One key problem in understanding remote ecosystems is limited data against which to measure ecosystem changes. Recently, the use of ancient DNA preserved in sediment records (ancient eDNA) has emerged as a useful tool to understand past ecosystems for which no long-term records exist. Here, we present reconstructed biological timeseries data from five short (< 40cm) sediment cores collected from the Western Antarctic Peninsula. We used metabarcoding to amplify three gene fragments for eukaryotic, vertebrate and mammalian species, and combined this data with age models generated using ^{210}Pb isotopes. Our data show a pronounced decline in marine mammal detections, particularly blue whales, coincident with twentieth-century industrial whaling. In contrast, the strongest community turnover occurs in the most recent decades, suggesting that anthropogenic climate change is driving broader ecosystem restructuring than historical exploitation. Overall, our data provides novel insights into the state of past ecosystems and offers a glimpse of a pristine Southern Ocean.

Comparison and Modification of Extraction Methods to Improve Recovery of Degraded DNA from Sediments

4. Sedimentary ancient DNA

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Abstract text: The growth of sedimentary ancient DNA (sedaDNA) research has led to novel insights that have significantly expanded our understanding of past environments. However, the recovery of sedaDNA is hindered by unique challenges, including increased inhibition and diverse sedimentary properties that affect DNA preservation. Given the significant impact of the extraction protocol on the recovery and purity of target DNA, it is critical to thoroughly evaluate extraction methods for successful recovery of sedaDNA. In this study, we compared the effectiveness of multiple extraction methods in the recovery of DNA from experimentally spiked sediment samples: an established aDNA protocol, commercially available soil DNA kits, and a novel method. All methods were evaluated for total DNA concentration (Qubit), DNA purity (NanoDrop), and amplification efficiency (qPCR), with significant differences found between all methods. By adapting the strengths of existing methods, we present a novel extraction protocol that offers high total DNA concentration, balanced removal of contaminants for optimal DNA purity, and the most efficient amplification of target DNA, suggesting high potential for success in downstream analyses. With greater accessibility, a reduced learning curve, and efficient processing time, this study introduces a novel extraction method that can easily be adapted for effective recovery of sedaDNA.

Cyanobacterial Sedimentary DNA records of two contrasting lakes from the Jorka River system, Poland

4. Sedimentary ancient DNA

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Abstract text: The Masurian Lakelands in north-eastern Poland contain thousands of lakes spanning a range of trophic levels, with diverse morphologies, and situated within catchments characterised by contrasting land-use histories. The Jorka River watershed contains five hydrologically connected lakes and has been described as a typical catchment within this region of high economic and cultural significance. The watershed has been extensively investigated since the early 1980s, with indications of increasing eutrophication and the development of cyanobacterial Harmful Algal Blooms over the past several decades.

To extend this perspective, we reconstructed ~140 years of cyanobacterial history using 16S rRNA amplicon metabarcoding and photosynthetic pigment analyses from sediment cores collected in two lakes within the watershed: one currently eutrophic and one mesotrophic.

From the late 1970s onward, both lakes exhibited shifts from cyanobacterial communities dominated by Synechococcaceae toward increasing contributions from Nostocaceae and Microcystaceae. These changes were strongest in the eutrophic lake with an agriculturally dominated catchment, while the mesotrophic, largely forested lake showed more moderate but still notable changes. We interpret these shifts in the context of historical, environmental, and anthropogenic pressures across the watershed.

Deciphering Methodological impact on Ancient Metagenomics: Nucleic acid Extraction-Dependent Taxonomic Skewing in Harappan Faunal Remains

4. Sedimentary ancient DNA

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Abstract text: Silica-based DNA extraction protocols employing chaotropic salts have been extensively optimized for ancient DNA research, with modifications in binding buffers, digestion conditions, and purification steps demonstrating variable efficacy across sample types. Building upon these established methodologies, this investigation evaluated chemically divergent extraction approaches for metagenomic DNA recovery from ancient faunal osseous remains excavated at Dholavira, a UNESCO World Heritage Harappan Civilization site (ca. 3000-1500 BCE) in Gujarat, India. Two GENECLEAN® Kit protocols were compared: a modified EDTA-based approach (DB1_E) incorporating overnight proteinase K/SDS/EDTA pre-digestion prior to guanidinium-based binding, versus the standard kit protocol (DB1_M) utilizing direct guanidinium thiocyanate lysis. Following Illumina shotgun sequencing (17.20 GB DB1_E; 29.24 GB DB1_M), taxonomic profiling revealed profound extraction-dependent compositional skewing. DB1_E yielded 68% unassigned reads with polyphyletic bacterial distribution across Gammaproteobacteria (48%), Alphaproteobacteria (37%), and Betaproteobacteria (12%), representing diverse orders including Pseudomonadales (61%) and Bacillales (36%). Conversely, DB1_M generated 15% unassigned reads but displayed marked taxonomic compression, with 98% Gammaproteobacteria overwhelmingly represented by Vibrionaceae (90%), predominantly *Vibrio* spp. This differential metagenomic DNA recovery pattern underscores that extraction chemistry influences paleomicrobiome characterization through cell wall lysis efficiency and DNA binding kinetics, necessitating multi-protocol validation strategies for microbial community reconstruction in archaeogenomic contexts.

Decoding Arctic HTM biodiversity: A comparative assessment of metabarcoding and shotgun sedaDNA sequencing

4. Sedimentary ancient DNA

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Abstract text: The Holocene Thermal Maximum (HTM) is considered an analogue of the present-day climate. It is a key research target for understanding the future of the polar oceans under anthropogenic warming. The APHRODITE project analyses sedimentary DNA (sedaDNA) from Arctic Ocean cores, among numerous proxies. The goal is to reconstruct the dynamics of biodiversity, productivity, and composition of marine ecosystems, with particular emphasis on lower trophic levels (phytoplankton, microzooplankton) and key species of potential economic importance (fish).

Selected stratigraphic units encompassing the HTM were subjected to sedaDNA extraction in the aDNA laboratory at Adam Mickiewicz University in Poznań, Poland. Two sequencing approaches were applied: shotgun metagenomic sequencing in the Illumina NovaSeq X platform and metabarcoding targeting selected markers (18S, 16S/12S). The authenticity of the ancient material was assessed based on fragment lengths, deamination profiles, and contamination indices. Bioinformatics pipelines and tools - including aMeta for shotgun data and taxonomic assignment supported by extensive reference databases - were used for both data types. Estimated alpha and beta diversity, community composition in major trophic groups, and detectability of rare taxa and keystone species were compared. The presented results provide a critical evaluation of the potential of two sedaDNA sequencing approaches in reconstructing pan-Arctic HTM ecosystems.

Dirt floor DNA retains a record of human and faunal behavior in open-air archaeological sediments

4. Sedimentary ancient DNA

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Abstract text: Sedimentary DNA from ancient settlements provides a novel means of learning about past societies and their lifeways, with DNA preserved directly within living and working spaces. Here, we present ancient DNA results from n=14 open-air Holocene settlements across Europe, spanning the Neolithic to Medieval times. Our n=183 sediment samples taken from different domestic contexts - such as alleys, houses and ditches - were captured for mammalian and human mitochondrial DNA. We identified a variety of ancient domestic and wild taxa, with compositions varying according to site, period and context, though domesticates clearly dominate. We found that the ancient faunal DNA did not always parallel the zooarcheological record, suggesting differences in the origins of DNA and remains. In more than half of the n=45 samples containing ancient human DNA, we were able to resolve haplotype mixtures or infer single mitochondrial haplotypes using a novel workflow. These haplotype distributions were consistent with the skeletal record when such a record was available, and for several archaeological sites this study represents the first genetic data for that location and time period. Our findings show that it is possible to contribute to the growing body of archaeogenetic research using sediment-derived sequences alone.

Ecosystem change throughout the Holocene in Northern Scandinavia

4. Sedimentary ancient DNA

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Abstract text: The postglacial recolonization of Fennoscandian flora and fauna was initiated when the land became accessible as the last ice sheet retreated. In northern Sweden, plants are represented in pollen and macrofossil records, but there is very limited genetic evidence from the first plants, animals or humans in the region, mainly owing to an absence of osteological finds. We have shotgun sequenced more than 400 lake sediments samples from nine lakes in middle and northern Sweden in order to reconstruct the ecosystem changes throughout the Holocene. For this purpose, we have also developed a ready to use bioinformatic pipeline optimised for sedimentary ancient DNA analysis. The final stages of the analyses are currently ongoing, but results will be ready by the time of the conference, since the outcomes will be presented in my PhD dissertation on 22 May 2026.

Environmental shifts accompanying Angkor's rise, peak, and decline revealed by sedimentary ancient DNA

4. Sedimentary ancient DNA

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Abstract text: The Angkor archaeological complex in Cambodia represents one of the world's largest pre-industrial settlements, supporting over 700,000 inhabitants at its peak between the 11th-13th centuries. Despite extensive archaeological research, many questions remain about human-environment interactions and ecosystem changes during the Angkor period. The decline of Angkor remains a compelling archaeological enigma, with proposed drivers including alternating droughts and floods, shifts in political authority, the failure of the city's vast hydraulic network and the spread of diseases.

Here we present shotgun metagenomic analyses of sedimentary ancient DNA (sedaDNA) from sediment sequences in three adjacent urban water bodies. These sequences form a temporal series roughly spanning the last thousand years, capturing Angkor's rise, peak, decline, and post-urban transformation. The three lakes represent contrasting social and functional environments: ritual waters directly adjacent to Angkor Wat, the state-scale reservoir of the West Baray, and a moat surrounding the densely occupied urban center Angkor Thom.

By reconstructing temporal patterns in plant, microbial, and eukaryotic community composition, this study investigates how biological signatures reflect shifts in water management, ecological conditions, and urban activity. Together, these analyses will offer new perspectives on the environmental and infrastructural dynamics that accompanied one of history's most significant urban transitions.

Evidence for sedaDNA preservation in a warm tropical lake and implications for palaeogenomic research

4. Sedimentary ancient DNA

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Abstract text: Tropical environments are significantly underrepresented in sedimentary ancient DNA (sedaDNA) research. However, growing evidence suggests that sedaDNA can survive over surprisingly long timescales in tropical sediments. We evaluated DNA preservation and reconstructed historic vegetation dynamics using sedaDNA extracted from the warm tropical crater Lake Nyabikere in Uganda. We collected a sediment core and metabarcoded plant community composition in horizons spanning from the present to ~1945 CE. The results confirm sedaDNA preservation on a decadal-century scale, with no indication of degradation. Most reads could be assigned to family level due to inadequate representation of tropical taxa in public databases. Musaceae appear only in upper horizons, likely reflecting local land-use intensification. The results underline several key opportunities for tropical sedaDNA research. First, sedaDNA preservation in warm tropical lakes is likely not exceptional. Second, reference sequences of agricultural plants and ecological key species will enhance sedaDNA interpretations. Third, lightweight piston corers are necessary to reach older sedaDNA in lakes with high sedimentation rates and difficult access. Fourth, sedaDNA studies will benefit from collaboration with local scientists throughout the research process, from sample collection to data generation, and the integration of oral histories to contextualise findings.

Genetic admixture between East and West European Gravettian-associated populations in Western Europe before the Last Glacial Maximum

4. Sedimentary ancient DNA

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Abstract text: Modern humans first settled in Europe at least 45,000 years ago. However, limited genomic data from individuals dating between 45,000 and 20,000 years ago still restricts our understanding of population dynamics and admixture during the Upper Palaeolithic. Before the Last Glacial Maximum, Gravettian culture-associated populations were widespread and genetically diverse, comprising at least two distinct genetic groups, referred to as the Fournol and Věstonice clusters. We present genome-wide data from two Gravettian-associated individuals from cave sites in the Franco-Cantabrian region (Chufín and Isturitz). These data reveal previously undetected gene flow linking the ancestry of 34,000-year-old individuals from Sungir (Russia) to Gravettian individuals from Western Europe, challenging the prevailing model of population continuity from the Aurignacian to the Solutrean. As osseous remains are scarce for this time period, DNA from sediments deposited by ancient humans opens a new possibility to obtain genomic data. We thus examine sedimentary DNA from Solutrean Layer 122 at El Mirón Cave (Cantabria, ~22,000 cal BP), recovering approximately 16,000 human SNPs, among the highest yields reported from a Palaeolithic context. Generating these data required over 1.15 billion sequencing reads, illustrating both the potential of sediment DNA for autosomal analysis and the technical challenges of the approach.

Genomic footprints of anthropogenic impact in Neolithic pile-dwelling sediments

4. Sedimentary ancient DNA

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Abstract text: Ancient DNA from cultural sediments opens a direct window into the human-environment interface of prehistoric life. We applied multi-marker metabarcoding (mammals, fish, eukaryotes, plants) to Neolithic cultural layers from Zurich-Parkhaus Opéra and Küssnacht-Immensee Dorfplatz, two pile-dwelling settlements in the Alpine Foreland dated to ~3000 BCE. These waterlogged deposits provide good preservation of organic material and serve as archives of both ecological and anthropogenic signals. Through the parallel analysis of terrestrial and aquatic DNA, we aim to trace the extent and nature of anthropogenic impact on surrounding lake ecosystems. The study integrates genomic data with archaeological and bioarchaeological records to evaluate how prehistoric economy and settlement activity influenced biodiversity, trophic structure, and the environment. By combining metabarcoding with established archaeological methods, we aim to reconstruct prehistoric human activity and its ecological consequences. The work represents a large-scale application of sedaDNA to cultural layers from Neolithic pile dwellings and provides insights into how humans shaped lakeshore ecosystems more than five thousand years ago.

Gotta capture 'em all: Advances in the analyses of ancient environmental hybridization capture data

4. Sedimentary ancient DNA

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Abstract text: The preservation of DNA in ancient sediments has enabled the reconstruction of past ecosystems despite difficulties connected to the low amounts of vertebrate and plant genomic material. To overcome this, many take advantage of hybridization capture for the enrichment of libraries prior to sequencing, with the aim of enriching DNA from targeted species or specific genomic regions. This requires, among other things, a well-designed bait-set, stringent laboratory workflow and bioinformatic considerations, but often results in fold enrichments of up to 100x for target regions compared to regular shotgun sequencing. However, bioinformatically, hybridization capture data is often analyzed like regular shotgun sequencing data, with few considerations being taken towards duplication biases and the non-randomness of the data, which can heavily inflate the results and thereby lead to misinterpretation of the data. We carried out an extensive review of the literature, aiming at setting a new direction in both bioinformatic analysis of hybridization capture sequencing data but also present a set of measures for a standardized comparison of the effectiveness of capture against shotgun sequencing. Furthermore, we developed a pipeline that heavily mitigates PCR-induced duplication biases for hybridization capture sequencing data.

High-latitude plant community assembly varied with Late Quaternary glacial-interglacial cycle strength

4. Sedimentary ancient DNA

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Abstract text: How did high-latitude plant communities assemble across different intensities of Quaternary glacial-interglacial cycles? Here, we explore this process by developing a modelling framework based on ecological niche models of 669 plant taxa to assess spatio-temporal changes of community composition in unglaciated Siberia and Alaska during glacial and interglacial stages of Late Quaternary. Model results were validated using sedimentary ancient DNA data compiled from ten lakes covering the last 24 thousand years. Our results highlight the recurrence of glacial legacy effects on subsequent interglacial plant assemblages, and the effect of interglacial legacy is not observed. In addition, we provide model-based evidence that the higher modern dispersal capacity of warm- than cold-adapted taxa may be shaped by their greater migration requirements during the past glacial-interglacial cycles, which is likely a result of an evolutionary trade-off between long-distance dispersal and local survival. Finally, we identify two long-standing biodiversity hotspots and four migration corridors for ecological protection. The sustainability of those hotspot sites is highly sensitive to glacial-interglacial cycle strength, and most of them are unable to persist beyond Marine Isotope Stage 4. These findings are important for devising long-term ecological conservation strategies in high-latitude ecosystems under climate change.

Holocene ecosystem change and Sámi-Norse land use transitions from an eight millennia sedaDNA record

4. Sedimentary ancient DNA

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Abstract text: Sedimentary ancient DNA provides a detailed record of Holocene ecological change and human land-use. We analyzed an ~8000-year sediment core from Lake Stabbevatnet in northern Norway using plant trnL and mammal 16S metabarcoding together with contemporary vegetation surveys to track long-term shifts in regional terrestrial, aquatic and riparian communities. Early to mid-Holocene sediments show a strong co-occurrence of *Populus* and *Castor fiber*, indicating well-wooded riparian habitats that supported beaver populations until about 2300 cal BP. Detections of *Castor fiber* sharply decline after c. 4300 cal BP, best explained by local hunting. Over the last one to two millennia, the record shows a clear transition toward human-modified landscapes, marked by rising *Plantago*, Poaceae (including *Poa*), *Achillea* and *Trifolium*, alongside the first occurrences of agricultural indicators such as *Avena*, Hordeinae, as well as domestic mammals including *Bos, Ovis* and *Capra*. This is followed by the sudden appearance of potatoes (Solanoideae) and Perca (European perch), which is most likely due to the northern travels of the well-known 'potato priests' in the post-medieval period. Taken together, these ecological signals align with archaeological evidence for early Sámi presence and pastoral activity in the region and are consistent with Norse settlement and expansion into northern Norway.

Inter-annual variability of plant DNA in a varved sediment record

4. Sedimentary ancient DNA

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Abstract text: Sedimentary ancient DNA (sedaDNA) is increasingly used to link past shifts in biodiversity to landscape and climatic changes, but its reliability depends on understanding DNA production, transport, deposition, and preservation ('DNA taphonomy'), which is still limited.

Assuming that vegetation community composition is stable across consecutive years, we analysed annual lamina (or varves) from a small boreal lake in northern Sweden to assess year-to-year variation in plant DNA signals. We find that vegetation community structure is similar between varves (years) with a consistent, transient change across the 30-year period, emphasizing the robustness of eDNA for whole-ecosystem analyses. Yet, taxon richness varied strongly among varves, with only ~15% being consistently detected in most varves, while ~45% are only sporadically detected. Variability appears influenced by terrestrial input and the presence of plant fragments. Hence, DNA-based detection of individual taxa need to be interpreted with caution in paleoecological studies.

Our results highlight how a better understanding of DNA taphonomy increases the reliability for DNA-based signal interpretation in sediment records.

Is less more: Do organelle genomes yield better species detection than nuclear genomes in sedaDNA samples?

4. Sedimentary ancient DNA

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Abstract text: In ancient sediment DNA research, mapping reads to organelle or nuclear genomes is a common strategy for taxonomic detection. Organelle genomes, with their high intracellular copy numbers, typically provide strong and reliable signals. Yet many datasets yield substantially more reads when mapped against complete nuclear genomes, raising questions about how organelle-based detection relates to the broader nuclear signal. In particular, it remains unclear whether nuclear mapping consistently improves sensitivity, how organelle and nuclear read abundances covary across taxa, and whether reliance on organelle references biases biodiversity inferences. This issue is especially important for ecologically significant eukaryotic groups—such as plants and mammals—that also pose analytical challenges due to their large nuclear genomes. Here, we analyse published ancient sediment metagenomic datasets to quantify the relationship between reads mapping to organelle versus nuclear genomes for plants and mammals. Although organelle references are expected to yield strong detection signals, multiple factors—including taphonomic processes, sample type, and stochastic read recovery—may obscure this pattern. By characterizing organelle-to-nuclear coverage ratios across differing depositional contexts, we assess whether consistent trends emerge and evaluate how organelle-focused strategies shape detection limits and ecological interpretations.

Marine ecosystem change in relation to climate conditions in the North Atlantic over the last 600,000 years

4. Sedimentary ancient DNA

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Abstract text: Understanding how marine ecosystems responded to past climate fluctuations is essential for resolving long-term interactions between climate, ocean circulation, and marine communities, as well as for anticipating the impacts of ongoing ocean warming. In particular, determining how the biological carbon pump operated under different climatic regimes is crucial for evaluating the strength and direction of future climate–carbon feedbacks in a rapidly warming ocean. Using shotgun sedimentary ancient DNA from four sediment cores recovered from the Icelandic Shelf and the Denmark Strait, we reconstruct 600,000 years of marine biodiversity change across all domains of life (viruses, archaea, bacteria, and eukaryotes) and spanning several glacial–interglacial transitions. A comprehensive analysis of more than 500 metagenomes revealed how high-latitude marine communities responded to large-scale climatic forcing, shifts in ocean circulation and polar–subpolar water-mass dynamics. Our results show a clear alternation between communities adapted to glacial and interglacial conditions across all levels of the trophic chain and enable detailed reconstructions of ecosystem structure and function under changing environmental regimes. An integrative network framework, combined with ecological and functional annotations, highlights the implications of these transitions for key biogeochemical processes, including carbon sequestration and export, remineralization pathways, and nutrient cycling.

Mediterranean Sapropels as Archives for sedaDNA: A 9000-Year-Old Vegetation Record from the Skopelos Basin (Aegean Sea, Greece)

4. Sedimentary ancient DNA

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Abstract text: Freshwater runoff into the Eastern Mediterranean Sea has repeatedly led to the formation of oxygen-depleted bottom waters and intense accumulation of organic matter, which has resulted in the deposition of organic-rich sediments under anoxic conditions („sapropels“). Based on sediment core KC5-6 retrieved from the Aegean Sea during R/V METEOR Expedition M144, we performed a pilot sedaDNA analysis on three sediment samples from (i) sapropel S1 (age: 9 ka before present), a pre-sapropel horizon (11 ka), and a post-sapropel layer (5 ka) deposited under oxic conditions. Shotgun metagenomic screening revealed no ancient DNA in the oxic, post-sapropel horizon, whereas both the sapropel and pre-sapropel samples contained abundant ancient DNA dominated by 30–60 bp fragments. Taxonomic assignments indicate that ~90% of the sequences from the 11-ka sample are from marine bacteria, while ~30% of the assignments from sapropel S1 correspond to plant taxa. Using a custom hybridization-capture bait set targeting matK and rbcL regions of Mediterranean and Afromontane shrub and tree species, we detected high levels of ancient grapevine DNA, along with sequences of *Populus*, *Quercus*, *Acer*, and *Corylus*. These results highlight the potential of Mediterranean sapropels as valuable archives for reconstructing regional vegetation and environmental dynamics during the early Holocene.

MEMELANDS: Towards a Molecular Ecology of Medieval European Landscapes

4. Sedimentary ancient DNA

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Abstract text: The recovery of ancient DNA from sediments (sedaDNA) is a potential step-change in our understanding of cultural biodiversity and Medieval landscape history. Much of the biodiversity characteristic of northwestern Europe today reflects Post-Roman landuse change and agricultural practices, with many influences from southern and eastern Europe, and the New World. A pertinent debate concerns the role of elites, including ecclesiastical, in this ecological transformation. These questions have previously been approached using macrofossils (seeds, bones) and pollen but both have limitations, some of which can be overcome using sedaDNA through both amplicon-sequencing and metagenomics. This approach also has the capacity to add data from other organism groups ranging from fungi to annelids. MEMELAND is producing high-resolution plant and animal data for the last 2000 years from over 100 lakes and related excavation sites. In particular the project will exploit the high taxonomic resolution for plants and animals in order to examine the role of elites and human mobility in the spread of valuable resources, such as crops, domesticated stock including related taxa (e.g. commensals) across NW Europe. A practical justification is that many of these species play essential roles in culturally mediated biodiversity, human nutrition, and long-term ecosystem functioning.

Optimizing sedimentary ancient DNA extraction for palaeoenvironmental reconstruction with organic-rich sediments

4. Sedimentary ancient DNA

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Abstract text: Palaeoenvironmental records preserved in sediments provide a window into the world of ancient humans, allowing researchers to understand how people of the past may have interacted with their environment. Sedimentary ancient DNA (sedaDNA) is one such palaeorecord that has great potential for expanding what can be recovered, particularly in combination with other palaeorecords like palynology and macrofossils. Unfortunately, the recovery of sedaDNA can be difficult in organic-rich sediments like peat due to high amounts of PCR-inhibiting humics. To remove these inhibitors, researchers apply stringent purification methods, typically resulting in the loss of considerable target DNA due to the coextraction and elution of DNA with humics. This loss of endogenous DNA decreases the taxonomic diversity recovered, thereby reducing the efficacy of sedaDNA analysis in peat palaeoenvironmental reconstruction compared to other palaeorecords. The aim of this study is to improve the recovery of sedaDNA from peat and other organic-rich sediments through comparative experimentation of commercial, published, and modified extraction and purification methods. By comparing methods optimized for improved DNA release from organic and mineral components and low fragment size recovery, we aim to maximize the retrieval of authentic sedaDNA from organic-rich sediments and improve taxonomic diversity and specificity of multiproxy palaeoenvironmental reconstructions.

Past and present reindeer-vegetation interactions inferred from environmental DNA

4. Sedimentary ancient DNA

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Abstract text: Herbivory plays a key role in shaping biodiversity and ecosystem functioning in Arctic terrestrial ecosystems. Knowledge on plant-herbivore interactions and its response to changing environments in a long-term perspective is essential for understanding the resilience of arctic ecosystems in the face of global changes. The ruminant reindeer (*Rangifer tarandus*) is the most abundant large herbivore in the Arctic, feeding on a unique and complex diet, and is of great cultural and socio-economic importance to indigenous peoples in the North. We will study past and present reindeer-vegetation interactions from the last 1500 years, and its effect on species diversity and ecosystem dynamics in northern Norway using eDNA. Using sedimental DNA from lake catchments, we investigate changes in past plant community composition along with past reindeer densities, with focus on the semi-domesticated reindeer at Nordvivatnet, a small lake at the Varanger Peninsula. Metabarcoding of sedimentary DNA will be applied targeting vascular plants to resolve a high time resolution of the past plant community. To obtain past densities of reindeer, ddPCR will be applied using reindeer specific markers targeting the mitochondria. The final objective is to link past and present reindeer-vegetation interaction by including dietary metabarcoding of reindeer faeces and contemporary vegetation analyses.

Preliminarily Metagenomics Analysis of Late Holocene Environmental DNA from the Sts'ailes Territory, British Columbia, Canada

4. Sedimentary ancient DNA

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Abstract text: Ancient environmental DNA (aeDNA) is becoming a key method for reconstructing past ecosystems and has proven particularly useful in deposits where the fossil record is limited or absent. This study presents a preliminary metagenomic analysis of sedimentary ancient DNA recovered from Late Holocene settlements within the Sts'ailes Territory in British Columbia, Canada. These settlement features reflect significant technological and socio-economic adaptations to the local environment. Sediment samples were collected from multiple floor layers and characterised by micromorphology and FTIR to capture temporal and spatial variation in species presence throughout each settlement's occupation. Shotgun metagenomic sequencing was employed to identify a wide spectrum of ancient plant and animal DNA preserved within these cultural deposits. To distinguish human interactions from background environmental variation, biodiversity profiles from the settlement features are compared to a natural baseline derived from a minimally impacted area. Preliminary results from this comparative approach may highlight patterns of species utilization, vegetation changes, and broader ecological dynamics associated with human settlement activities. Overall, the study highlights the value of metagenomic aeDNA for illuminating past lifeways and environmental dynamics in the Northwest Coast region.

Reconstructing late Holocene ecosystem change in the southern Arctic Ocean using sedimentary ancient DNA

4. Sedimentary ancient DNA

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Abstract text: The southern Arctic Ocean, located north of Svalbard and along the pathway of Atlantic waters entering the Arctic Ocean, has experienced strong anthropogenic pressures over the past 400 years, first due to whaling in the 17th to 19th centuries, which nearly extirpated local whale stocks, and more recently from ‘Atlantification’ in response to global warming. To investigate the ecosystem impacts, we analysed sedaDNA from 35 cm-long marine sediment cores collected from two continental slope locations north of Svalbard. Our records span the last 1500 years, allowing us to reconstruct the southern Arctic Ocean ecosystem before and after commercial whaling. Our dataset also provides a late Holocene baseline prior to anthropogenically induced climate change. We detect a broad range of taxa from across the ecosystem using metagenomics and metabarcoding approaches, with a strong and consistent detection of baleen whale DNA in the bottom half of both cores. This enabled us to determine the species composition and biological sex of the whale environmental genomes. However, in recent centuries and synchronous with a strong reduction in whale sedaDNA, we observe a transition in diatom community composition and a loss of marine invertebrate diversity, which we interpret as the ecosystem consequences of commercial whaling.

Reconstructing Subsurface Microbial Community Dynamics Through Time in Marine Arctic Sediments

4. Sedimentary ancient DNA

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Abstract text: Subsurface microbial communities are typically assumed to be structured primarily by present-day in situ conditions such as availability of electron donors-acceptors, and physical properties of the sediment. However, emerging evidence indicates that the vertical distribution of subseafloor microbiome may instead mirror the paleo-depositional environments at the time of sediment burial. Testing this hypothesis requires well-resolved deep temporal records of sedimentary microbiomes combined with independent reconstructions of past environmental change from diverse settings. Here, we analyze four sediment cores recovered from the Northwest Greenland margin during IODP Expedition 400. Our dataset comprises ~180 samples spanning the last ~900 kyr (~21 MIS cycles). We target V4 region of the 16S rRNA gene of bacteria and V1–V2 region of archaea, complemented by shotgun metagenomics for taxonomic and functional characterization. In parallel, organic geochemical proxies are used to reconstruct paleoenvironmental variations. We present preliminary results demonstrating successful DNA recovery across multiple sediment depths and effective amplification using selected primer sets, establishing the feasibility of generating high-resolution microbial community profiles from the Arctic subseafloor sediments. By integrating microbial distributions with paleoclimate-derived environmental shifts, this collaborative study evaluates how variations in paleo-depositional conditions influenced the vertical structuring of sedimentary microbiome in the Northwest Greenland margin.

Reconstructing the impact of land use on meadow vegetation with sedaDNA

4. Sedimentary ancient DNA

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Abstract text: Mountain ecosystems are sensitive to changes in both climate and anthropogenic disturbances like pastoral- and arable farming. With the introduction of farming to the European Alps ca 7000 years ago, people have started to change the composition and structure of the natural vegetation. They have opened the closed forests, to create space for animals and crops, thereby lowering the timberline and creating meadows, leading to a mosaic of different habitats and increased biodiversity. However, these highly diverse meadows are threatened by current climate change. Increasing temperatures, but also land abandonment, will lead to an upwards shift of mountain forests, which will cause changes in biodiversity and threaten present-day meadow species.

Here we will present the first *sed*aDNA results from two lake sediment records from the Eastern Alps spanning the entire Holocene. The two lakes have contrasting land use histories (e.g. arable vs pastoral farming); this contrast will be used to reconstruct the impact of different farming activities on the composition of meadow and ruderal vegetation communities. This will help to better assess the impact of future climate change and anthropogenic disturbance on mountain vegetation.

SedaDNA and the Stonehenge Landscape, Insights into the Hunter Gatherer-Early Farmer Transitional Environment

4. Sedimentary ancient DNA

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Abstract text: The relationship between late hunter gatherers and the early farmers of Europe is one of the most long-running archaeological debates and particularly in relation to key European sites and landscapes across Europe. Here we present sedaDNA (both metabarcoding and shotgun) data alongside pollen evidence from a transect of sites in Southern England that reveal that the area around Stonehenge held a mosaic of habitats, including both grasslands and open woodland in the Later Mesolithic. We argue that the cause of this was the interaction between long-duration Mesolithic resource management, particularly of large herbivores identified in the sedaDNA data, and the naturally thin calcareous soils of Salisbury Plains. This created a predominantly open environment rich in grazing resources and pre-adapted to the requirements of early-mid Neolithic farmers. A critical element in this model is the complimentary use of sedaDNA and pollen which provides improved taxonomic and spatial precision and can avoid the bias caused by the long-distance transport of tree pollen. When viewed together with the sedaDNA data, evidence from the archaeological record suggests that this early geographical advantage was part of the reason that Stonehenge eventually became a supra-regional centre of power.

SedaDNA down under: recovering ancient DNA from Australian cave sediments

4. Sedimentary ancient DNA

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Abstract text: The application of sedimentary ancient DNA (sedaDNA) from caves remains nascent, with fewer than 30 studies published to date; most within the past few years with a bias towards the Northern Hemisphere. Essential groundwork is therefore still required before the full potential of cave sedaDNA can be realised. In stark contrast to recent advances in understanding the sources and processes influencing aeDNA records from lakes, virtually nothing is known about these aspects in caves. We are contributing to addressing these knowledge gaps in a study of cave sedaDNA across south-eastern Australia. Through combining DNA preservation metrics with cave climate records and mineralogical data we aim to improve understanding of sedaDNA taphonomy, allowing us to model theoretical age limits of DNA preservation across the Australian landscape and detect sedaDNA preservation hotspots; reducing the time and costs associated with screening for suitable sites. Different library protocols were tested to determine the optimal method in terms of tradeoff between cost, time and data quality. Our data also provides new insights into Australian biodiversity change through time, some of which have direct applications in areas of conservation current management.

Sedimentary ancient DNA analysis of the Aurignacian layers at Hohle Fels cave in southwestern Germany

4. Sedimentary ancient DNA

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Abstract text: Human groups associated with the Aurignacian lithic industry of the Swabian Jura produced a remarkable record of material culture, including the world's earliest known mobile art dated to approximately 43,000-35,000 BP. During this period, the cave site of Hohle Fels experienced episodes of intensive human occupation and ongoing use as a refuge for diverse animal species, underscoring its long-standing ecological and cultural significance. Limestone caves, which maintain relatively stable temperature and moisture levels, as well as shield sediments from UV light, are considered favorable environments for preserving sedimentary ancient DNA (sedaDNA).

Here, layers associated with Aurignacian human occupation at Hohle Fels were systematically sampled. Genetic libraries generated from DNA extracted from 185 loose sediment samples were processed using shotgun sequencing as well as targeted enrichment approaches. Employing a bioinformatic pipeline designed for sedaDNA authentication, metagenomic analysis of eukaryotic taxa provided insights into ancient DNA preservation, spatial taxonomic distribution, and genomic diversity across the Aurignacian stratigraphic layers. Therefore, sedaDNA analysis from Hohle Fels offers a valuable opportunity to reconstruct archives of past genetic diversity and to reveal patterns of human and animal occupation within their depositional contexts.

Sedimentary ancient human nuclear DNA from open-air Holocene archaeological sites in Europe

4. Sedimentary ancient DNA

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Abstract text: The successful retrieval of ancient human nuclear DNA directly from sediment samples has opened up the possibility of conducting population genetic analysis in regions or periods for which ancient materials, such as bones, are limited or unavailable for sampling. While hominin nuclear DNA of Palaeolithic populations has previously been isolated and analysed from cave sediments, it has not been shown how well such an approach can work for more recent open-air archaeological contexts. Here, we present results from a wide-spanning project exploring the role of sedimentary ancient DNA taken from living spaces at several open-air Holocene settlements from throughout Europe. A key challenge when attempting to isolate and reliably analyze sedimentary nuclear DNA is distinguishing between genetic material originating from human or non-human sources. We outline and demonstrate novel methods to successfully overcome and mitigate the impact of faunal DNA on analysis. We then proceed to use contemporary ancient population genetic approaches to uncover new insights into the ancestry of people who lived at three distinct Neolithic and Bronze Ages archaeological sites, and reveal genetic connections to other contemporaneous areas, using only nuclear DNA isolated from sediment samples.

Sedimentary DNA and fossil archives reveal long-term phytoplankton shifts and their biogeochemical influence in a subtropical lake

4. Sedimentary ancient DNA

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Abstract text: Understanding long-term phytoplankton community dynamics is essential for assessing ecological resilience and informing lake management under global change. However, centennial-scale patterns of phytoplankton succession remain poorly resolved due to the limited taxonomic resolution of traditional fossil-based approaches. In this study, we integrated sedimentary DNA (sedDNA) with subfossil diatom analysis to investigate two centuries of phytoplankton succession and associated sedimentary biogeochemical responses in a subtropical lake. The sedDNA data captured major shifts in both eukaryotic and cyanobacterial communities, revealing distinct ecological phases linked to human activities and regional climate warming. Under near-natural conditions, phytoplankton communities typically exhibit low diversity and were characterized by oligotrophic taxa such as xanthophytes and *Gyrosigma*. Moderate human interventions, such as dam construction, can alter hydrodynamic regimes, promoting the expansion of macrophytes and creating niches for epiphytic phytoplankton such as *Staurosira*. In recent decades, intensified anthropogenic pressures combined with regional warming have driven a shift toward more diverse phytoplankton assemblages enriched in cyanobacteria, reflecting elevated nutrient inputs and rising temperatures. Random forest models further highlighted the role of phytoplankton in mediating carbon burial and biogenic Ca precipitation. These findings illustrate long-term phytoplankton community dynamics and underscore the value of sedDNA for reconstructing ecological trajectories in lake ecosystems.

The ancient subglacial precipitate microbiome

4. Sedimentary ancient DNA

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Abstract text: Beneath Earth's glaciers and ice sheets lies an aquatic realm where ice, water, rock, and microbial communities interact, driving chemical reactions that can collectively influence Earth's global carbon cycle, polar oceans, and climate. Efforts to describe subglacial microbial communities have been limited by the challenge of cleanly drilling through hundreds of meters of ice, such that only a few sites have ever been sampled. Here we use ancient metagenomics to present a spatiotemporal characterization of subglacial bacterial and archaeal communities. We extracted DNA from 25 subglacial precipitates, sedimentary accumulations of minerals that form in subglacial waters prior to exposure on the ice sheet surface. The precipitates studied here formed between 16,000 and 550,000 years ago beneath the Antarctic and the Laurentide Ice Sheets. Postmortem DNA damage patterns can reliably distinguish between ancient subglacial taxa and modern surface taxa, and that this approach can reconstruct subglacial microbial communities across space and time. Subglacial microbial communities neatly separate into two clusters distinguished by redox conditions, irrespective of geography or age. Geochemical measurements of redox state reproduce these same two clusters independently. We outline a framework describing how subglacial water redox states are held in balance by microbes, hydrology, and meltwater oxygen input.

The dirt on sediment DNA: Where does it really come from?

4. Sedimentary ancient DNA

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Abstract text: Living organisms are constantly shedding DNA in to their environment. Some portion of that DNA may eventually become bound to sediments, buried, and later recovered in an ancient DNA laboratory. Many studies have used such ancient DNA from sediments to study past ecosystems, or to zoom in on the population genetics of specific organisms. The source, the specific route that this DNA took on its way to adhering to a mineral particle, and the subsequent fate of that mineral particle are critically important to the interpretation of the genetic results, yet in many studies are unknown. Here we examine data from several studies to investigate the source of ancient DNA in lake, terrestrial, and archaeological sediments.

The influence of sediment mineralogy on DNA preservation and recovery in Bronze Age archaeological sites

4. Sedimentary ancient DNA

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Abstract text: Sedimentary ancient DNA (sedaDNA) is increasingly used in palaeoenvironmental and archaeological research for exploring past environments and human occupations. Yet, our understanding of how sediment mineralogy affects DNA preservation and recovery remains limited. Minerals exhibit distinct DNA adsorption and preservation properties. Clays, for instance, can effectively preserve DNA through adsorption, but this can also hinder extraction, yielding only a small fraction of the preserved molecules.
In this study, we examine the impact of sediment characteristics on DNA preservation and recovery using sediment from Bronze Age sites in south-west England. We analyzed peat sediments from a log coffin and clay-rich sediments from two settlements, characterizing their mineralogical composition, pH, and organic content, as well as for the presence of ancient DNA. We then demonstrate how DNA adsorption to the observed minerals is impacted by the body fluid from which it originates.
These results allow us to discuss the interplay among mineralogy, DNA adsorption, and taphonomy, how they influence sedaDNA preservation in archaeological archives and the geochemical processes that retain DNA. This knowledge will bring key insights into unlocking sedaDNA's potential by maximizing DNA recovery.

The Muskox Way: Plant and mammals DNA from N and NE Greenland

4. Sedimentary ancient DNA

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Abstract text: The oldest muskox bones in N and NE Greenland are from Independence I culture sites (4.5-3.9 ka) in Wandel Dal, northern Greenland, and «the muskox way» from Canada to N and further to NE Greenland may have been important for plants, herbivores and humans. We have analysed two lakes in Wandel Dal (Latesommersø and Midsommersø) and one at Zackenberg. In Wandel Dal, the plant DNA metabarcoding indicates that the climate was warmer than today about 7-3.9 ka year ago, with an abrupt change in the flora and sedimentation rate at 3.9 ka, especially at Midsommersø. Muskox was found contiguously from 7 ka at Midsommersø, thus millennia before humans arrived. Zackenberg dates back to 12.2 ka, with arctic forbs, grasses, ferns and crowberry in the earliest layers, willow from 8.2 ka and birch from 7.2 ka, but muskox only the last 2.5 ka. For all sites, we provide the full mammal and plant record with first arrival date, and it is clear that human arrived millennia after the first megafauna and had little impact on its populations. Ongoing shotgun sequencing will further elucidate if there were single or multiple immigrations per species.

The potential of early colonization and northern refugia in Doggerland

4. Sedimentary ancient DNA

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Abstract text: Prior to the formation of the present-day North Sea during the mid-Holocene, North-Western Europe was connected through the Doggerland landmass. Whilst it has been known for the past century that Doggerland was forested, it has not been clear when the onset of forestation occurred or whether the environment was more habitable for humans than surrounding European areas. In this study we reconstruct the palaeoecology of a river system, the Southern River, from the Late Pleistocene to the late Holocene using sedimentary ancient DNA (sedaDNA). We identify secure and insecure sedaDNA signals by integrating sedimentological and sedaDNA data into a taphonomic model. Secure sediments reveal the presence of several temperate tree genera such as *Quercus*,*Ulmus* and *Corylus* over 16000 years ago in the Late Pleniglacial, and thermal indicator genus *Tilia* several thousand years earlier than has been recorded for surrounding European areas. In this area we also detect an anomalous signal of the genus *Pterocarya*, considered extinct in the region since the Hoxnian Stage (~400ka). These observations are consistent with colonization from nearby northern glacial refugia, suggesting a favourable environment in which the cultural Mesolithic could develop.

The Reconstruction of Early Patagonian Occupation Histories by a Comprehensive Sedimentary Ancient DNA Study at Baño Nuevo 1

4. Sedimentary ancient DNA

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Abstract text: Patagonia was first inhabited by humans 14,000 years ago and has a fragmented record of early human presence that is only partially understood. Occupations were often discontinuous, and archaeological sites with long stratigraphies are extremely rare. Here, Baño Nuevo 1 provides uniquely well-preserved archaeological and palaeontological deposits. The cave's sequence spans 16,000 years and contains late Pleistocene megafauna, intermittent human activity and the burials of ten early Holocene individuals (about 10.2 kya BP). The late Pleistocene (layers 5–4) and early Holocene deposits (layer 3) show minimal disturbance, making Baño Nuevo 1 a key reference site for studying early Patagonian history.
Here, we present the first comprehensive sedaDNA project on a late Pleistocene site in Patagonia. The analyses are correlated with human occupational analyses as well as fauna studies. Through the combination of different techniques, we aim to identify different periods of human presence as well as draw conclusions about the relationship between megafauna and human populations in the early stages of the colonisation of Patagonia by modern humans.

Tracing Large Mammal Community Composition and Turnover in the British Upper Palaeolithic Through Sedimentary Ancient DNA

4. Sedimentary ancient DNA

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Abstract text: The Upper Palaeolithic (~50,000 to 12,000 BP) was characterised by substantial climatic variability, with repeated stadial-interstadial oscillations influencing the distribution of mammals across Europe. These climatic fluctuations drove regional extirpations and spurred large scale range shifts as species tracked suitable habitats. High-resolution reconstructions of faunal community composition and turnover remain limited due to a paucity of dated, morphologically identifiable fossils.

To address this, sedimentary ancient DNA was recovered using mammalian mitochondrial capture from pre Late Glacial Maximum (LGM) Upper Palaeolithic deposits at two British cave sites located in disparate regions of the UK: Pin Hole in Derbyshire and Wogan Cavern in Pembrokeshire. The former provides the type fauna for MIS 3 Britain, while the latter contains a rare example of an intact Pleistocene sequence in Britain that has been excavated with modern techniques. Sediment samples were derived from a broad vertical distribution within the sequences, with 12 samples analysed from Pin Hole and 26 from Wogan. The resulting per-layer taxonomic profiles document large mammal communities at the sites with a granularity beyond that of the local fossil record. By synthesising these faunal signals with available palaeoclimatic records and interpreting habitat preferences of the identified taxa, we infer local environmental conditions.

Tracking Muskoxen in Northern Greenland using Sedimentary Ancient DNA

4. Sedimentary ancient DNA

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Abstract text: Muskoxen on Greenland (*Ovibos moschatus wardi*) have the lowest genome-wide heterozygosity of any vertebrate herbivore. However, questions remain as to how many times muskoxen from mainland North America colonized Greenland, when exactly the bottleneck responsible for their lack of genetic diversity occurred, and if the underlying cause can be more attributed to climatic or anthropogenic pressures. Our project aims to characterize the plant and vertebrate life of northwestern Greenland since before the arrival of the earliest people (ca. 4.0 kyr BP) to the modern day, with a specific focus on the relationship between muskoxen and humans. Sedimentary ancient DNA is unique among environmental proxies for its ability to track the presence of animals through time at high taxonomic resolution, even when more traditional proxies for them, e.g. bones, are absent or few. Here we present initial metabarcoding and metagenomic results from five lakes on Warming Land, Wulff Land, and Nares Land. In addition to muskoxen, we also present records of collared lemmings, ptarmigans, arctic hares, and plants, and discuss these in the context of the island's archaeological record.

Turning Trash into Treasure: Reconstructing microbial community change across the marine–freshwater transition in the Late Pleistocene

4. Sedimentary ancient DNA

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Abstract text: The Pleistocene–Holocene transition (~13–11 ka BP) represents one of Earth's most abrupt climatic shifts, yet its microbial dimension remains poorly resolved. Although sedaDNA increasingly informs past vegetation and vertebrate histories, microbial reads in ancient sediments are rarely analysed in detail and often dismissed as contamination. Here, we re-mine metagenomic sedaDNA from the Jossavannet basin (northern Norway) to reconstruct microbial community turnover across a marine–freshwater transition spanning 13.070 to 12.800 kyr BP. Taxonomic profiling (Kraken2) and β-diversity analyses (PERMANOVA, dbRDA) showed that environment and site together explained ~26% of community variance. Indicator species analysis identified environment-specific taxa, including *Alteromonas pelagimontana* and *Streptomyces* sp. in marine sediments and *Pyxidicoccus parkwasys* and *Celeribacter ethanolicus* in freshwater. SIMPER highlighted *Synechococcus* lineages and *Aequihabitans* sp. as major contributors to marine–freshwater differences. Sequences aligning to these genomes exhibited short fragments and elevated terminal C→T and G→A misincorporations consistent with authentic ancient DNA, and SourceTracker distinguished environmental from host-associated and kit-derived sources. By de novo reconstructing the microbial diversity of Jossavannet, we aim to explore functional shifts in carbon fixation, methanogenesis, antimicrobial resistance, and stress-response pathways across deglacial warming. Originally generated for eukaryotic analyses, these metagenomes contain overlooked microbial "trash" that can be transformed into ecological insight.

Using sedaDNA to reconstruct the past landscape of Lake Lednica: a case study for Molecular Ecology of the European Medieval and Historical Landscape

4. Sedimentary ancient DNA

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Abstract text: Understanding how human activities during historical periods have shaped landscapes provides valuable insights for contemporary landscape management, biodiversity and human well-being. The state-of-the-art sedimentary ancient DNA (sedaDNA) approach offers a molecular, high-resolution reconstruction of past landscape dynamics. Here, we present a case study from the MEMELAND project based on sediment cores from Lake Lednica in central-western Poland. The lake core sediments span the last ~2,000 years and are located near the early Polish polity's capital, with the richest Medieval archaeological remains from the previous archaeological records. Using the sedimentary ancient DNA (sedaDNA) metabarcoding method, we reconstructed how landscape composition and biodiversity responded to successive phases of human influence, including the establishment and expansion of settlements, the intensification of agriculture and deforestation, the development of pasturelands, the rise of royal authority and military fortifications (including elite residences and bridges connecting the islands to the mainland), the adoption of Christianity in 966 CE, and the eventual collapse of the polity. This study demonstrates how sedaDNA can illuminate long-term social–ecological interactions and the legacy of human activities on landscape evolution.

Viking to Christian Landscapes (V2C): Environmental Genomics Across the Norwegian Sea

4. Sedimentary ancient DNA

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Abstract text: Reconstructing how Norse expansion and later Christianisation reshaped northern landscapes requires biological archives capable of capturing fine-scale ecological change. The Viking to Christian Landscapes (V2C) project applies sedimentary ancient DNA (sedaDNA), metabarcoding, fecal biomarkers, and sedimentological analyses to examine long-term shifts in vegetation, crops, livestock, and associated pathogens between c. 500–1500 CE across the Norwegian Sea region.
Ongoing analyses from lake sediments and archaeological deposits in Orkney, Shetland, and northern Norway are generating high-resolution profiles of plant and animal communities linked to farming and land-use practices. These datasets provide new opportunities to track changes in agricultural intensity, grazing regimes, crop choices, commensal species, and ecological resilience during the transition from Viking Age societies to Christianised medieval communities.
By integrating genomic, archaeological, and paleoenvironmental evidence, V2C aims to clarify how mobility, religious transformation, and evolving systems of governance shaped agrarian strategies and landscape development. Comparative analysis across contrasting cultural and environmental settings highlights regional variability in responses to social and climatic pressures. The emerging results demonstrate the potential of sedaDNA to transform our understanding of Norse environmental impact and the broader dynamics of medieval biocultural change in northern Europe.

5. Museomics

A glimpse into the past of Asiatic Cheetah from the Indian subcontinent

5. Museomics

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Abstract text: The population of the critically endangered Asiatic cheetah have been reduced to a fraction with only 20 individuals surviving in Iran. Once occurring widely across western and southern Asia, the Asiatic cheetah is at the brink of extinction. Historic samples can provide a glimpse into their past genomic diversity and help identify the factors responsible for local extirpation. In this study we sequence multiple historic samples from the Indian subcontinent. We provide the first complete mitogenome of the Asiatic lineage. We also confirmed the historic import of African cheetah in the early 20th century to India which is also reported in the literature. Comparison with other subspecies of African cheetah confirm the erosion of genomic diversity and build of inbreeding in the Asiatic lineage as well. The study highlights the importance of museum collections and the urgent need to safeguard and preserved the remaining individuals of this sub-species in Iran.

A Pest's Path to Perfection: Genomic Evolution of the German Cockroach Across 150 Years

5. Museomics

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Abstract text: Museum specimens provide a unique window into evolutionary change, particularly in pest species like the German cockroach (*Blattella germanica*). *B. germanica* is one of the most globally distributed indoor pests and has repeatedly evolved resistance to a wide range of synthetic insecticides. Unlike its closest relatives, this species is characterized by the loss of flight and an active avoidance of light, key adaptations for remaining hidden while living alongside humans.

A time series of specimens spanning over 150 years, collected on cruise ships, freight packages, and kitchens, enabled us to reconstruct genomic changes across a century that captures the onset of chemical pest control, including the widespread use of DDT.

Using minimally invasive DNA extraction, we generated whole-genome data from specimens dating back to 1887 and compared them with modern populations. The historical genomes yielded broad coverage sufficient for genome-wide analyses of *B. germanica* and its endosymbiont *Blattabacterium*. This century-long time series documents dynamic changes in transposable element copy number, evidence of previously unrecorded invasions that may have supported recent adaptive responses.

Our results highlight the power of museum collections for studying genome evolution, showing how *B. germanica* has changed genomically over a century of increasing chemical control.

Ancient DNA of medieval manuscripts

5. Museomics

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Abstract text: Parchment is a reservoir of ancient DNA, containing genetic material from animals, humans, and microbiota. DNA is retrieved using a non-destructive method: manuscripts are gently rubbed with a PVC eraser, the resulting crumbs are collected, and DNA is extracted from these crumbs before being sequenced by Next Generation Sequencing.

Medieval manuscripts provide a detailed snapshot of a period of cultural connectivity across Europe. There is, however, ongoing debate within the manuscript community regarding their geographical origins, with many repositories keen to determine where their manuscripts were produced. Interestingly, a single manuscript can represent an entire herd of cattle, revealing potential biological kinship among animals whose skins appear within the same book or across different books. Analysing manuscript DNA can give us clues to medieval parchment production and past animal management practices.

Additionally, questions remain as to which animal species were used to produce specific manuscripts, the role of sex in parchment production, the manuscript microbiome, and the predominant origins and sex of the human users. Our study investigates these questions using a dataset of Irish and continental European manuscripts to illuminate their origins, production processes, and handling.

Ancient DNA unveils the evolutionary history and palaeoecology of the extinct mātuhituhi bush wren

5. Museomics

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Abstract text: Reconstructing ecosystem responses to environmental change has historically focused on large vertebrates. In contrast, small vertebrates have been neglected in palaeogenetic studies despite their utility as fine-scale environmental proxies. Aotearoa New Zealand's Acanthisittid wrens are a speciose group of tiny, phylogenetically basal, perching birds, of which the mātuhituhi bush wren (*Xenicus longipes* subsp.) only went extinct in the 1970's. However, little is known about these enigmatic birds. We sequenced mitogenomes and nuclear ultra conserved elements from 32 historical bush wrens to reconstruct their evolutionary history. We also genetically-sexed specimens and reanalysed their plumage to reconstruct aspects of bush wren palaeoecology. Our analyses showed bush wrens evolved 6.6 Mya, with North and South Island populations diverging 2.6 Mya during narrowing and closure of Plio-Pleistocene seaways. This was followed by rapid glacier-driven diversification of South Island populations 470-94 Kya. Genetic sexing allowed an accurate reconstruction of ontogenetic, sexual, and geographic plumage variation, and consequently taxonomic revision. Our research highlights that ecosystems can buffer against environmental change up to a tipping point, which has important lessons for conservation management in a fast-changing world. It also lays the groundwork for functional (palaeo)genomic analyses across Acanthisittid wrens and how they compare to other perching birds.

Contamination or miscommunication? DNA analysis of historical palm-leaf manuscripts revealed use of exotic plants and cheaper plant surrogates

5. Museomics

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Abstract text: Palm-leaf manuscript (PLM) production is an ancient, region-specific craft from South and Southeast Asia that involves the use of various plants other than palms. This craftsmanship has largely ceased today; therefore, its study is possible only retrospectively. We present a novel, highly promising molecular approach to the material analysis of PLMs that reveals social and ethnobotanical aspects of their production. We collected 50 fallen fragments from five PLMs originating from Tamil Nadu (South India) and analysed them for historical plant DNA. About 250 unique taxa were identified, c. 35% of which originated from plants not known from India. The use of these plants is not mentioned in the literature on PLM production. However, DNA of these exotic plants was absent from negative controls and cannot be attributed to modern contamination. Instead, this DNA appears to derive from adulterants and surrogates historically used in place of more expensive ingredients. For example, we identified cheaper *Tagetes* sp. and *Carthamus tinctorius* applied for seasoning palm leaves instead of the expensive spice *Crocus sativus*. Among the introduced plants was *Couroupita guianensis*, often venerated locally as the 'sal tree', i.e. *Shorea* sp. Both examples demonstrate the importance of studying the social context of plant use.

Exploring ancient DNA preservation in archaeological museum materials

5. Museomics

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Abstract text: Archaeological museum materials are an invaluable resource in archaeogenomic research. However, these materials have been relatively underexplored. With advances in sequencing technology and research into the mechanisms of DNA preservation, this study aims to explore cultural materials that could be ideal reservoirs for preserving ancient DNA and, therefore, hold answers to archaeological questions at the biomolecular level. We analysed objects stored under various conditions, including Iron Age daub, medieval daub and rope from two museum collections, and a medieval wooden bowl, freshly excavated and stored under controlled frozen conditions.

Materials were analysed using metabarcoding of plants and animals. Shotgun sequencing was also conducted to assess the damage patterns and levels of potential contamination from modern DNA. Results show that these materials have good preservation of species that point to the use-history of the material as well as the depositional environment. DNA from one piece of unworked medieval rope in particular had a high number of marine species. These results together with the archaeological context suggest it was used on a fishing boat. We further highlight differences in DNA preservation among material types and discuss how damage pattern analyses can shed light on the life history and handling of these objects.

Molecular dissection of century-scale flowering adaptation using historical plant genomes

5. Museomics

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Abstract text: Climate change is reshaping biological traits globally, yet the molecular basis of these century-scale shifts remains unclear. Nowhere is this gap more evident than in the worldwide advance of flowering time, a shift with striking ecological and agricultural impacts whose genetic foundations are poorly understood. Here, we integrate 200-year timelines of flowering phenotypes and whole-genome data from European *Arabidopsis thaliana* herbarium specimens to dissect the molecular basis of this shift. Phenophase scoring combined with reconstructed historical climate conditions yielded high-resolution flowering estimates that minimized noise from sampling bias and developmental plasticity. Modeling revealed a robust ~10–20-day-per-century advance in flowering across central and southern Europe, consistent with global, cross-species patterns and clearer than in uncorrected estimates. We whole-genome sequenced 304 herbarium specimens and conducted a GWAS for loci associated with model-predicted flowering time. Pairing each historical genome with geographically and genetically proximate modern ecotypes highlighted genetic variants showing strong temporal divergence. We will functionally revive these candidate alleles through targeted genome editing to determine how historical genetic change rewired flowering pathways. This will provide the first mechanistic insight into the genetic shifts that advanced flowering and establish a foundation for understanding and predicting plant developmental adaptation under climate change.

Museum specimens characterize natural repertoire of antimicrobial resistance in wildlife and reveal human impact of antibiotic use.

5. Museomics

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Abstract text: Antibiotic use has resulted in the spread of antimicrobial resistance genes (ARGs) throughout the environment. Contamination is so widespread that virtually no unaffected regions remain to serve as baselines for comparing against current ARG levels. However, fossilized host-associated oral microbiota (dental calculus) enable characterization of environmental resistomes pre-dating anthropogenic contamination. These historical resistomes can be used to identify geographic and taxonomic reservoirs of ARGs and better understand the response dynamics of oral microbiota to AMR selection pressures leading to ARG transfer and spread into clinically-relevant microbes. In this study, we used host-associated microbiota from historical, museum-preserved specimens to characterize the ARG repertoires of 34 mammalian species spanning the 19th to 21st centuries. We found evidence of many ARGs circulating in the environment decades before they were reported in clinically-relevant pathogens, including ARGs conferring resistance to synthetic and last-resort antibiotics. We also determine elements of host biology and ecology that affect ARG diversity and abundance in the oral microbiome. We found significant increases in total oral microbiome AMR load across all species after the mid-20th century intensification of antibiotic production. This allows us to link human actions to changes in environmental resistomes, driving evolution, diversification, and spread of naturally-occurring ARGs.

Prospecting for Novel Orthopoxvirus Reservoir Diversity in the Smithsonian institutes African Mammal Archives

5. Museomics

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Abstract text: Prior to its eradication in 1977, smallpox was a major global health threat, responsible for an estimated 300–500 million deaths in the 20th century alone. Despite its immense historical impact, the evolutionary origins of its causative agent, Variola virus (VARV), remain poorly understood, in part due to the limited characterization of viral diversity among its closest Orthopoxvirus relatives. In this project, a broad range of animal pelts from the Smithsonian Institution's African mammal collection are being screened and sequenced to uncover novel Orthopoxvirus reservoir diversity that may refine estimates of the timing and geographic origin of VARV's divergence from its closest relatives. This project is targeting specimens collected from animals that occupied similar temporal, geographic, and ecological contexts as the singular Taterapox virus specimen isolated in 1968 (VARV's closest known relative), as well as species that are underrepresented in contemporary Mpox related wildlife viral screenings. Our strategy will utilise Orthopoxvirus qPCR assays optimized for ancient DNA to efficiently screen large numbers of specimens, with whole-genome sequencing and targeted enrichment applied to any positives in order to generate high-quality Orthopoxvirus genomes. This poster will be discussing the overall project goals/design, as well as preliminary results.

Reconstructing the Evolutionary History of Australian Feral Cats Using Museum-Based Ancient DNA

5. Museomics

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Abstract text: For at least two centuries, feral cats (*Felis catus*) have had severe impacts on Australian biodiversity and have contributed to range contractions and extinctions of many native species. Although several modern genetic studies have examined contemporary cat populations, they provide only a snapshot of present-day patterns and cannot fully reconstruct the long-term population dynamics that shaped the establishment and spread of feral cats across the Australian continent. To address this gap, this project uses historical cat specimens curated in Australian museums and heritage sites to generate whole-genome ancient DNA data. These time-stratified samples offer a unique opportunity to directly investigate invasion dynamics, including past population structure, diversity, and dispersal. Genomic data from a subset of specimens are evaluated for authenticity, endogenous content, and suitability for downstream analyses. These genomic datasets are integrated with historical and ecological information to trace multiple potential introduction routes, assess demographic changes through time, and identify genomic signals associated with the early stages of feralisation and adaptation to the Australian environment. This work will provide the first temporal genomic framework for one of Australia's most impactful invasive predators.

Recovering hepatitis B virus genomes from great ape museum specimens

5. Museomics

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Abstract text: In recent years, numerous studies have provided insights into the genetic diversity of pathogens infecting past human populations. Yet data on the evolutionary history of infectious diseases including viral diseases in our closest living relatives remains scarce. Previously, only one study successfully recovered ancient viral genomes of monkeypox (MPV) and hepatitis B (HBV) from museum samples of great apes. Here, we add a temporal perspective on HBV genetic diversity in nonhuman great apes, based on chimpanzee, gorilla and orangutan museum specimens dating back as far as 1838. Using in-solution hybridization capture targeting HBV, 16 high coverage genomes were obtained, with a mean depth of coverage ranging from 8-fold to 4158-fold and a breadth of coverage varying from 87.52% to 100%. Phylogenetic analysis revealed that they mostly cluster within the viral diversity infecting their respective host species. However, we also found evidence pointing to cross-species-transmission, as suggested by the phylogenetic placement of an HBV genome obtained from a gorilla specimen within the *Pan* HBV diversity. This work emphasises the importance of further elucidating the evolutionary history of pathogens infecting great apes.

Recovering Phylogenomic Signal from Archival Marine Mollusc Shells of Nautilus and Spondylus

5. Museomics

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Abstract text: Museum collections represent an invaluable but underused source of genomic material, particularly for marine molluscs. Yet extracting usable DNA from decades-old shells remains technically challenging. Here, we present our efforts to optimize protocols for recovering DNA from archival *Nautilus* and *Spondylus* specimens, some nearly 100 years old, preserved dry in natural history collections. We tested multiple extraction approaches using powdered shell, dried ligament tissues and formalin preserved tissue, comparing lysis conditions and purification methods designed for highly degraded, low-yield templates. Initial results show differences in DNA recovery between tissue types and species, with ligament material generally producing higher concentrations and more consistent fragment sizes. We also obtained amplifiable DNA from several powdered shell samples, indicating that skeletal material can serve as a viable substrate when soft tissues are absent. Building on these optimized protocols, we are generating phylogenomic datasets for both *Nautilus* and *Spondylus,* combining contemporary and archival specimens to evaluate the evolutionary informativeness of historical DNA. We present phylogenomic trees for each taxon and compare the placement and branch lengths of historical versus modern samples. Together, these analyses highlight the feasibility and added value of integrating decades-old museum material into phylogenomic frameworks and the potential of natural history collections.

Should we re-wild the white tiger?

5. Museomics

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Abstract text: Tiger coat colour variation has fascinated scientists and the public alike. White tigers originally occurred in the central Indian forests, and the last wild white tiger was hunted in 1958. This phenotype is caused by a recessive mutation in the SLC45A2 gene. Today, there is a proposal to rewild Central Indian forests with white tigers as a conservation measure. Such plans require scientific insights: were historical wild white tigers different from others in the same landscape? Does the white allele still exist in the wild? Are captive white tigers appropriate sources for reintroduction?

We generate the first ever genomic data (average depth of mapped regions = 18X) from wild historical white (n= 6) and normal tigers from central India (n=9), and captive white tigers (n=28, depth> 10X). Historical white (and normal) tigers had overall higher (but not significantly different) genetic diversity than modern wild individuals. Historic tigers did not cluster based on phenotype, while modern captive whites were highly inbred with low diversity. Field sampling of over 300 fecal samples across India suggested the white mutation is either absent or at very low frequency.

In conclusion, re-wilding the white allele may prove detrimental for tiger conservation in the long run.

Signals of hybridization between commercial and wild bumblebees revealed by museum genomics

5. Museomics

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Abstract text: Hybridization between domesticated and wild species can lead to the transfer of (mal-)adaptive genes. The buff-tailed bumblebee (*Bombus terrestris*) has been bred for crop pollination since 1987 and commercial colonies are traded globally. Hybridization between commercial and wild lineages was found in Spain and Poland, but not in Great Britain or Sweden. However, despite the high dispersal capabilities of bumblebees, these studies assigned unadmixed individuals by using limited spatial distances.

To further investigate hybridization between commercial and wild bumblebees in Great Britain and Sweden, we generated genomes for dry-pinned museum specimens (~50) collected before the first distribution of commercial hives. The historical samples serve as a baseline to detect signals of hybridization across modern samples (~170).

Contrary to previous results limited to modern data, we find evidence of hybridization between commercial and wild bumblebees in both Sweden and Great Britain in population structure and D-statistics. In a divergent region on chromosome 10, putative hybrids show similarities with commercial bumblebees, indicating transfer of potentially adaptive genes. The presence of commercial-type alleles on chromosome 10 in the wild is limited to modern samples. Our findings highlight the importance of museum genomics to complement modern genomic data with a temporal perspective.

Tracking 150 years of genomic erosion in tigers with museomics

5. Museomics

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Abstract text: In the age of the sixth extinction, temporal genomics is uniquely positioned to decipher the evolutionary history of endangered species. Tigers today occupy only 6% of their 1900 AD range, yet hundreds of trophy specimens from extensive historical hunting exist in museums and private collections worldwide, representing an untapped genomic archive. Indian populations are fragmented, with isolated populations like Ranthambore in Rajasthan showing signatures of inbreeding and reduced heterozygosity. While recent work suggests purging of highly deleterious variants, the temporal trajectory of genomic erosion and genetic baseline of historic Rajasthan tigers remain unknown.

We have assembled a unique sample collection spanning the late 1800s to the mid 1900s from museum collections in the UK and, for the first time in museomics research, from private collections in Rajasthan. Using this temporal sampling we investigate changes in mitochondrial and nuclear diversity, levels of inbreeding, identify genomic regions that maintain diversity despite temporal erosion, and attempt to distinguish the effects of serial bottlenecks. We will present preliminary results, including the comparisons between private and museum-preserved collections. We will expand the scope of this study to tigers across India to understand historical connectivity to suggest genetic rescue strategies for populations with higher extinction risk.

Tracking molecular mechanisms of plant adaptation to climate change with herbaria

5. Museomics

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Abstract text: To live across diverse environments, plants have to balance taking up CO2 to grow with the concomitant loss of water through their leaf stomatal pores. Increasing CO2 concentrations, together with climate change induced droughts and increasing temperatures should strongly alter this balance. However, while the genetics of stomata development in Arabidopsis thaliana are well-characterized, little is known about the natural variation of stomata genes across the climatic gradients of the plant's geographic range, let alone across the last centuries of climate change.

Using the 1001 A. thaliana genomes resource and genetic variation across a unique set of ~200 historical herbarium specimens dating as far back as 1817, we describe the global natural variation in core stomata genes. By combining published mutant phenotypes for these stomata genes with their genetic variation over time, we develop an experimentally-informed polygenic score for stomatal density to infer phenotype change over 200 years of climate change. Integrating a model organism's historical specimens and a molecularly understood phenotype allows us to understand how this species adapted in the past, at a phenotypic, genetic and ultimately a functional-molecular level. It thus provides a unique opportunity to decipher in detail whether and how plants respond to climate change.

Understanding the history of herring periods (Sillperioder) on the West Coast of Sweden: a temporal genomics approach

5. Museomics

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Abstract text: Historical records and high abundance of herring bones at 18th-19th centuries fishing sites on the West Coast of Sweden indicate that herring populations have gone through episodic phases of high density ("Sillperioder"). These population expansions contributed to the development of the local and national economy and to the industrialisation of the region. However, whether high herring abundance resulted from an invasion from distant populations in the Atlantic or from increases in local stock densities is still unclear. Additionally, the environmental drivers of these population increases remain unknown.

To address these issues, we built a dataset comprising more than one hundred modern and historical whole genome sequences of individuals from the West Coast of Sweden and the North-Eastern Atlantic, sampled before and after different Sillperioder. Using population genomics and demographic modelling, we aim to answer the following questions: (1) are the Sillperioder the consequence of increases in local stock abundance or massive migrations from other stocks? (2) are fluctuations in population sizes the consequence of fluctuations in environmental conditions (e.g. temperature)? Answering these questions will deepen our understanding of this economically and ecologically important species and clarify how climate and population dynamics influence its demography and evolution.

Using century-old fish collections to study rapid adaptation across space and time in the epicenter of marine diversity

5. Museomics

Marianne Dehasque

Abstract text: Much of Earth's biodiversity has been shaped by rapid bursts of adaptive evolution. Rapid evolution through natural selection may be a critical survival mechanism for species facing fast-changing environments (*i.e.*, evolutionary rescue). Yet our understanding of the genomic architecture and origin of adaptive variation remains limited due to a lack of data spanning relevant temporal and spatial scales. In this study, we leverage historical fish collections from the Philippines to test the hypothesis that local adaptation provides the raw substrate for rapid evolution through time. Using historical and modern collections of the delicate round herring (*Spratelloides delicatulus*), a small and widely distributed coastal fish, we will test (1) if local adaptation across geographic regions maintains genomic variation and (2) if this variation has served as the substrate for rapid evolution over the last century. To test these hypotheses, we have generated ten haplotype-resolved assemblies and are now whole-genome sequencing over one thousand historic and contemporary individuals from multiple locations to identify genomic regions under selection across time and space. Overall, this project will uncover the broad patterns and generalizability of rapid adaptation and its importance for population persistence in the face of climate change.

Using historical butterfly specimens to track genomic erosion in clouded apollo populations in Sweden

5. Museomics

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Abstract text: The clouded apollo (*Parnassius mnemosyne*) experienced strong decline throughout Europe in the last century. In Sweden, the clouded apollo persists in the wild in three geographically isolated and differentiated populations that display low genetic diversity. We generate whole-genome sequences of historical specimens from museum collections, including samples from within and from outside of Sweden, to shed light on the processes that account for the Swedish population's current genomic status. We compare modern Swedish genomic sequences against historical counterparts to describe the impact of recent population decline on the genetic diversity found in Swedish clouded apollo. In addition, we compare the historical Swedish population against historical populations that existed closer to the species' central range and closer to presumed glacial refugia in the Alps and the Balkans. This second comparison provides perspective on what level of genetic diversity can be considered typical, thus allowing for a more accurate estimation of the impact of rapid population decline. Furthermore, by comparing across both space and time, we aim to disentangle the effects of recent population decline from factors such as the Swedish position at the periphery of the species' distribution and the species' post-glacial colonization of Sweden.

Using museuomics to investigate the historic dispersal of Rattus norvegicus to Europe

5. Museomics

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Abstract text: Today, brown rats (*Rattus norvegicus*) are among the most globally successful commensal species, as their adaptability allows them to thrive in a variety of ecological niches. Due to the anthrodependence of rats, their expansion out of northeast Asia was propelled by globalised human networks. Multiple lines of evidence suggest that the expansion of the *R. novegicus* range only occurred in the last ~300 years. Still, historical reports are inconsistent, and archaeological specimens are difficult to date precisely because of burrowing behaviour and imprecise radiocarbon chronologies during the post-medieval period.

The RATTUS project is investigating the spread of the brown rat into Europe by adding temporal data. During our collaborations with multiple museums across Europe, we have investigated DNA preservation in various tissue types, considering the sampling impact on each individual specimen. This led to testing the use of minimally-invasive polishing papers to recover historic rat DNA from pristine specimens. This effort will enable the integration of ancient genomic data from ~100 specimens (securely dated archaeological brown rats and museum specimens dating to the 19th and 20th centuries) with modern *R. norvegicus* genomic data. Here, we will present preliminary phylogenetic results integrated with the existing scholarship on brown rat mobility.

6. Domestication

A 5,000-year-old water buffalo genome reveals the involvement of extinct wild B. mephistopheles in swamp buffalo domestication

6. Domestication

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Abstract text: Two subspecies of domestic water buffalo, the river buffalo (*Bubalus bubalis bubalis*) and the swamp buffalo (*B. bubalis kerebau*), are generally considered to share the same wild ancestor, the Asian wild water buffalo (*Bubalus arnee*). However, all extant Asian wild water buffaloes share closer genetic relationship to the river buffalo but distinct from the swamp buffalo, raising the possibility that the swamp buffalo might have an alternative wild ancestor.We sequence a 5,000-year-old specimen from Yunnan, China, which carries the mitochondrial haplotype belonging to an early divergent swamp buffalo lineage, while its nuclear genome clusters with *B. mephistopheles*, an extinct wild species previously thought to have never encountered domestic buffaloes. We further generate genomic data of 6 ancient Chinese swamp buffalo, 6 *B. mephistopheles*. Integrating them with published modern domestic buffalo genomes, we identify gene flow from *B. mephistopheles* into domestic water buffaloes. Our findings provide a novel perspective on the domestication origins of the swamp buffalo.

A multi-species study of domestic animals in Neolithic Sweden

6. Domestication

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Abstract text: The relationship between humans and domestic species has been central to the development of human cultures, societies and migrations. Advances in ancient genomic approaches have led to an increasing number of ancient animal genomes from time periods going as far back as the Paleolithic. However, most studies have focused on continental level questions related to domestication origins and large scale population patterns. More local scale questions focusing on sociocultural aspects within sites and regions, such as kinship and relatedness, can offer unique cases to study mobility and breeding patterns of domestic animals through time, while also providing further insights of disease prevelance and pathogen evolution. In this study, we delve into local genetic patterns of domestic species from Neolithic sites found in the area of Falbygden in western Sweden, where previous studies on humans have reconstructed pedigrees of up to six-generations and found evidence of plague. By using >200 genomes from domestic cattle, pigs and dogs, we explore patterns of relatedness and inbreeding within and between sites from Sweden. Our results highlight the importance of local scale studies to provide new insights into domestic management strategies, livestock trade networks and husbandry in Neolithic Scandinavia.

Animal husbandry practices during the Medieval "Green Revolution" in Iberia

6. Domestication

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Abstract text: The conquest of Iberia by Islamic groups from the 8th century CE, resulting in the formation of Al-Andalus, brought with it innovations in agricultural and animal husbandry practices. This period, sometimes referred to as the "Islamic Green Revolution", transformed the agricultural landscape of Iberia and resulted in dramatic changes to diet and the exploitation of domestic animals. This research focuses on several important domestic animal species (cattle, sheep, and goat), and aims to generate a dataset spanning the period of the "Green Revolution" across Al-Andalus (6th-16th centuries CE). Through the analysis of a number of key sites, including intra-site comparisons between different cultural contexts, we aim to assess the genetic impact of this millennium of changing political control on the animal herds.

Bioinformatic curation of mitogenomes for delimitation of wild and domestic lineages in Fennoscandian reindeer (Rangifer tarandus L.)

6. Domestication

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Abstract text: From phylogenetic inference to functional analysis, sequence alignment is required for genome-wide exploration studies, and its quality relies on the completeness of Whole Genome Sequences (WGS) and the efficiency of data mining approaches. Here we show the bioinformatic workflow with which we have curated extant and paleo *Rangifer tarandus* WGS from Northern Fennoscandia deposited in NCBI. We aim to build a reference library for subsequent phylogenomic analyses and haplotype annotations of the zooarchaeological specimens. WGSs were first assembled into mitogenomes and then quality-checked so that only complete, circular chromosomes were retained. After manual curation of instances of reverse complementarity and uneven sequence start, quality-filtered mitogenomes were retained for phylogenetic analyses. Manually curated mitogenomes were analysed together with published complete mitogenomes of reindeer samples from across the Holarctic range, using Maximum Likelihood and Neighbor-Joining approaches. The moose (*Alces alces*) mitogenome was used as an outgroup in all phylogenetic analyses. Resulting phylogenetic analyses supported separation between Fennoscandian wild and domestic lineages as sister subclades. We plan to further extend this georeferenced and dated reindeer mitogenome reference library to be used for the identification of newly collected zooarchaeological specimens based on a phylogenetic placement approach.

Cattle at the crossroads: ancient cattle genomes reveal human interactions across South, East and Southeast Asia and early gaur management

6. Domestication

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Abstract text: At the crossroads of South, East, and Southeast Asia, Southwest China is a critical hub for prehistoric human movements and harbors rich cattle diversity. To understand the formation of cattle diversity and associated human activities, we generated 42 nuclear genomes and 112 mitogenomes from *Bos* samples spanning ~4000–800 BP in Southwest China. We identified three waves of cattle introduction associated with different groups of people: taurine cattle arrived ~3300–3000 BP from northern East Asia, East Asian indicine arrived ~2300–2000 BP from Southeast Asia or southern China, and South Asian indicine arrived ~1700–1500 BP directly from South Asia. These incoming cattle replaced the locally utilized gaur, with a strong sex bias in the transient gaur–cattle gene flow suggesting human management of female gaurs. Interestingly, we identified two almost contemporaneous but genetically distinct cattle populations around 2300–1800 BP, associated with two human settlements only ~1 km apart but belonging to culturally different groups—the local Dian people and newly arrived Han people—reflecting potential cultural interactions. Together, these results provide important insights into human interactions across southern and eastern Asia and their livestock management practices.

Comet: Investigating the genome of the first 1,000 guineas bull

6. Domestication

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Abstract text: Born in 1804, Comet was a bull that impressed. He was the first ever bull sold for £1,000 (the equivalent of £127,882/149,370€ today) and was widely regarded as a high quality bull. He was one of the foundational sires of the Shorthorn breed which was first developed in 18th century England and was later used to improve or develop as many as 40 other modern breeds. The legacy of Comet continues on in many modern developed breeds that are responsible for a large portion of the world's meat and dairy products.

For this project, the genome of Comet was sequenced to a coverage of 15X. This genome was used to investigate the legacy of Comet in modern developed breeds. Genetic continuity between Comet and modern Shorthorn individuals can be shown, across 200 years of selective breeding. Comparing runs of homozygosity between Comet and modern individuals shows changing approaches in livestock husbandry. Identity-by-descent segments shared between Comet and modern individuals reveals the extensive use of Shorthorns for breed improvement and indicate that some selected traits common in modern developed breeds can be traced back to this foundational sire.

Describing early domestic genetic diversity using ancient sheep genomes from Asikli Höyuk, in Central Anatolia.

6. Domestication

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Abstract text: Sheep was amongst the earliest livestock species to be domesticated in the Fertile Crescent around 12.000-10.000 years ago. However, the region, process and demographic changes that led to this domestication are poorly understood. Recent genetic studies suggested that this domestication may have started somewhere in Anatolia from a wild population significantly different from the extant Anatolian mouflon.

To disentangle the history of early domestic sheep, we sequenced 72 high quality ancient genomes from Aşıklı Höyük, a site reflecting the earliest stages of sheep management and domestication, in addition to other Early Pre-Pottery Neolithic sites in southwest Asia, including Göbekli Tepe and Nevali Cori, both early megalithic sites in Anatolia built by communities of foragers. The pooling of these ancient genomes along publicly available (modern and ancient) genomes enables us to elucidate the genetic structure of pre-domestic and early domestic sheep populations in Neolithic southwest Asia. By then focusing on a vertical-sampling of an Early Neolithic site with over a millennium of occupation we were able to describe the transition from hunting to herding this species, and we were then able to describe the relationship of these early domestic sheep with later Early Neolithic sheep from other regions.

Evidence of multiple integrations of Endogenous Viral Elements in parasitoid wasps of the subfamily Rogadinae (Hymenoptera: Braconidae)

6. Domestication

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Abstract text: Some lineages of parasitoid wasps —whose larvae develop at the expense of a host — have established mutualistic interactions with viruses. In some of these lineages, domesticated endogenous viral elements (dEVEs), such as polydnaviriforms, have been well-documented. One of these wasp lineages are the members of the family Braconidae (Ichneumonoidea). We aim to comprehensively explore the incidence and evolutionary history of mutualistic DNA viruses in members of the subfamily Rogadinae (Braconidae), which comprises eight tribes and approximately 1,350 described species. We analyzed genomic data (including five complete genomes) from 64 species representing all Rogadinae tribes using homology searches and targeted identification of ancient core genes (ACGs). Preliminary phylogenetic analysis of seven ACGs revealed putative dEVEs clustering with *Filamentoviridae*, known to include domesticated viral species, in members of three tribes (Aleiodini, Yeliconini and Stiropiini). Additionally, putative dEVEs related to *Alphanudivirus* (*Nudiviridae*), another group with mutualistic wasp viruses, were identified in two species from Aleiodini. These findings suggest multiple integration events or ancestral infections followed by lineage-specific losses. Ongoing work focuses on genome annotation and characterizing the genomic architecture of these viral sequences to determine if they represent dEVEs and to elucidate their functional roles and evolutionary impact on this group.

Following the Cat Trail: Mobility and Diet in Medieval Northern Europe

6. Domestication

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Abstract text: Domestic cats (*Felis catus*) provide key insights into mobility, resource use, and human-animal interactions in past urban environments. We analysed 92 archaeological cats from two major northern German sites - the Viking emporium of Haithabu (8th-11th c. CE) and the medieval town of Schleswig (11th-13th c. CE) - combining ancient DNA and stable isotope evidence to reconstruct their biological and ecological histories.
Mitochondrial DNA points to clade IV (*Felis lybica lybica*), primarily subclades A and C, with subclade D occurring exclusively in Viking-related contexts. This pattern reflects the connected nature of Haithabu and Schleswig, shaped by trade-driven movement of animals. Nuclear genomic data reveal a predominant domestic ancestry closely related to the North African wildcat lineage, yet also show substantial admixture with European wildcats (*Felis silvestris*). These genomic signatures indicate that domestic cats interacted genetically with local *F. silvestris*, resulting in notable introgression.
Isotopic analysis indicates broad, opportunistic diets. Several cats show elevated carbon and nitrogen values consistent with access to fish, likely obtained through scavenging or human provisioning, highlighting their close ecological association with urban environments. Integrating genomic and isotopic evidence, this study highlights medieval cats as bio-cultural indicators of connectivity, economy, and shared urban ecologies in northern Europe.

Genetic Legacies of the First Ancient South American State in Archaeological Maize

6. Domestication

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Abstract text: Moquegua Valley in South Peru has an ancient legacy of pre-Hispanic maize cultivation, but when and in what form maize arrived in South Peru is still a mystery. Over thousands of years, the people of the Moquegua Valley shifted from subsistence farming to intensive maize cultivation. Trade networks were well developed between the peoples of the Valley and the high-altitude regions of the Andes, including the Tiwanaku state. This research explores the co-evolution of humans and maize by analyzing genetic changes in maize over 1,500 years of human occupation in the Moquegua Valley. By examining highland and lowland maize alleles and tracking traits under selection, we assess how the expansion of the Tiwanaku state influenced maize genomics. Using AMS-dated archaeological maize samples, we map the genetic changes in maize from ancient times to better understand the impact of Tiwanaku colonization on local maize varieties. Comparisons to modern maize help assess the legacy of these processes and put ancient specimens in context. Moreover, broader impacts will empower local farmers through documentation and curation of diverse regional germplasm, provide educational opportunities through training of undergraduate and graduate students, and establish a meaningful link between the past and the present for future researchers.

Genomic composition of Migration Period horses in the Carpathian Basin

6. Domestication

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Abstract text: Previous studies have successfully recovered general trends in the horse domestication process. These revealed that the ancestors of all domesticated lineages originated from a 2nd millennium BCE radiation from the western steppes, and a population turnover around the beginning of the second millennium CE leading to the foundation of the majority of modern breeds. However, little is known about details and regional variation of these processes, especially in Central Europe during the early medieval period. To fill this gap, we shotgun sequenced more than 150 horse genomes from the territory of modern day Hungary, Slovakia and Romania to an average of ~1x fold genomic coverage, mostly belonging to the 4th to 8th centuries CE. We use uniparental-based, allele-frequency-based and IBD methods to find answers for breeding customs, commerce and general genomic composition of the prevailing populations in the region. Moreover, we aimed to co-analyse the dataset with human ancient DNA data (i.e. the horse and its rider) where possible, and to compare the results with morphological ones and historical records in a multidisciplinary manner. The project is embedded within the ERC HistoGenes Synergy Grant.

Genomic Insights into Animal-Human Interactions from the Mesolithic to Iron Age in Northern Iran through the Re-analysis of Legacy Collections

6. Domestication

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Abstract text: This project investigates the interactions between animals and humans during the Mesolithic-Neolithic transition in Central Eurasia, specifically within the corridor connecting the Levant to Central Asia. Using a One Health framework, which decenters human health to examine the interconnectedness of human, animal, and environmental systems, we are analyzing how intensifying animal husbandry practices altered the genomic landscapes of animals and their microbiomes. To this end, we are combining traditional zooarchaeological methods with archival research and genomic sequencing to demonstrate how legacy collections can provide insight into complex bioarchaeological questions without the need for new, destructive excavations. More specifically, we focus on a sample of ten ovicaprid teeth representing a range of archaeological contexts from a 1951 excavation of Hotu Cave, Iran (~10,000 BCE–200 CE), currently housed at the University of Pennsylvania Museum of Archaeology and Anthropology. Both the dental calculus and pulp chamber of these teeth will be sampled to reconstruct the genomic profiles of the ovicaprids and detect any shifts in microbiome profiles. Through this work, we aim to clarify the species of these particular ovicaprid teeth and fit their genomic profiles into local population histories already identified in the transition from hunting to animal husbandry.

Livestock on the margins: maximizing what can be learned from poorly preserved ancient specimens.

6. Domestication

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Abstract text: Extracting reliable genomic data from poorly preserved archaeological materials remains challenging in ancient DNA research. Here we present two case studies reflecting how marginally preserved samples can still retain useful population genetic signals. First, we assess caprine specimens from Ireland: Haughey's Fort (Bronze Age) and Carrickfergus (Late Medieval). Proteomic and genetic analyses confirmed goat identification and molecular sex determination, representing the oldest reliably identified goat specimens from Ireland. Genome-wide data from Haughey's Fort reveals genetic continuity linking Late Bronze Age and Medieval populations to modern Old Irish Goats, a greatly-depleted indigenous breed. Carrickfergus specimens show variable inbreeding patterns reflecting diverse herd management strategies in Medieval Ireland. In our second case study, we recovered genome-wide data from worked goat leather (~7,250-7,000 BP) from Cueva de los Murciélagos (Albuñol, Spain). This specimen is among the oldest low latitude or altitude soft tissues yielding nuclear DNA. Despite tanning, modification, and handling, the specimen preserved host DNA. Genetic analysis places this individual within early European domestic lineages with strongest affinity to modern Bermeya goats, demonstrating long-term Iberian ancestry continuity over seven millennia. Together, these case studies illustrate the robustness of many population genetic approaches to low coverage and the value of marginally-preserved specimens.

Paleogenomic data evidence the origin and demographic history of ancient goats from the Canary Islands

6. Domestication

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Abstract text: Archaeological, linguistic and genetic evidence supports a North African origin for the indigenous people of the Canary Islands. Radiocarbon dating indicates that, apart from a temporary Roman purple dye workshop established in the first century BCE, the indigenous human occupation of the islands began in the first centuries CE and persisted until the European conquest in the 15th century.

The most abundant domesticate found in Canarian indigenous sites are goats, offering a proxy for investigating the origin and the temporal evolution of indigenous herds. Also, they represent an opportunity to characterize the North African populations at the time of the islands' colonization, providing paleogenomic data on this understudied region.

We obtain a total of 36 low-coverage genomes, including individuals from the Roman, indigenous and post-conquest periods. Ancestry inference analyses support an African ancestry for both the Roman and indigenous goats, placing the most probable origin in the northwestern region. We detect a temporal continuity from the Roman and indigenous times until modern-day goats. However historical goats show a minor European input due to the introduction of goats after the conquest. Finally, we identify signatures of isolation such as high inbreeding and low heterozygosity values.

Paleogenomics sheds light on the principal biological mechanisms that determined the long domestication process of the cat

6. Domestication

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Abstract text: The domestication process and the spread of the domestic cat have been approached by various scientific fields including history, archaeozoology and genetics, but are still subject of controversy and elusive. To compensate for weaknesses and gaps in previous studies, we undertook a large genomic study of ancient cats covering the entire Holocene and a large geographic region from the southern shores of the Mediterranean Sea to the North Atlantic. We performed a high resolution analysis of more than 100 well-covered genomes including key specimens from various locations and periods. Our results complete but also contradict some previous studies and reveal the major processes determining the domestication process of the cat such as hybridization, mating and behavioral patterns, as well as disparate interactions with various societies at various periods. Taken together, they document the complexity of the process.

Reconstructing the Demographic History of Early Domestic Goats in the Zagros Region

6. Domestication

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Abstract text: The Central Zagros Mountains of Iran provide some of the earliest evidence of goat management, indicating caprine domestication as early as 8,200 BCE during the Neolithic period. Previous studies suggest that early domestic goats initially exhibited low inbreeding, which increased during the Neolithic, likely due to human-driven herd movement, and later declined as herd sizes expanded and management strategies were improved. Based on these findings, we aim to reconstruct a detailed demographic history of the earliest managed goats and assess the effects of early human management practices. To achieve this, we will present 20 high coverage ancient goat genomes from key Neolithic sites such as Tepe Abdul Hosein and Ganj Dareh,and applying genomic approaches that infer past population sizes and demographic trends from patterns of runs of homozygosity (ROHs) identity by descent (IBD), and recent demographic history based on linkage disequilibrium (LD). These analyses will provide new insights into the domestication process of one our first livestock species.

The evolution and spread of Andean maize revealed through archaeogenomics

6. Domestication

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Abstract text: Modern Andean maize represents the most genetically distinct group of maize due to repeated founder effects during its spread into the region. However, little is understood about its movements through the Andes and how it passed between cultural groups. We surveyed 185 archaeological maize samples spanning the last 2,300 years from across a geographical range extending from the northwest coast of Peru to northern Argentina to retrieve archaeological genomes.

Surprisingly, we found that pre-Columbian maize forms a genetic group distinct from modern Andean maize, suggesting that modern landraces have been influenced by homogenizing introgression, perhaps facilitated by the colonial Spanish. Ancient Andean maize shows distinct lineages that depict its spread through the region over time and its local replacement associated with cultural movements.

Coastal and upland genomes are differentiated, with evidence of selection that may pertain to altitudinal adaptation and nutritional changes. Later upland genomes appear to have arrived from coastal regions but acquired an upland genetic signature through adaptive introgression.

The differing genomic structures of Andean maize in the northern and southern Andes appear to mirror human genomic patterns, suggesting a close link between crop dispersal and cultural interactions across the region in late prehistory.

Tracing the genomic history of domestic cats in North Africa and Southwest Asia

6. Domestication

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Abstract text: The domestic cat (*Felis catus*) descends from the North African and Near Eastern Wildcat (*Felis lybica lybica)*. Despite its global distribution, the limited genomic data from the Near and Middle East and North Africa leave unanswered questions about cat domestication, particularly regarding the contributions of the Neolithic Levant and Pharaonic Egypt. Recent archaeogenomic studies redefined the timing of its dispersal, indicating that domestic cats were introduced to Europe within the last 2,000 years, later than previously assumed.

To address this gap, we generated 60 low-coverage (0.1- to 0.6-fold) genomes from cat remains from North Africa and the Near and Middle East, dated from the 7th millennium BCE to the 15th century CE, along with 23 low- to mid-coverage (0.4- to 15-fold) genomes of present-day and museum wildcats from the Levant and Central and North Africa. Our findings raise the possibility that North Africa may have represented an original centre of cat domestication. As domestic cats later moved into the Levant and the Middle East, they may have incorporated Levantine ancestry through admixture with local *F. l. lybica* populations. These patterns hint at a more complex domestication process and invite further investigation into the origins of domestic cats across Southwest Asia.

Two centuries of historical genomes reveal the consequences of closed breeding in purebred dogs

6. Domestication

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Abstract text: Implementation of breed standards and pedigrees during the Victorian-era led to a dramatic increase in the phenotypic diversity of dogs. Consequently, many contemporary purebred dogs show reduced genomic health compared to mixed breed individuals including reduced heterozygosity and increased genetic load, largely linked to breeding practices. Lack of historical genomes, however, has made it difficult to disentangle the timing and drivers of such declines given complex and breed-specific demographic histories, artificial selection, and crossbreeding. Here, we sequenced genomes from 60 museum specimens of dogs spanning the 19th and 20th centuries, and representing 11 breeds/landraces, to directly assess the consequences of contemporary breeding practices on genomic diversity and health over time. For “extinct” breeds such as the Turnspit and Tweed Spaniel, we characterised their genomic legacy in modern breeds, including the inheritance of breed-defining traits. For globally-popular breeds including the German Shepherd and Saint Bernard, we leveraged time-series data to quantify the effects of popular sires and the Second World War on genomic health. Combined, our results indicate that declines in the genomic diversity and health of purebred dogs occurred not at the onset of breed formation, but throughout the last century, as a result of repeated population bottlenecks.

When pathways constrict: A Neolithic bottleneck in caprine dispersal to Iberia

6. Domestication

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Abstract text: Sheep and goats represent the earliest domesticated livestock animals brought under human control, and played a central role in the emergence of agriculture and pastoralism in Southwest Asia. Caprines later formed the backbone of the Neolithic Mediterranean migration, fueling migrant farmer communities along the Mediterranean. This migration advanced rapidly, ~2,500km in ~300 years. Reaching the Iberian coast by ~5600 BCE, caprines became a major economic resource in the peninsula. How this rapid migration influenced caprine genetics is not yet understood. To investigate, we sequenced twelve Neolithic Iberian caprines (5 goats, 7 sheep) and two southern French sheep. Neolithic Iberian and French caprines exhibit lower genetic diversity and unique phylogeographic affinities, distinct from Anatolian and eastern European populations. Both species exhibit high cumulative sums of runs-of-homozygosity (ROH) and increased identity-by-descent (IBD) between settlements involved in the Mediterranean migration. While sheep and goats display similar trends, goats have exceptionally high ROH and IBD, indicative of a long-lasting bottleneck accompanied by an extremely small population. Using SLiM, we simulated the dispersal bottleneck to determine its scale and explore interspecies differences and similarities. These results point to dispersal bottlenecks of differing severities during the Mediterranean migration, laying the genetic basis of local livestock herds.

Wild Phenotypes Far Away from Home: Investigating a Stratified Model of Domestication with Brazilian Archaeological Maize

6. Domestication

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Abstract text: Maize was domesticated in the lowland Balsas valley, Mexico from its wild ancestor, Balsas teosinte, at approximately 9000 BP. The crop rapidly expanded throughout South America between 6500-6300 BP. Archaeological maize from the Teohuacan valley were found to have partial domesticated genotypes (Ramos-Madrigal et al., Current Biology 2016; Vallebueno-Estrada et al., PNAS 2016). Dated at 5300 BP, this postdates the initial domestication and spread of maize by thousands of years. A stratified model of South American maize domestication (Kistler et al., Science 2018) proposes the crop was transported from Mexico in a partially domesticated state.

Within the sites Lapo do Boquete and Lapa da Hora from Peruaçu Caves National Park, Brazil, fourteen archaeological maize specimens (1010-570 BP) share unique teosinte-like morphologies not yet found elsewhere in South America (Costa, et al. Science Advances 2024). To explore this phenomenon through the context of a stratified domestication model, this project has generated archaeogenomes from teosinte-like and maize-like phenotypes from Peruaçu. These genomes are being analyzed to determine their domestication statuses and, if proven to be partial domesticates, they will become the first known of its kind discovered outside of Mexico.

7. Lab methods

Assessing the Effect of Proteinase K on Ancient DNA Recovery from Archaeological Dental Calculus

7. Lab methods

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Abstract text: Dental calculus is one of the richest biomolecular sources in the archaeological record, preserving both host and microbial signals. Most extraction protocols for ancient DNA (aDNA) rely on proteinase K (PK) digestion. However, in studies that aim to recover both aDNA and proteins from the same sample, omitting PK would enable fully combined protocols. Yet its impact on microbial DNA recovery from dental calculus, particularly whether PK improves efficiency or biases yield, remains poorly understood.

In this study, we selected archaeological dental calculus from three 18th century individuals from St James's Gardens Burial Ground (London, UK) and subdivided each into six subsamples. For each individual, three subsamples were extracted using a standard EDTA + PK digestion, while three were processed with EDTA alone, following our combined DNA-protein extraction protocol that omits PK. Extracts were converted into double-stranded libraries and sequenced to assess human DNA content, fragment length distributions, damage profiles, and microbial community structure.

By directly comparing paired subsamples, this pilot study quantifies the impact of PK on the recovery of human and microbial aDNA and evaluates how a PK-free workflow affects the representation of different taxa. These results will inform best-practice protocols for multiomics analyses of ancient dental calculus.

Checkpoint Assays and Sample-Specific Optimizations for Improved Ancient DNA Recovery

7. Lab methods

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Abstract text: Ancient DNA (aDNA) researchers contend with molecular damage and complex environmental chemistry that challenge every stage of the laboratory workflow, requiring innovative, aDNA-tailored genomic approaches to maximize downstream success. Because preservation state and inhibition differ between samples, some workflow decisions must be made on a per-sample basis to improve aDNA recovery and mitigate sample failure. To simplify this process, we have developed a dynamic framework with workflow optimizations and diagnostic checkpoint assays for a range of source materials, including bone, sediment, and coprolites.

To address inhibition-driven failures, we refined the Inhibition Index assay that characterizes inhibition via quantitative PCR and integrates with a predictive model to identify samples at a heightened risk for downstream complications, allowing tailored template inputs. In parallel, we implemented a droplet digital PCR assay as a quantitative proxy for the presence of authentic aDNA molecules in an extract, leveraging microfluidic reaction partitioning to overcome challenges associated with low-copy, damaged, and inhibited templates. Each assay is paired with open-access data-processing tools to reduce subjectivity and standardize aDNA decision-making. Our integrated framework aims to equip researchers with diagnostic data throughout the aDNA workflow to improve downstream success and maximize the yield of palaeogenomic data from finite source materials.

Comparative Analysis of Single- vs. Double-Stranded LibraryPreparation Methods for Ancient DNA Recovery

7. Lab methods

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Abstract text: Ancient DNA (aDNA) studies rely on efficient library preparation methods tomaximize the recovery of degraded genetic material. In this study, we compare theefficiency of the Meyer & Kircher double-stranded library preparation method (Meyer & Kircher, 2010) with two single-stranded approaches: the Santa Cruz method (Kappet al., 2021) and the single-stranded library method published by Gansauge et al. (2017, 2020). Our dataset consists of ancient human and mammoth bones spanningdifferent time periods and exhibiting varying degrees of preservation. In addition to comparing library preparation efficiency, we assess the impact of uracil-DNA glycosylase (UDG) treatment, which removes characteristic aDNAdamage, by analyzing both UDG-treated and non-UDG-treated libraries for eachmethod. The primary aim is to determine which approach recovers the highest proportion of authentic aDNA fragments while also considering factors such as timeand resource efficiency. We will compare the library complexity, endogenous content, and fragment length across methods to evaluate their performance in different preservation conditions. The findings of this study will contribute to refining best practices in aDNA research, particularly for highly degraded specimens, and provideinsights into method selection based on sample condition and available resources.

Enhancing aDNA extraction from unconventional anthropogenic sources

7. Lab methods

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Abstract text: Recent breakthroughs have demonstrated the viability of recovering ancient DNA from unconventional and non-skeletal sources including coprolites, pendants, chewed birch, and sediments. Yet, even as the technical capabilities of the field expand, conceptual frameworks have remained narrow. In practice, ancient DNA is often treated as an isolated line of evidence to be extracted from an object, rather than as something shaped by and embedded within the object's material and contextual history. Furthermore, for non-human material, the retrieval of ancient DNA has been underexplored, particularly when it comes to recovering information beyond raw material sources and taxonomic identification. In the same vein, ancient DNA studies often overlook "invisible actors," or agents that played meaningful roles in past human environments but left little durable traces in the archaeological/genomic record. This poster will present research that addresses this gap in its exploration of differential ancient DNA preservation in underutilized anthropogenic sources, particularly of the skin microbiome from naturally mummified remains, tools, and plaster floors. Finally, it will also situate the metagenomic analysis from these sediments and indirect sources within the archaeologist's toolkit for better understanding human presence, activity, and lived experience.

Novel DNA Extraction Pipeline for Microbiome Analysis using Palaeofeces and Sediment deposited in Sacral Foramina.

7. Lab methods

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Abstract text: PCR inhibiting substances that are co-extracted with aDNA from bones, sediment and mummified tissue are one of the main methodological problems in aDNA extraction protocols. These substances make PCR amplification difficult and are the main cause of PCR failure. Here we present an optimized version of the Rohland et al. (2018) extraction protocol for highly degraded DNA that reduces inhibition by adding a density separation step and inhibitor PCR. We tested our optimized aDNA extraction pipeline in coprolites, a DNA source for which laboratory protocols are not well defined. We also used this pipeline for sediment covering human sacra, which until now has been widely ignored as a possible source for aDNA recovery and gut microbiome reconstruction. We studied 33 coprolites from Mexico, Peru and Portugal, as well as sediment deposited on the sacra of 9 individuals from the Carnuntum archeological site in Austria. Furthermore, we tested the variation in DNA preservation at different sampling locations, for example the interior and exterior layers of a single coprolite sample. We also compared the sediment covering different areas of a sacrum and the sediment deposited inside its sacral foramina. Finally, we compared our microbiome analysis results from coprolites to that of sediment.

Quantifying sequencing methods to access unattainable epigenetic information

7. Lab methods

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Abstract text: Analyzing the epigenome of ancient individuals offers valuable insights into their lifestyles. Bioinformatic processing utilizes differential deamination patterns in methylated CpGs to enable the inference of methylation levels by estimating sample-specific deamination rates. However, this approach does not allow for CpG-specific estimates, rather relying on the study of DMRs (differentially methylated regions).

To increase precision, we developed a laboratory pipeline to directly quantify methylation levels from ancient human genomes and thereby providing high quality estimates of single CpG methylation rates. This involves optimizing whole genome bisulfite sequencing, while in parallel establishing Oxford Nanopore sequencing for ancient bone tissue (*Pars petrosa ossis temporalis*).

The efficiency of the bisulfite sequencing protocol was established by first sequencing a bisulfite conversion control, followed by single-stranded libraries, resulting in three high coverage genomes. A preliminary shallow nanopore run delivered promising results and identified protocol steps currently undergoing optimization. Furthermore, for all individuals used in this project additional high coverage (~20X) genomes were generated using our standard aDNA protocols.

Through the integration of wet-lab and computational methods, we aim to enhance precision in methylation detection by building a model capable of assimilating these multiple data streams into concise estimates.

The effect of long-term storage on ancient DNA samples.

7. Lab methods

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Abstract text: aDNA research frequently relies on remains stored for prolonged periods, yet studies examining the long-term storage effects on aDNA samples remain limited. For my master's thesis, we examined the effect of 8 years of long-term storage on aDNA samples from different preparation stages: bone powders, extracts and indexed libraries. Specifically, eleven individuals processed in 2015 were reprocessed in 2023.

We report significant differences in preservation across sample types: extracts showed increased degradation, whereas preservation improved for indexed libraries and bone powders.

Additionally, we found a significant increase in unique reads rate and mean fragment length in samples processed in 2023. These improvements are probably due to the differences in sequencing platforms available in 2015 compared to 2023. All samples were stored at constant cold temperatures. Long-term storage of aDNA samples has only recently emerged as a concern and no study has examined the long-term storage effects on aDNA samples from different preparation stages. Our findings suggest that the best suited sample types for storage are powders and indexed libraries, therefore extracts should not be kept for an extended period. Our research emphasizes that through sequencing technologies continuous improvement and storage conditions optimisation, the consequences of aDNA degradation can be mitigated.

Unlocking Archives: Evaluating the preservation of ancient DNA in archival waterlogged archaeobotanical assemblages

7. Lab methods

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Abstract text: Ancient DNA from archaeological plant tissues allows researchers to directly investigate the history and adaptability of crops and wild taxa across millennia. Although most studies have focused on desiccated archaeobotanical specimens, well-preserved waterlogged plant remains are increasingly recognised as a genetic resource to address complex palaeogenomic questions. Nevertheless, many waterlogged archaeobotanical assemblages exist as decades-old collections where the primary objective was to protect morphological features using antimicrobial preservatives. It remains unclear whether such storage conditions negatively impact DNA preservation or introduce contamination. To better understand how archaeobotany curation practices might constrain palaeogenomic methods, we have generated sequencing data from dozens of waterlogged prehistoric uncharred crops stored in different antimicrobial preservatives. Our results show that high-quality genetic information can be obtained from some archived waterlogged archaeological plant material, but DNA preservation varies within a site and depending on storage conditions. In particular, our experiments shed new light on whether treatment with thymol or ethanol may compromise genomic testing. These findings already guide our work on crop history in the context of the Alpine pile dwellings. We hope this work will 'unlock' existing collections to plant palaeogenomics and inform future curation practices for the long-term storage of waterlogged plant tissues.

8. Computational methods

A spatially-explicit reconstruction of muskox genomic data responding to climate change and human hunting.

8. Computational methods

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Abstract text: Investigating the effects of environmental changes on species distributions has been the central focus of biogeography studies over the past 50 years. This has been usually done by employing ecological niche models (ENMs) and, more recently, by incorporating ENMs into spatially-explicit population models (SEPMs). Given that the ecological processes that shape species distributions also determine patterns of genomic diversity, translating these spatially- and process-explicit ecological models into genomic simulations might provide new opportunities to better understand evolutionary processes in space and time, determine the genomic signatures of extinction and resilience, and directly evaluate the effects of environmental changes on the genome. We developed a pipeline for translating ecological models into genomic simulations. Using muskox as a case-study, we simulated 21,000 years of population growth, extirpation, and dispersal responding to changes in environmentally suitable conditions and hunting by humans. Gridded maps of simulated population abundances were used to simulate muskox genomic data, allowing to directly sample genomes across space and time, for any SEPM. Our framework provides a way forwards towards genomically-informed process-explicit analyses of species distributions, to ultimately unveil the impacts of environmental changes at multiple biodiversity levels.

Accurate genotype likelihoods for ancient DNA

8. Computational methods

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Abstract text: Genomic data of ancient samples are typically available only at low depth, consist of short fragments, and are affected by post-mortem damage (PMD). As a result, it is not possible to call genotypes accurately, and downstream analyses should account for genotype uncertainty, for instance by using genotype likelihoods.

Here, we present a fully updated version of the Analysis Tools for Ancient and Low-depth Samples (ATLAS 2.0), a user-friendly collection of methods to infer accurate genotype likelihoods for ancient DNA, and to use these genotype likelihoods to characterize many aspects of genetic diversity. ATLAS 2.0 further enables the use of many existing tools to assess population structure, infer selection or perform genotype imputation by encoding genotype uncertainty in the requested formats, or accurately infer allele counts from population samples. Additionally, ATLAS 2.0 offers convenience tools to characterize and filter sequencing data and is ten times faster and uses ten times less memory than previous versions. We demonstrate the usability of ATLAS 2.0 by performing large-scale downsampling experiments on paleogenomic data of several species and show that it outperforms existing approaches in both speed and accuracy.

ADAPT: An Ancient DNA Analysis Pipeline for planTs

8. Computational methods

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Abstract text: Recent advances in ancient DNA analysis have enabled researchers to reconstruct the histories of both extinct and extant species, providing deeper insights into past ecosystems and evolutionary processes. The history of crops and wild plants could provide valuable perspectives on these themes, but many bioinformatic tools for palaeogenomics are not optimised for large and complex plant genomes. Building upon best practices in the field, we present a dedicated workflow for archaeological and historic plants: ADAPT, the Ancient DNA Analysis Pipeline for planTs. This Nextflow pipeline dynamically allocates computational resources to process degraded plant DNA and assess common metrics like fragmentation, degradation and endogenous content across a range of genome sizes. Importantly, the approach builds upon past methods to identify ploidy, based on competitive mapping and breadth of coverage. Here we showcase the effectiveness of this pipeline on major crops such as polyploid wheat and diploid flax. We assess ADAPT's utility using shotgun sequencing and target enrichment data and compare it with other pipelines in terms of ease of use, computational resource requirements, and runtime. By identifying the most efficient pipelines for these crops, our findings aim to ensure reproducibility and high-quality results for downstream analyses of species with complex genomes.

Alignment of aDNA fragments to panmitogenomes and inference of hominin sources for low-coverage data

8. Computational methods

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Abstract text: Pangenome graphs reduce reference bias by encoding population-level variation as a genome graph rather than a single linear reference. In the mitochondrial context, these graphs are known as panmitogenomes. We introduce SAFARI, a sensitive graph-based aligner optimized to recover highly damaged, short, and post-mortem modified ancient DNA fragments. This increases usable read yield for low-coverage libraries. We demonstrate that panmitogenome alignments enable robust haplogroup assignment using HaploCart.. Finally, we show that our approach supports source inference in low-coverage mixtures of archaic hominins and modern humans.

Developing a human ancient epigenetic clock: promises and limitations

8. Computational methods

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Abstract text: Robust age-at-death estimation of archaeological remains is central to palaeodemographic research. While osteological methods are widely established and particularly effective for subadults, adult age estimation is often burdened by large uncertainties and wide age ranges, especially when skeletal remains are fragmentary. Epigenetic clocks have emerged as powerful predictors of age in modern humans, and recent work in ancient horses has shown that age-associated methylation patterns can be recovered when leveraging their deamination profiles in combination with a dedicated mathematical transformation framework. This raises the question of whether similar strategies could be implemented to unlock ageing information in ancient humans. Here, we adapt and evaluate this correction framework for human ancient DNA using established CpG clock panels to a dataset of 36 high-coverage (>10X) genomes. Our aim is to assess how well corrected values follow modern reference distribution and whether age-associated signals become detectable. We also evaluate the reliability of the transformed data by examining chromosome X methylation differences between sexes and general methylation distribution in CpG islands and promoter regions. This work highlights the need for bone-derived modern reference datasets and optimized sequencing strategies, laying the groundwork for future applications of human epigenetic ageing in palaeogenomics, and potentially reviving palaeodemography.

Estimating Genetic Kinship in Admixed Populations from Low-Coverage Genomes

8. Computational methods

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Abstract text: Genetic kinship estimation is central to research areas ranging from forensics to the ancient DNA (aDNA) studies, particularly for studying prehistoric social structures. However, accurately inferring biological relatedness from aDNA remains challenging, particularly when dealing with very low-coverage sequences. Furthermore, most of the existing methods overlook population structure and admixture, assuming a homogeneous background, which leads to biased or incorrect kinship inferences in heterogeneous populations. Here, we introduce a new approach for estimating kinship coefficients designed to explicitly address the challenges of population heterogeneity and admixture in low-coverage data. Unlike previous tools that assume homogeneous populations and fail to account for admixed ancestries, our approach substantially improves the accuracy of genetic kinship estimates in admixed and diverse populations by incorporating individual genetic backgrounds into relatedness estimation. Therefore our approach enables more reliable inferences about social organization and practices in prehistoric communities that were previously obscured by methodological limitations.

Genomic Approaches for Betula Species Delimitation in Ancient Sedimentary DNA

8. Computational methods

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Abstract text: SedaDNA cannot distinguish Betula nana (tundra shrub) from B. pubescens (boreal tree), the two species representing contrasting ecosystems but somehow possessing near-identical chloroplast genomes. This taxonomic limitation prevents niche reconstruction of Arctic shrubification, a key process in understanding ecosystem responses to climate change.

We present two complementary approaches using whole-genome sequencing data (15× coverage). First, we are developing a k-mer-based machine learning framework: comparative k-mer analysis (k=31) to identify species-specific genomic signatures per species, which were used to train a Random Forest classifier achieving >95% species identification accuracy (species-specific kmers are observed in our early tests). Second, we employed GeneMiner to extract single-copy nuclear genes directly from raw reads, followed by phylogenomic analyses to validate species boundaries and evolutionary relationships.

The k-mer approach offers critical advantages for sedaDNA applications: alignment-free, robust to DNA fragmentation and low coverage, and directly applicable to shotgun metagenomes. We demonstrate species identification at low coverage and short length, which can be representative of ancient DNA.

This dual-methodology framework addresses a fundamental limitation in Arctic paleovegetation research, hopefully enabling accurate species-level reconstruction of past vegetation dynamics, with potential to be transferable for other challenging taxa within sedaDNA context.

Geolocating Neanderthal Introgression using spatial simulations

8. Computational methods

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Abstract text: The last two decades have seen significant progress in the study of archaic human groups, such as Neanderthals and Denisovans, and their interactions with the ancestors of present day humans. Questions of when, where and how many times these groups interbred, have stood at the forefront of the field. Genetic simulations have played an important role in studying these interactions, by allowing us to model and test competing hypotheses, but spatiality; a crucial aspect of population theory, is still largely omitted.We use Slim and its non Wright-Fisher spatial simulation capabilities to investigate different admixture scenarios. We model an expanding 'modern human' population and a smaller and more static 'archaic' population, controlling for the exact location of introgression. We test different scenarios of admixture, such as a short vs a prolonged coexistence of the two populations and a single vs multiple encounters scenario. We generate hundreds of iterations of each scenario and for each one of them, record a number of summary statistics pertaining to introgression, exploring which can best illuminate the origin of an introgression event in deep time. We then compare the summary statistics of our simulations to those generated from real data to assess possible locations of introgression.

Graph variant explorer, a workflow for identifying structural variants in ancient DNA reads

8. Computational methods

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Abstract text: Ancient DNA (aDNA) sequencing is a powerful tool for studying evolutionary processes, but because DNA degrades and fragments over time, most analyses must be restricted to single-nucleotide polymorphisms (SNPs), even though genomic structural variants (SVs) represent a larger source of genetic diversity. Methods to detect aDNA SVs would therefore be valuable. A key challenge is the failure to map short, damaged reads to a reference assembly (i.e., reference bias), especially when those reads contain alternative alleles. While linear assemblies lack variant information, pangenome graphs efficiently store variation between constituent assemblies, so mapping to graphs significantly improves detection of alternative alleles. For ultra-short aDNA reads, graph references could enable detection of historical genetic variation undetectable using linear references. We present GRAVE (graph variant explorer), a reproducible Nextflow workflow for aligning aDNA reads to pangenome graphs, authenticating aDNA data, and identifying both SNPs and SVs. The workflow produces output files compatible with standard population genomics analyses. We expect that by incorporating diverse haplotypic backgrounds during mapping, grave will enhance the recovery of authentic endogenous DNA while reducing reference bias and unlocking complex SVs for aDNA research. Although our initial application focuses on sheep domestication, the pipeline is broadly applicable across study systems.

High-resolution oral microbiome analyses by mapping metagenomic data on a new curated genomic database of oral microbes

8. Computational methods

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Abstract text: The oral microbiome situates at the interface between the environment and host and influence local and systemic health. Recent metagenomic studies have clarified its taxonomic composition, but significant gaps remain in understanding variation across multiple dimensions—including pangenomic, strain-level diversity, and encoded functions—across scales (individual to population) throughout time and geography. While *k-mer*-based methods are widely employed to classify reads, their utility for deeper analyses at these levels is limited. To advance this, we constructed a comprehensive, non-redundant database of oral microbial genomes to map ancient and modern oral metagenomes. Our approach captures genome-wide data from most oral species, enabling *i*)accurate taxon detection, with strain-level resolution, *ii*)simultaneous genotyping of hundreds of taxa for evolutionary analyses (e.g.,selection), *iii)*phylogenomic and phylogeographic analyses, and *iv*)exploration of species pangenomes and functional variation. Applied to ancient oral metagenomes (dental calculus and birch pitch), our method significantly reduced false positives and environmental noise, yielding cleaner oral profiles. Additionally, using diversity analysis used in human population genetics, we detect geographic structure at whole-community scale. Our approach represents a significant methodological advance to deepen our understanding of the oral microbiome's dynamics and composition, to investigate the evolutionary trajectories of associated species, and their implications for human health and disease.

IBDemography: A Workflow for interpreting Identity-by-Descent sharing patterns through demographic simulations

8. Computational methods

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Abstract text: Improvements in imputation of low-coverage DNA have made Identity-by-Descent (IBD) analysis a standard approach for understanding relationships between human populations over time. However, there is no standardized framework for interpreting IBD results, with many studies using ad-hoc cut-offs for IBD segment length, leading to inconsistent conclusions. To better understand expected IBD sharing distributions under different demographic scenarios, we simulated genetic data investigating shared IBD proportions between populations, accounting for population size changes, structure, admixture, and varying sampling times. Our results demonstrate that using short IBD segments (<4cM) can lead to incorrect interpretations about recent relationships, as these segments are predominantly >100 generations old. For longer IBD segments, researchers must consider demographic changes (population size, admixture events, split times) to accurately interpret results. We find that what is considered very long IBD in the field (IBD>8cM) strongly depends on population history. For instance, even in the case of 90% admixture, observing IBD above 8 cM between target and source populations is rare when population size >5,000. Here, we also introduce IBDemography, a computational workflow that enables researchers to simulate specific demographic scenarios and compare their empirical IBD results against simulated expectations, facilitating more accurate interpretation of population relationships and demographic history.

Improved ancient human DNA alignment using GRCh38 and telomere-to-telomere (T2T) human reference genomes.

8. Computational methods

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Abstract text: Ancient DNA (aDNA) research predominantly relies on the GRCh37 human reference genome, despite the availability of more recent and complete assemblies such as GRCh38 and telomere-to-telomere (T2T). In parallel, graph-based reference genomes, incorporating population-level genomic diversity, have recently emerged as a promising framework for reducing reference bias. However, transitioning to newer reference genomes is challenging, as this requires extensive computational work such as remapping thousands of published genomes to avoid a mapping bias in population genetic studies. To quantify the potential improvement of remapping ancient data, we benchmark aDNA mapping performance across the linear reference genomes GRCh37, GRCh38, T2T, and a graph reference genome. We evaluate the mapping performance for published ancient genomes accounting for factors such as population background, post-mortem damage, and library preparation strategies. We observe a consistent increase in the number of aligned reads from GRCh37 to GRCh38 and further to T2T. The alignment quality also improves, as reflected by a reduced number of mismatches and reduced duplication rates. While analyses on the graph genome are ongoing, our preliminary results already highlight the advantages of updated linear references and point toward the potential added value of graph-based approaches as the next step for the aDNA field.

Improving taxonomic inference from ancient environmental metagenomes by masking microbial-like regions in reference genomes

8. Computational methods

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Abstract text: Detecting ancient plant and animal DNA in environmental samples relies on using extensive eukaryotic reference genome databases for profiling metagenomics data. However, many eukaryotic genomes contain regions with high sequence similarity to microbial DNA, which can lead to the misclassification of microbial reads as eukaryotic. This issue is especially problematic in ancient eDNA datasets, where plant and animal DNA is typically present at very low abundance. In this study [1], we present a method for identifying microbial-like sequences in eukaryotic genomes and apply it to nearly 3000 reference genomes from NCBI RefSeq and GenBank (vertebrates, invertebrates, plants) as well as the 1323 PhyloNorway plant genomes from nordic regions. We find that microbial-like regions are widespread across eukaryotic genomes and provide a comprehensive resource of their genomic coordinates and taxonomic annotations. This resource enables the masking of microbial-like regions during profiling analyses, thereby improving the reliability of ancient environmental metagenomic datasets for downstream analyses.

[1] Nikolay Oskolkov, Chenyu Jin, Samantha López Clinton, Benjamin Guinet, Flore Wijnands, Ernst Johnson, Verena E Kutschera, Cormac M Kinsella, Peter D Heintzman, Tom van der Valk, Improving taxonomic inference from ancient environmental metagenomes by masking microbial-like regions in reference genomes, *GigaScience*, Volume 14, 2025, giaf108, https://doi.org/10.1093/gigascience/giaf108

Optimising imputation and IBD segments retrieval in ancient genomes

8. Computational methods

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Abstract text: Ancient DNA has revolutionised the study of genetic variation and population movements over time. However, significant gaps in ancient genetic data hinder fine-scale characterisation of genomic structure and relatedness between individuals and/or archaeological sites. Here, we evaluate an imputation pipeline using a two-step approach to improve genotype accuracy and reduce genotype missigness in low-coverage ancient genomes. First, we impute individual samples with GLIMPSE using the 1000 Genomes Project reference panel. Second, we build a multi-individual dataset of high-confidence GLIMPSE calls and run Beagle5 for an additional round of imputation and phasing. To benchmark our imputation pipeline, we downsampled high-coverage ancient genomes, including shotgun sequences and 1240k target enrichment data. We investigated each step of the pipeline testing different filter thresholds, including genotype posterior probability after the imputation steps. Our findings highlight that a second round of imputation reduces the missingness of imputed genotypes for both shotgun sequences and SNP capture samples. Finally, we evaluate the performance of the second imputation with the identification of Identity-By-Descent (IBD) shared fragments between individuals using refinedIBD software, including long fragments, by examining known parent-offspring pairs. In conclusion, this study sheds light on improving ancientDNA analysis methodologies offering insights into population genetics and evolutionary dynamics.

sedimix: A workflow for the analysis of hominin nuclear DNA sequences from sediments

8. Computational methods

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Abstract text: The ability to extract DNA from archaeological sediments opens up the potential to study individuals at a given archaeological site when access to skeletal remains is limited. In recent years, several studies have demonstrated the promise of this approach by recovering hominin DNA from prehistoric sediments, including those dating back to the Middle or Late Pleistocene. However, a lack of open-source workflows for analysis of hominin sediment DNA samples poses a challenge for data processing and reproducibility of findings across studies. Here we introduce a snakemake workflow, *sedimix*, for processing genomic sequences from archaeological sediment DNA samples to identify hominin sequences and generate relevant summary statistics to assess the reliability of the pipeline. By performing simulations and comparing our results to two published studies with human DNA from ~25,000 years ago (including shotgun data from a sediment sample and capture data from touch DNA recovered from a deer tooth pendant) we demonstrate that *sedimix* yields accurate and reliable inferences. *sedimix* offers a reliable and adaptable framework to aid in the analysis of sediment DNA datasets and improve reproducibility across studies.

Time to rethink the analysis of ancient collagen?

8. Computational methods

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Abstract text: Ancient protein analysis has emerged as a powerful tool for palaeogenetics, yet conventional proteomic software continues to struggle with the unique challenges posed by ancient collagen, the target for ZooMS and many palaeoprotemics studies. Collagen presents a perfect storm of analytical difficulties that expose the limitations of software optimized for modern, intracellular proteins. Its unusually high proline and hydroxyproline content causes proline-induced fragmentation suppression during mass spectrometry, yielding spectra with incomplete fragment series. The repetitive Gly-X-Y motifs create ambiguous peptide identifications where single sequences map to multiple proteins. Beyond these intrinsic properties, ancient collagen accumulates extensive post-translational modifications: not only the biological hydroxylations and glycosylations critical for structural function, but also diagenetic modifications including deamidation, oxidation, and sample preparation artifacts. There is a fundamental mismatches between the assumptions underlying conventional proteomics workflows and the biological reality of ancient samples. The field requires analytical frameworks that can handle extensive modification landscapes, phylogenetic variation, and degraded material without sacrificing statistical rigor. This presentation will examine why current approaches systematically fail for ancient collagen and discuss the logical foundations required for next-generation analytical strategies tailored to the unique demands of ancient protein research.

Tree Inference from Low-depth Next-generation Sequencing Data with distAngsd

8. Computational methods

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Abstract text: The field of ancient DNA relies heavily on next-generation sequencing data. However, such data is difficult to work with when sequencing depth is low, as is often the case for ancient DNA. At sites in the genome covered by few reads, sequencing error may result in the detection of false variants – or vice versa – true heterozygous sites may be discarded as sequencing error. As we attempt to recover DNA from increasingly older sources, the challenges inherent to analysing such data will be exacerbated. To address this, methods tailored to ancient DNA move towards the use of genotype likelihoods. In contrast to variant calling, which results in a single genotype per individual per site, genotype likelihoods allow multiple genotypes to be considered with varying likelihoods, accounting for uncertainty resulting from the characteristics of ancient DNA. Genotype likelihoods also allow for a more nuanced handling of heterozygous sites. distAngsd generates one-to-one evolutionary distance estimates based on genotype likelihoods; we expand the tool to generate full phylogenetic trees, providing a novel genotype likelihood-based tree inference software. With the addition of new user capabilities, we aim to increase distAngsd's versatility as a tree inference method within the study of closely-related ancient populations.

tSNP: A dimensionality reduction algorithm for genetic data

8. Computational methods

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Abstract text: Population structure reflects non-random genetic relationships shaped by geography, culture, and history. Dimensionality reduction methods, most notably principal component analysis (PCA), are widely used to visualize genome-wide single-nucleotide polymorphism (SNP) data in two or three dimensions while trying to preserve patterns of population structure. However, these generic methods do not explicitly exploit the ternary nature of SNP genotypes, which encode the count of reference alleles per locus (either 0, 1, or 2), and may therefore fail to capture subtle structure.

Here, we introduce tSNP, a dimensionality reduction algorithm specifically tailored to ternary genetic data. It represents SNPs as lines, and genotypes as dots, and finds a two-dimensional embedding that optimizes geometric relationships between them in a way that captures allele-sharing patterns that are informative about population structure. We benchmark its performance against PCA, UMAP, and t-SNE on multiple simulated and empirical datasets, and examine cases where tSNP outperforms other methods in revealing large-scale patterns of population structure. These results indicate that directly exploiting the ternary representation of SNP data is a promising direction for dimensionality reduction in population genetics.

Unravelling Spatio-Temporal Admixture Dynamics in the Neolithic Using Spatially Explicit Paleogenomic Simulations

8. Computational methods

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Abstract text: Interpreting paleogenomic diversity in terms of interactions between prehistoric populations requires computational models that account for both space and time. We present a spatially explicit simulation–inference framework to reconstruct population dynamics between European hunter-gatherers and early farmers during the Neolithic transition. Using high-quality paleogenomic data from 67 individuals, we simulated range expansion, long-distance dispersals, and biological interactions under multiple demographic scenarios. An Approximate Bayesian Computation approach was then used to select the most plausible model and estimate key parameters. The best-supported scenario involves a temporal increase in admixture with hunter-gatherers at each step of the farmer's progression along the Continental route, rather than constant gene flow through time. This suggests that genetic exchanges were initially rare and increased during the cohabitation between both populations, following a similar process across all regions along the route. We further estimated a ~5-fold higher effective population size for farmers relative to hunter-gatherers and rare long-distance dispersal events. Our approach shows that spatially explicit demogenomic models integrating admixture, competition, and migration can disentangle spatial from temporal drivers of genetic change. This framework paves the way for further models exploring the role of admixture pulses and heterogeneous environments, and advances ancient DNA analyses beyond descriptive inferences.

Using ancient DNA methylation to Predict Exposure to Smoke in Ancient Societies

8. Computational methods

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Abstract text: DNA methylation in blood of present-day individuals has been shown to provide reliable prediction of exposure to smoke. Using this predictive model for ancient societies might provide insights on their patterns of fire use. However, reconstructed levels of DNA methylation in ancient genomes is characterized by increased standard errors and lower resolution compared to modern methods. Moreover, modern predictive models were developed for blood, whereas ancient DNA methylation maps typically represent skeletal tissues.

To overcome these limitations, we developed a multi-step framework. First, we used DNA methylation data across multiple tissues to develop a predictive pan-tissue model. Second, we adapted the predictive model to the distinctive features of ancient DNA methylation. We validated the framework using simulations.

We applied the model to 53 ancient genomes and predicted levels of smoke exposure. Together with temporal and spatial information, as well as cultural context, we identified patterns of smoke exposure changes across time, space and culture.

9. Other

A rodent's view of Middle Pleistocene Beringia

9. Other

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Abstract text: Rodents offer unique insights into Middle Pleistocene ecosystems in Beringia, acting as both ecosystem participants and preservers of environmental information. We integrate genomic data from rodent palaeofaeces, permafrost sediments, and skeletal remains to reconstruct Middle Pleistocene ecosystems. Permafrost preservation has allowed assembly of high-coverage mitochondrial genomes, including ca. 700,000-year-old ground squirrel (*Urocitellus* sp.). By using shotgun and targeted sequencing we also recover diverse plant, invertebrate, and vertebrate taxa, of which many are absent from conventional fossil records. Our integrated palaeogenomic approach demonstrates the value of combining skeletal remains with ancient environmental DNA to reconstruct Middle Pleistocene ecosystems, highlighting the rodent perspective as a powerful lens for understanding deep-time biodiversity and ecological interactions.

Ancient RNA expression profiles from the extinct woolly mammoth

9. Other

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Abstract text: The analysis of ancient DNA has recently gained considerable momentum, allowing the study of extinct and extant organisms that lived up to 2 million years ago. This has enabled the reconstruction of genomes and historical ancestry of multiple extinct species, as well as revealing the complex nature of the bygone ecosystems where they once thrived. However, current DNA sequencing techniques cannot alone provide information about tissue identity, gene expression dynamics or transcriptional regulation – all of which is encoded in the RNA fraction, and critical to fully understanding the biology of these now lost species. Here we report RNA expression profiles from 10 woolly mammoths dating to the Late Pleistocene. One of these, dated to ~39,000 YBP, yielded sufficient detail to recover tissue-specific biological functions essential for skeletal muscle

and skin metabolism. Our findings represent the oldest ancient RNA sequences recorded to date, enabling the reconstruction of transcriptional signatures in the extinct woolly mammoth. With our results, we showcase the potential to study ancient RNA molecules decoding preserved transcriptomes from deep time, and propose future directions and perspectives on the unrealized potential of RNA to illuminate developmental biology, infectious disease history, and the dynamic regulatory landscapes of ancient life.

Ancient seeds reveal millennia of agriculture on the Canary Islands

9. Other

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Abstract text: The colonised history of the Canary Islands has been shaped by isolation and globalisation with profound consequences for the islands' agriculture. On most islands the original crop package, brought to the arhipelago in the early centuries of the Common Era by Amazigh colonisers, was decimated while the islands were isolated from the mainland and each other, prior to the arrival of Eurpopean seafarers. Only on Gran Canaria was the full crop package retained.

The indigenous inhabitants of Gran Canaria carved out grain silos in remote mountain locations and used them for long-term storage of their harvest surplus. In these silos, well-preserved seeds can still be found. We have genetically analysed lentils dating back to the 7th century, the first ever analysis of aDNA in lentils. Comparisons with present-day Canarian lentils reveal continuous cultivation of the lentils brought to the archipelago by the original colonisers. We further find support for inter-island isolation prior to the arrival of European seafarers and for continuous cultivation also on island lacking archaeological finds of lentils. A lasting genetic impact of Canarian lentil export to the mainland, after the isolation was broken is suggested.

Beyond palaeogenomics: benchmarking the Survival and Authenticity of Pre-Holocene Enamel Proteomes

9. Other

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Abstract text: Palaeoproteomics offers the potential to extend the molecular record significantly beyond the temporal limits of ancient DNA. However, the precise boundaries of protein survival remain difficult to define, as wide-scale studies documenting degradation patterns across geological time are lacking. Here, we report on a broad-scale investigation of all pre-Holocene enamel proteomes published to date. By reanalysing these datasets, we define consistent trends in diagenetically induced modifications and damage patterns that serve as key indicators of authenticity in deep time.

We observe the robust recovery of enamel matrix proteins and distinct sequence regions that display clade-specific survival patterns. By contextualizing these results against amino acid racemization data, we establish a predictive framework for initiating new deep-time projects, allowing researchers to gauge expectations of protein survival based on independent diagenetic markers. Overall, our results indicate that valid proxies for authenticity depend on data volume, implying that reports of isolated peptides cannot be substantiated, excluding distinct cases where specific mineral-binding mechanisms are established. Finally, we demonstrate that while high sequence conservation restricts resolution at lower taxonomic levels, it ensures the resulting phylogenetic signal is highly accurate and rarely misleading, provided strict validation criteria are applied.

Each bead tells another story: ZooMS reveals unexpected complex sourcing of personal adornment durng Bronze Age

9. Other

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Abstract text: During rescue excavations at Ożańsk in south-eastern Poland, an atypical burial of an adult woman was uncovered within a settlement of the Early Bronze Age Mierzanowice culture. The body was partially burned, likely due to a collapsed burning beam and accidental death cannot be ruled out. She was buried with numerous artifacts, considered rich for this cultural context, including a necklace made of multiple beads, many of which were partially fire damaged.

Anthropological analysis of the poorly preserved skeleton revealed little, but the accompanying artifacts provide valuable insight into social practices and cultural identity. We applied Zooarchaeology by Mass Spectrometry to determine the faunal origin of the beads, overcoming challenges posed by poor preservation and burning.

ZooMS analysis identified a diverse assemblage of wild and domesticated species, including hare, red fox, dog/wolf, pig/wild boar, domestic sheep, cattle, and possibly hawk. This multispecies selection may reflect practical use of available materials, symbolic or ritual significance, or both.

These findings demonstrate the potential of ZooMS to uncover new dimensions of Early Bronze Age material culture in south-eastern Poland, revealing aspects of mortuary practices, personal adornment, and human-animal relationships that were previously inaccessible due to preservation issues and limited application of biomolecular methods.

Historical RNA expression profiles from the extinct Tasmanian tiger

9. Other

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Abstract text: Paleogenomics continues to yield valuable insights into the evolution, population dynamics, and ecology of our ancestors and extinct species. However, DNA sequencing cannot reveal gene expression patterns, cellular identity, or gene regulation. Pioneering studies have shown that useful RNA can be extracted from ancient specimens preserved by permafrost or desiccation, but no previous attempts have been made on extinct species. We extracted, sequenced, and analyzed historical RNA from muscle and skin tissue of a ∼130-year-old Thylacine preserved by desiccation at room temperature in a museum collection. The transcriptional profiles closely resembled those of extant species, revealing specific anatomical features such as slow muscle fibers and blood infiltration. Kraken analyses, RNA damage, tissue-specific expression profiles and exon-spanning sequences further confirmed the authenticity of the sequences. RNAs were used to refine gene annotations and increase the number of annotated thylacine microRNAs from 62 to 325 - including novel marsupial sequences. Finally, we detected traces of viruses, suggesting the possibility of tracing RNA virus evolution. Our results represent the first successful attempt to obtain transcriptional profiles from an extinct animal species, and have implications for the study of RNA molecules across the vast collections of natural history museums.

Millennia of evolution and adaptation between Mediterranean human coastal populations and Atlantic bluefin tuna

9. Other

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Abstract text: For millennia, Mediterranean coastal communities have relied on tuna fishing as a primary source of sustenance, with evidence of this practice dating back 9000 years. Understanding the historical extent of human dependence on coastal resources is therefore essential for assessing long-term socio-economic development, human health, and the anthropogenic impact on the environment. Among the apex predators of the Mediterranean Sea, the Atlantic bluefin tuna (*Thunnus thynnus*) servs as both a keystone species and a vital resource for traditional sustenance. Its exploitation was historically related to small-scale subsistence fisheries conducted by coastal and islands communities and then to more complex systems, such as the traditional tuna traps, which activated the first commercial activities. This study aims to examine adaptive changes in ancient and contemporary Mediterranean bluefin tuna populations, as well as among past and present communities engaged in traditional tuna fishing practices. Our study shows: potential adaptive responses of tuna to prolonged human influence; possible differences in allele frequencies of pollutant-detoxification genes between populations with a historical reliance on fish consumption and those without such dietary traditions. Although tentative, this research will provide a comprehensive understanding of the long-term interactions between Atlantic bluefin tuna and human populations in the Mediterranean area.

Molecular dating of rodent remains as a means to date Late Pleistocene sites

9. Other

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Abstract text: Establishing absolute chronologies is fundamental in palaeontological and archaeological research, enabling the interpretation of evolutionary processes, cultural phases, and faunal turnover. Radiocarbon dating (^{14}C) and thermally or optically stimulated luminescence (T/OSL) are the most widely applied methods for dating Late Pleistocene materials and sediments. Although highly effective, these approaches have limitations and cannot always be used.

Molecular dating, based on a specimen's placement within a time-calibrated phylogeny, represents a complementary or alternative approach. It has been previously applied to Late Pleistocene human and animal remains, typically relying on mitochondrial DNA. However, in large mammals, low mutation rates limit the temporal precision of such estimates. Rodents, in contrast, have faster mutation rates due to short generation times, and their remains are abundant at many Late Pleistocene sites, offering higher resolution and broader applicability.

Here, we present molecular age estimates based on mitogenomic datasets from five rodent species widespread across Eurasia during the Late Pleistocene. The analysed specimens originate from a range of sites, including caves and open-air localities. We compare the molecular age estimates with available absolute dating results and discuss the potential and limitations of applying rodent-based molecular dating to multilayer Late Pleistocene sites.

Molecular Persistence in Deep Time: Amino Acid Preservation in Enamel from Modern and Fossil Mammals

9. Other

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Abstract text: Proteomic research demonstrated that proteinaceous residues preserved in tooth enamel can provide insights into sex, diet, and evolutionary relationships. Enamel contains about 1% organic material, yet its dense mineral structure protects endogenous peptides and amino acids by acting as a closed system during chemical alteration. Over long timescales, proteins break down and may persist mainly as short peptides or free amino acids. Earlier studies largely focused on amino acid racemisation in relatively young (Quaternary) samples.

To address this gap, a protocol was developed to detect and semi-quantify THAAs and FAAs. To investigate protein resistance, twelve amino acids were quantified using HPLC, confirming that both THAAs and FAAs can persist in enamel for up to 28 million years. The study assesses THAA/FAA ratios to determine how long amino acids remain peptide-bound, how they change over time, and when they shift toward predominantly free forms or complete degradation.

Amino acid data from modern and fossil Proboscidea and Rhinocerotidae show that Asx maintains a stable THAA/FAA ratio, indicating comparable preservation across both clades. In contrast, Gly, Ser, Tyr, and Arg display increasing ratios with age, suggesting contributions from preserved peptide fragments and demonstrating enamel’s reliability as an archive of ancient biomolecules over time.

SmallRNA preservation in >41000 year old permafrost: Evidence from a Pleistocene moth

9. Other

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Abstract text: Ancient DNA has become a powerful and increasingly routine tool for reconstructing genomes and evolutionary history of extinct organisms. While DNA reveals genomic potential across deep time, ancient RNA fills major gaps in uncovering gene activity, regulation and biological function directly. To date, successful recovery has been reported from large, megafaunal tissues mostly preserved in permafrost, the oldest being 39,000 years.

Here, we demonstrate the persistence and improved yield of endogenous smallRNA from a single leg of an exceptionally preserved moth *Agrotis fatidica* recovered from a > 41,000 year old layer of Siberian permafrost. Alongside its historical and modern representatives, we reconstruct its microRNA repertoire and identify highly conserved, as well as *bona fide* species specific microRNAs suggesting deep regulatory continuity along lineage specific innovations. Comparative analysis across 3 time points reveals trace changes in presence, abundance and sequence variations, reflecting ancient population specific mutations or long term evolutionary trends where present. We report successful small RNA recovery from one of the oldest known invertebrate specimens, highlighting the potential for preservation of smallRNA beyond currently understood limitations. We hereby illuminate the viability of the emerging field of paleotranscriptomics to complement traditional paleogenomics by revealing functional and regulatory dimensions of ancient organisms.

Transcriptomic data from RNA preserved for more than 500 years

9. Other

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Abstract text: The three Children of Llullaillaco, dated to around 1480 CE, are among the best-preserved mummified human remains. Non-invasive sampling provided a multi-omic dataset including high-coverage human genomes, multiple pathogen genomes and an authentic gut microbiome profile. Given their exceptional preservation, we attempted the recovery of RNA from six nucleic acid extracts obtained from surface swabs of the mummies. Using RNA library preparation protocols tailed to small RNA fragments, we retrieved a low coverage transcriptome. Among reads mapping to the human genome, up to 65% were falling in exons, and variants within these reads matched the genomic variants of the respective individuals. Strikingly, a fraction of up to 16.5% of the mapped reads shows signatures of splicing at canonical splice sites. We also found that the most abundant gene products in the individual datasets are specific to the body part where they were sampled from (human gut from an anal swab, human skin from a skin swab). Even though the overall yield was limited, we conclude that it is possible to obtain authentic transcriptomic data from human remains preserved for five centuries.

Zooarchaeology by Mass Spectrometry (ZooMS) protocols for optimized taxonomic identification of fossils from a submerged cave system

9. Other

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Abstract text: Heightened hydrolysis of fossil DNA, alongside complicated sampling requirements, limit ancient DNA research in submerged and underwater environments. In such contexts, fossil proteomics and collagen-based analyses might be better approaches since proteins are more resistant to hydrolytic diagenesis. Zooarchaeology by Mass Spectrometry (ZooMS) uses the MALDI-ToF fingerprinting of trypsinated Collagen Type I to determine the taxonomic identity of otherwise unidentifiable fossil fragments. Here, we present a comparison of ZooMS protocols targeted at both acid-insoluble and acid-soluble collagen components of a largely fragmented cohort of skeletal specimens (n = 200), from underwater assemblages ranging from 250 ka to post-colonial (1788) ages found within the Green Waterhole-Tank Cave complex of southeast South Australia. We discuss the suitability of tested ZooMS protocols on submerged fossil assemblages, reviewing success rates, potential for taxonomic identification and present palaeoecological reconstructions derived from our results. Our analyses suggest significant preservation of acid-insoluble collagen in submerged assemblages up to ~60 ka in age, allowing for family-level taxonomic identifications. Through this, we highlight how submerged cave environments provide good conditions for biomolecular survival despite higher water availability and emphasize the benefits of ZooMS in a multi-proxy molecular reconstruction of Australian ancient ecosystems.

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Stone, Anne C.
Stoof-Leichsenring, Kathleen
Stoof-Leichsenring, Kathleen R.
Story, Jo
Strandberg, Nichola
Strang, Alex
Straus, Lawrence G
Stringer, Chris
Suchwoska-Ducke, Paulina
Sun, Xin
Sun, Zhouyong
Sundset, Monica Alterskjær
Suo, Mingjie
Swali, Pooja
Swarts, Kelly L.
Szeifert, Bea
Szpak, Paul

van der Valk, Tom
Van Doorn, Kelly
Van Neer, Wim
van Schaik, Katherine
van Vugt, Lieveke
Vandorpe, Patricia
Vanni, Margherita
Vaquer, Jean
Varlık, Nükhet
Vartanyan, Sergey
Varul, Liivi
Vassou, Despoina
Veiberg, Vebjørn
Velsko, Irina
Velušček, Anton
Vera Cortés, Jose Luís
Vera Cortés, José Luis
Vergnaud, Luc
Verheijen, Ivo
Vernot, Benjamin
Verry, Alex
Vida, Tivadar
Villa-Islas, Viridiana
Villagrasa, Amaia
Villalba-Mouco, Vanessa
Vinner, Lasse
Visagie, Johann
Viti, Aurora
Vizzari, Maria Teresa
Vogel, Nicola
Vogel, Nicola Alexandra
Vogel, Nicola
Vollmar, Nele Manon
Vukovic, Nikola
Vukovikj, Maja
Vuković, Sonja
Vulković, Sonja