ABSTRACT BOOK

10th Meeting of the International Society for Biomolecular Archaeology (ISBA)

New Horizons in Biomolecular Archaeology

13th–16th September 2023
Estonian National Museum, Tartu, Estonia


Website: Flickr.com Photo: Ragnar Vutt

Welcome Letter

Dear colleagues,

A warm welcome to the 10th Meeting of the International Society for Biomolecular Archaeology (ISBA) entitled "New Horizons in Biomolecular Archaeology," hosted by the University of Tartu!

Set against ISBA's inaugural meeting in 2004, the ISBA community has undergone a scientific journey spanning two decades. Marking the tenth anniversary of the ISBA conference, ISBA10 stands as a testimony to ten years of multidisciplinary biomolecular research and as an outlook for the years to come.

Biomolecular archaeology is a tapestry woven from the threads of biomolecular disciplines held together by archaeology. Archaeology as a discipline stretches back over centuries. Through the more recent addition of biomolecular methodologies, the discipline was able to evolve well beyond its more humble beginnings and reconstruct much more complex pictures of history than we ever could have expected.

Picture, if you will, our ISBA meetings as a family gathering, where the innovation of youth harmoniously converges with the knowledge born from experience, generating a dynamic ever-evolving synergy. More profoundly, this meeting marks the first in-person meeting following the devastating COVID-19 pandemic, which diminished multidisciplinary exchange and impacted all our lives.

The present holds sway over our understanding of the past and vice versa, and this truth is evident in science too. The war that Russia started against Ukraine has cast a substantial shadow over research endeavours in Estonia. Within this context, the University of Tartu vehemently condemns the Russian military's aggression within Ukrainian borders. As a result of this principled stand, the ISBA10 will bear the consequence of absent 'family members' from the global academic community. The decision serves as a tangible reminder that academic exchange is deeply intertwined with ethical considerations and geopolitical realities. It reflects the commitment of institutions to uphold values even in the face of academic discourse, ultimately underscoring the intricate interplay between the past, present, and the pursuit of knowledge.

May this meeting be a source of interaction, inspiration, and productivity. Enjoy the vibrant exchange of ideas, the cultivation of novel concepts and the forging of multidisciplinary partnerships!

- The ISBA10 organising committee

Table of Content

ORGANISING COMMITTEE

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University of Tartu, EE

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Committee “Biomolecular archaeobotany”:

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Committee “Archaeological fieldwork, curation and pre-screening methods for biomolecular research”:

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Sara Gummesson (Stockholm University, SE)
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Birgitte Skar (NTNU University Museum, NO)

VENUES

Conference:
Estonian National Museum
Muuseumi tee 2
60532 Tartu, Estonia

Conference Dinner:
University of Tartu Museum
Lossi 25
51003 Tartu, Estonia

How to get to the Estonian National Museum?

~ 30 min

On foot: from the city center it takes ca **30 minutes to walk** to the Estonian National Museum. Take Roosi St and you will reach Muusemi tee where the venue is located.

~ 15 min

By bus: From the centre of the city you can take **Bus no 7**, which takes you next to the Estonian National Museum. The public transportation is free for the ISBA 10 conference attendees, you just need to have your conference badge with you. The bus stops in the centre are shown on the map.

~ 10 min

By bike: You may use the bikes of the Tartu Smart Bike Share. This is free for the conference attendees. In order to unlock a bike you need to create a **bike share account**, either on-line (ratas.tartu.ee) or via the mobile app (**Tartu Smart Bike**), and connect it to a credit card. To use the free ride insert the code **ISBA10SMARTBIKE**. There is a bike station right next to the entrance of the Estonian National Museum.

~ 10 min

By taxi: you can use the **Bolt** app in Tartu. Some other taxi companies and their phone numbers are listed here: Elektritakso: (+372) 1918; Takso Üks: (+372) 742 0000, Tartu Taksod: (+372) 455 5555, Tartu Taksopark: (+372) 730 0200, Minu Takso: (+372) 733 3333, SV Takso: (+372) 734 3333, Vatex Takso: (+372) 736 6566, Välk Takso: (+372) 557 7550.

Website: Flickr.com Photo: Ragnar Vutt

10th Meeting of the International Society for Biomolecular Archaeology
“New Horizons in Biomolecular Archaeology”

13th–16th September 2023
Estonian National Museum, Tartu, Estonia

Organised by:

The University of Tartu
&
The Estonian Genome Foundation

Supported by:

Faculty of Science and Technology, University of Tartu

Faculty of Arts and Humanities, University of Tartu

The Collegium for Transdisciplinary Studies in Archaeology, Genetics and Linguistics, University of Tartu

Institute of History and Archaeology, University of Tartu

Institute of Genomics, University of Tartu

International Society for Biomolecular Archaeology

European Union through the HORIZON Coordination and Support Actions under grant agreement no 101079396 (PaleoMIX).

Centre for Genomics, Evolution and Medicine (cGEM) of Institute of Genomics, University of Tartu (within the European Union’s Horizon 2020 grant no 810645).

Tartu City

UNIVERSITY OF TARTU 1632

UNIVERSITY OF TARTU Institute of Genomics

UNIVERSITY OF TARTU Faculty of Arts and Humanities

UNIVERSITY OF TARTU Faculty of Science and Technology

Co-funded by the European Union

The Collegium for Transdisciplinary Studies in Archaeology, Genetics and Linguistics, University of Tartu

PaleoMIX

Centre of Genomics, Evolution & Medicine cGEM

ISBA

TARTU

Wednesday
13th September

8.00-9.00	Registration	
9.15-9.30	Welcome to ISBA10!	
9.30-10.30	Keynote: Anne Stone	
10.30-11.00	Coffee break	
11.00-12.30	Session 1A: Kinship and social structure	Session 1B: Ancient foodways I
12.30-14.00	Lunch	
14.00-15.30	Session 2A: Domestication	Session 2B: Methodological advancements
15.30-16.00	Coffee break	
16.00-16.30	Invited talk: Melanie Roffet Salque	
16.30-17.00	Invited talk: Giedrė Motuzaitė Matuzevičiūtė	
17.00-17.30	Flash talks I	
17.30-18.30	Poster session I	
18.30-19.30	Annual general meeting for ISBA members	
19.30-21.00	Reception at the ENM	

🟧 Lobby Reception Area

🟥 Jakob Hurt Hall

Thursday
14th September

9.00-9.30	Invited talk: Benjamin Vernot	
9.30-10.00	Invited talk: Beatrice Demarchi	
10.00-10.30	Coffee break	
10.30-12.00	Session 3A: Community, sustainability & environment I	Session 3B: Ancient fauna
12.00-13.30	Lunch	
13.30-15.00	Session 4A: Human population genetics I	Session 4B: Health and disease I
15.00-15.30	Coffee break	
15.30-17.00	Session 5A: Ancient foodways II	Session 5B: Community, sustainability & environment II
17.00-17.30	Flash talks II	
17.30-18.30	Poster session II	
18.30-19.30	Break / Guided tours at the ENM (optional)	
19.30-00.00	Dinner at the University of Tartu Museum	

Friday
15th September

9.00-10.00	Keynote: Carl Heron	
10.00-10.30	Coffee break	
10.30-12.00	Session 6A: Diet & environment	Session 6B: Pleistocene
12.00-13.30	Lunch	
13.30-15.00	Session 7A: Health and disease II	Session 7B: Origins, dating & authentification
15.00-15.30	Coffee break	
15.30-17.00	Session 8A: Human population genetics II	Session 8B: Novel Approaches
17.00-17.30	Coffee break	
17.30-18.00	Invited talk: Martin Petr	
18.00-18.30	Closing of the conference	
18.30-19.30	Guided tours at the ENM (optional)	

Saturday
16th September

9.00-...	Excursions (optional)

PROGRAMME

Wednesday, 13th September

9.15–9.30	**Welcome to ISBA10!**					
9.30–10.30	**Keynote:** Anne Stone – Ancient DNA research since the first ISBA conference					
10.30–11.00	**Coffee break**					
11.00–12.30	**Session 1A: Kinship and social structure**			**Session 1B: Ancient foodways I**		
	KSS-001	Guido Alberto Gnecchi- Ruscone	Ancient DNA-based large pedigrees and haplotype-IBD networks provide unprecedented insights into the social structure of steppe descent Avar period communities	AF-001	Léa Drieu	Widen the perspectives: expanding the range of identifiable content in African pottery
	KSS-002	Frederik Seersholm	An Outbreak of the Stone Age Plague in a Large Extended Family	AF-002	Jasmine Lundy	Investigating the adoption of rice and millet by hunter-gatherer-fishers of central Japan using organic residue analysis
	KSS-003	Éadaoin Harney	The Genetic Legacy of African Americans from Catoctin Furnace	AF-003	Shinya Shoda	Regional differences in stone cooking in the Japanese Palaeolithic as revealed by lipid residues
	KSS-004	Ian Armit	Ancient DNA and kinship analysis at the Iron Age cemetery of Wetwang Slack, East Yorkshire, UK	AF-004	Edward Standall	Investigating the use of broomcorn millet (P. miliaceum) in culinary activities across East Kazakhstan throughout the Bronze Age
	KSS-005	Eirini Skourtanioti	Investigating the population history of present-day Georgia using diachronic archaeogenomic data	AF-005	Rachel Vykukal	From Dates to Hens: Exploring Lipid Biomarkers for Novel Commodities in Roman Britain
12.30–14.00	**Lunch**					
14.00–15.30	**Session 2A: Domestication**			**Session 2B: Methodological advancements**		
	DOM-001	Marcello Mannino	Mixed diets at the Mesolithic-Neolithic transition? Bulk and compound-specific isotope evidence for the interaction between hunter-gatherers and farmers at Grotta dell'Uzzo (Sicily)	MET-001	Nicola Alexandra Vogel	euka – Robust characterisation of eukaryotic taxa from sedimentary ancient DNA with pangenome graphs
	DOM-002	Marcela Sandoval-Velasco	Exploring the domestication of Agave – Preliminary results from the Tehuacán Valley Caves in central Mexico	MET-002	Bharath Anila Bhuvanendran Nair	Investigation of protein degradation using LC-MS/MS, MALDI-MS, and Amino Acid Racemization: A case study with Beta-lactoglobulin

Wednesday, 13th September

	DOM-003	Anders Bergström	The genetic identity of Europe's first dogs	MET-003	Théo Cavinato	Using ancient and modern DNA from relatives to reconstruct a missing genome
	DOM-004	Áine Halpin	Origins and genomic trajectory of the domestic sheep	MET-004	Irina M. Velsko	Extensive diversity of unnamed Anaerolineaceae taxa in ancient dental calculus revealed through de novo genome assembly
	DOM-005	Marco De Martino	Paleogenomics of European wild and domestic cats	MET-005	Katia Bougiouri	Imputation of ancient dog genomes informs on their inbreeding history since the onset of domestication

15.30–16.00	**Coffee break**		
16.00–16.30	**Invited talk:** Melanie Roffet Salque – Advancing the application of lipids in archaeological and palaeoenvironmental reconstruction		
16.30–17.00	**Invited talk:** Giedrė Motuzaitė Matuzevičiūtė – A biomolecular approach to millet journey across time and space		
17.00–17.30	**Flash talks I**		
	CEP-009	Yi Wang	A 14-thousand-year high resolution metagenomic exploration of Lake Constance
	METP-019	Femke Reidsma	Fundamental Fire: laboratory-based chemical research into the effect of diagenesis on heated bone and its implications for the study of fire proxies and other biomolecules in the deep past.
	DENP-001	Donikë Sejdiu	Herbarium DNA confirms 20th-century presence in Europe of Phytophthora lineage that caused Irish Potato Famine
	METP-023	Adrià Breu Barcons	Caution! Contents were hot: experiments exploring the suitability of novel high-temperature lipid biomarkers detected in Mediterranean neolithic pottery
	NOVP-005	Nikolay Oskolkov	aMeta: an accurate and memory-efficient ancient Metagenomic profiling workflow
	ODAP-007	Jack Sharpen	Assessing Biomolecular Degradation using a multi-omic approach
	NOVP-011	Liam T. Lanigan	Multi-omic analyses of palaeofaeces from Viking Age Ribe, Denmark
	METP-041	Lucas Anchieri	Assessing ancient DNA sampling strategies for natural selection inference with time-series data
	NOVP-017	Isabel Wiltshire	Using a multi-pronged approach to the analysis of absorbed lipid residues to investigate chronological trends in pottery use from the Neolithic to the Iron Age in Saxony
	HDP-011	Ian Light	Molecular evolution of Y. pestis using ancient and modern genomes
	PLEP-001	Palesa Madupe	Paranthropus robustus first dental enamel proteome
17.30–18.30	**Poster session I**		
18.30–19.30	**Annual general meeting for ISBA members**		
19.30–21.00	**Reception at the Estonian National Museum**		

Thursday, 14th September

9.00–9.30	**Invited talk:** Benjamin Vernot – Metagenomics Reveals the Past					
9.30–10.00	**Invited talk:** Beatrice Demarchi – Ancient proteins in archaeology					
10.00–10.30	**Coffee break**					
10.30–12.00	**Session 3A: Community, sustainability & environment I**			**Session 3B: Ancient fauna**		
	CE1-001	Rita Peyroteo Stjerna	Researchers' perspectives on the ethics of human remains research: from tissue to biomolecules	FAU-001	Merlin Szymanski	A systematic evaluation of hominin and faunal DNA preservation in Pleistocene sediments
	CE1-002	James Fellows Yates	Building a community-based consensus for ancient sequencing data metadata reporting with MInAS	FAU-002	Aurélie Boilard	Reconstructing faunal diversity from the last Glacial period in northern Norway using zooarchaeology and bulk-bone metabarcoding
	CE1-003	Andre Carlo Colonese	Biomolecular archaeology meets ocean conservation in biodiversity hotspots	FAU-003	Courtney Hofman	A Ghost on the Coast: Lessons from the Extinction of the Sea Mink (Neogale macrodon) and Conservation Implications for the American Mink (Neogale vison)
	CE1-004	Oya Inanli	Metagenomic perspectives on traditional beer brewing: New insights from Scandinavian yeast rings	FAU-004	Geneviève Pothier-Bouchard	Exploring question-oriented mass sampling strategies to integrate ZooMS into zooarchaeological analyses of prehistoric faunal collections
	CE1-005	Elena Essel	Tracing touch through time: Ancient human DNA recovered from a Palaeolithic pendant	FAU-005	Jorune Sakalauskaite	Spondylus Palaeoproteomics: tracing the iconic shell of prehistory
12.00–13.30	**Lunch**					
13.30–15.00	**Session 4A: Human population genetics I**			**Session 4B: Health and disease I**		
	HG-001	Cosimo Posth	Comparing demographic and cultural histories of Brazilian Sambaqui societies	HD1-001	Iseult Jackson	Contrasting evolutionary and adaptive histories revealed for three oral pathobionts recovered from Bronze Age Irish remains
	HG-002	Yusuf Can Özdemir	Genetic history of the Altai Population 4th–14th centuries	HD1-002	Kay Prüfer	Down syndrome in ancient societies
	HG-003	Mehmet Somel	In the pursuit of CNVs in palaeogenomes	HD1-003	Kerttu Majander	High-coverage genomic data of ancient treponemal bacteria allow multifaceted analyses on the evolution and adaptations of Treponema pallidum
	HG-004	Luciana G. Simões	Northwest African Neolithic ignited by migrants from Iberia and Levant	HD1-004	Richard Ågren	Recent increase in allele frequency of the common norovirus-protective FUT2 variant
	HG-005	Javier G. Serrano	The peopling of the Canary Islands	HD1-005	Gunnar Neumann	The evolutionary path of the Salmonella enterica Para C lineage
15.00–15.30	**Coffee break**					

Thursday, 14th September

15.30–17.00	**Session 5A: Ancient foodways II**			**Session 5B: Community, sustainability & environment II**		
	AF2-001	Aleksandra Laura Pach	Palaeodietary reconstruction from chewed birch pitch using shotgun metagenomics	CE2-001	Camilla Speller	Mapping long-term changes in the biodiversity of Pacific Herring
	AF2-002	Joannes Dekker	Recovering proteins from foodcrust, biased from the start	CE2-002	Elisabetta Cilli	Historical ecology and species diversity of Mediterranean marine apex predators
	AF2-003	Eleftheria Orfanou	Biomolecular and macro-botanical evidence sheds light on millet consumption in Late Bronze Age Central Germany	CE2-003	Anne Marie Høier Eriksen	Exploring Degradation of Arctic Heritage through metagenomics
	AF2-004	Lindsey Paskulin	Proteomic Insights to Foodways among the Moche of North Coastal Peru	CE2-004	Yvan Moënne-Loccoz	Metabarcoding and metagenomic assessment of microbial stains on the walls of Paleolithic Lascaux Cave
	AF2-005	Rachèl Spros	The make-up of skeletons to make-up a city	CE2-005	Lennart Schreiber	Deciphering climate change impacts on Arctic marine mammals using sedimentary ancient DNA
17.00–17.30	**Flash talks II**					
	AFP-006	Ester Oras	Farmers hunt: multi-proxy analysis reveals complex subsistence systems at the dawn of early farming in the NE Baltic			
	METP-030	Lei Huang	Exploring allele frequency dependencies of F4-statistics for investigating fine-scale population structure			
	CEP-002	Christina M. Carolus	How the Steppe was Sown: Transcontinental Origins and Local Innovations at Mongolia's Earliest Sites of Indigenous Agriculture (c. 250 BC–150 AD)			
	METP-022	Matthew Williams	The Limits of Ancient DNA Analysis in Resolving Recent Human Genetic History			
	CEP-004	Elisabetta Cilli	Using ancient genomes to investigate responses to climate and anthropogenic impacts in the Atlantic bluefin tuna			
	HDP-018	Daniel Kolbe	Current allele distribution of the human longevity gene APOE in Europe can mainly be explained by ancient admixture			
	FAUP-008	Magdalena Krajcarz	Advances in single amino acid nitrogen isotopic analysis of carnivore trophic position			
	KSSP-004	Ruairidh Macleod	Palaeogenomics of Stone Age Hunter-Gatherers at Lake Baikal			
	METP-010	Yun Chiang	Going de novo? The suitability of de novo sequencing for ancient proteins			
	NOVP-020	Niall Cooke	Complex analyses of ancient soil samples from burial context			
	PLEP-002	Diyendo Massilani	The high-coverage genome of a male Neandertal			
	METP-032	Francesco Montinaro	Assessing ancestry through Principal component analysis			
17.30–18.30	**Poster session II**					
18:30–19:30	**Break / Guided tours at the Estonian National Museum (optional)**					
19.30–23.00	**Dinner at the University of Tartu Museum**					

Friday, 15th September

9.00–10.00	**Keynote:** Carl Heron (Feat. Moderators Ian Barnes & Oliver Craig) – Biomolecular archaeology and museums: History, curation and engagement					
10.00–10.30	**Coffee break**					
10.30–12.00	**Session 6A: Diet & environment**			**Session 6B: Pleistocene**		
	DEN-001	Carlo Cocozza	Detection of protein malnutrition using amino acid isotopic tracers	PLE-001	Alba Bossoms Mesa	Fine-scale genetic history of North-Western European Late Neandertals
	DEN-002	Izzy Davis	Towards a more sensitive method for detecting freshwater resource use in archaeological pottery	PLE-002	William Marsh	Using ancient biomolecules to reveal the social structure and behaviours of the Upper Palaeolithic Magdalenian at Gough's Cave, UK
	DEN-003	Dorothée Drucker	New determination of C, N, O and S stable isotopes Trophic Enrichment Factors in bone collagen and apatite of carnivorous mammals from Białowieża Forest (Poland)	PLE-003	Marco Rosario Capodiferro	Geographical and Chronological patterns of archaic introgression in ancient Human genomes
	DEN-004	Cynthianne Spiteri	The potential of Sequential Thermal Desorption/Pyrolysis-Gas Chromatography-Mass Spectrometry in the analysis of human dental calculus: a case study from the Bronze Age Aegean	PLE-004	Dorothea Mylopotamitaki	Proteomic and mtDNA species identification of archaeological bone remains in cave Ilsenhöhle Ranis (Germany).
	DEN-005	Willemien de Kock	Bioarchaeological record reveals millenia-long use of North African seagrass meadows by endangered green turtles	PLE-005	Arev Pelin Sümer	High coverage genomes of two of the earliest Homo sapiens in central Europe
12.00–13.30	**Lunch**					
13.30–15.00	**Session 7A: Health and disease II**			**Session 7B: Origins, dating & authentification**		
	HD2-001	Arthur Kocher	An ancestral recombination graph for the hepatitis B virus	ODA-001	Marc Dickinson	Advances in amino acid dating of mammalian tooth enamel: testing for endogeneity, and the effects of taxonomy and taphonomic alteration
	HD2-002	Christina Wurst	Atherosclerotic cardiovascular disease in mummies - A polygenic risk score based on a genetic enrichment approach	ODA-002	John Meadows	The collagen, the whole collagen, and nothing but the collagen: testing alternative extraction protocols for dating large numbers of poorly preserved mid-Holocene bones at Vráble, Slovakia
	HD2-003	Bárbara Sousa da Mota	Investigating the ecological suicide ("ecocide") theory in Rapa Nui with ancient DNA data	ODA-003	Davide Bozzi	Towards predicting the geographical origin of ancient samples with metagenomic data
	HD2-004	Cindy Gilda Santander	Optimising sampling and analysis strategies for detecting epidemic-driven selection: a simulation-based tool.	ODA-004	Victor Yan Kin Lee	An Algorithm for Optimally Partitioning Spatiotemporal Archaeological and Genetic Data

Friday, 15th September

	HD2-005	Aurélie Manin	Ancient chicken remains reveal the origins of virulence in Marek's disease virus	ODA-005	Lisa Briggs	DNA from ancient shipwrecks: where it comes from and why it matters
15.00–15.30	**Coffee break**					
15.30–17.00	**Session 8A: Human population genetics II**			**Session 8B: Novel Approaches**		
	HG2-001	Xavier Roca-Rada	Living on the edge: 5,000 years of human occupation of Portugal	NOV-001	Eleanor Green	Community signatures of past human lifestyles are preserved within faecal concretions
	HG2-002	Michal Feldman	Post-Lapita human genomes provide insights on 2,000-years of genetic history in Fiji	NOV-002	Rowan McLaughlin	New spatiotemporal tools for the meta-analysis of stable isotope measurements from organic tissue
	HG2-003	Harald Ringbauer	Inferring IBD segments in ancient DNA - What next?	NOV-003	Maria Codlin	Palaeoproteomic approaches for identifying avian remains from archaeological sites: current potential and future possibilities
	HG2-004	Kelly Blevins	A test of pretreatment and DNA extraction methods for uncovering endogenous content in Neolithic human remains from the Near East	NOV-004	Zandra Fagernäs	Cleaning the Dead: Decontamination of skeletal elements for palaeoproteomics
	HG2-005	Nada Salem	Genomes from Pastoral Neolithic Sahara reveal ancestral north African lineage	NOV-005	Alexander Hübner	Reconstruction of Middle and Late Paleolithic metagenomes to access natural products
17.00–17.30	**Coffee break**					
17.30–18.00	**Invited talk:** Martin Petr – Charting ancient past through modern genomics					
18.00–18.30	**Closing of the conference**					
18.30–19.30	**Guided tours at the Estonian National Museum (optional)**					

Saturday, 16th September

9.00–… **Excursions (optional)**

Key contacts:

Organising committee: isba2023@ut.ee
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POSTER PROGRAMME

Posters will be placed across the entire accessible part of the Museum.
Posters will be on display throughout the conference in the order listed below (provided the presenter has provided them by the start of the conference) but presenters will only be available in the listes poster session.

Poster Code	Poster Session	Presenter	Abstract title
AFP-001	I	Anne-Julie Bilodeau	Understanding Early Pottery Uses and Social Interactions at two Late Archaic Shell Rings in the Southeastern United States through Organic Residue Analysis
AFP-002	II	Margherita Cantelli	Expanding our knowledge of prehistoric cooking technology through the chemical analysis of heat-altered stones
AFP-003	I	Shidong Chen	Multi-proxy Analysis of Starchy Plant Consumption: A case study of pottery food crusts from Late Iron Age settlement at Pada, NE Estonia
AFP-004	II	George Janzen	Archaeolipidomic investigation of dietary practices in treveri society: A comparison of two eras
AFP-005	I	Karine Taché	Northeast North American archaeology, lipid analysis, Late Woodland pottery, Iroquoian foodways
AFP-006	II	Ester Oras	Farmers hunt: multi-proxy analysis reveals complex subsistence systems at the dawn of early farming in the NE Baltic
CEP-001	I	Elsa Peters	Assessing Age-related Post-Mortem Metagenomic Diversity in Historical and Ancient samples
CEP-002	II	Christina M. Carolus	How the Steppe was Sown: Transcontinental Origins and Local Innovations at Mongolia's Earliest Sites of Indigenous Agriculture (c. 250 BC-150 AD)
CEP-003	I	Annabelle de Vries	Herbariomics: genetic diversity of Trochetiopsis (Malvaceae) through anthropogenic pressures
CEP-004	II	Elisabetta Cilli	Using ancient genomes to investigate responses to climate and anthropogenic impacts in the Atlantic bluefin tuna
CEP-006	II	Teri Hansford	SedaDNA analysis of Durrington Walls: a new class of Neolithic monument
CEP-007	I	Dawn Lewis	Sedimentary Ancient DNA across Australia
CEP-008	II	Caroline Orr	Reconstructing Microbial Communities Within Roman Turf Ramparts: A Proof-of-Concept Study
CEP-009	I	Yi Wang	A 14-thousand-year high resolution metagenomic exploration of Lake Constance
CEP-010	II	Maciej Krajcarz	Millennia-long human-wildlife co-existence recorded in mesocarnivoran isotopic signal
CEP-011	I	Robin Singleton	Paleogenomic Analysis of Archaeological Rockfish Diversity in the North Pacific: Insights into Past Human-Fish Interactions and Contemporary Ecological Challenges
CEP-012	II	Hope Loiselle	Insights Into the Ecology and Extinction of the Japanese Sea Lion Using Ancient DNA and Stable Isotope Analysis
CEP-013	I	Patricia Pecnerova	Diving into palaeogenomic analyses of shipwreck ivory

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Poster Code	Poster Session	Presenter	Abstract title
CEP-014	II	Robin Singleton	Animal management and sacrificial power: Using ancient genomics to study golden eagle (Aquila chrysaetos) sacrifice in Teotihuacán
CEP-015	I	Lydia Furness	The impacts of human exploitation on marine life: a comparative analysis of extant and extinct sirenians
CEP-016	II	Jakob Hansen	A comparative study of commercially available minimally invasive sampling protocols on Early Neolithic humeri analysed via palaeoproteomics
CEP-017	I	Céline Bon	beDNA: A project for systematic collection of archaeological human samples for palaeogenetics purposes
CEP-018	II	Louise Le Meillour	Towards more sustainability in palaeoproteomics? A digestion time comparison for cost and electricity reduction in ancient bones analyses
CEP-019	I	Alice Di Muro	Tracking the role of marine resources to food security and livelihoods in postcolonial southern Brazil through chemical analysis of pottery
CEP-020	II	Léa Drieu	Working with AROLD. What is the ARchaeological Organic residues Literature Database?
DENP-001	I	Donikë Sejdiu	Herbarium DNA confirms 20th-century presence in Europe of Phytophthora lineage that caused Irish Potato Famine
DENP-002	II	Eva Chocholová	Palaeoproteomic and Genomic Analyses of Bronze Age Population from Unětice Culture, Moravia, Czech Republic
DENP-003	I	Meaghan Mackie	Exploring Dietary Change in Ireland through Proteomic and Lipid Analysis of Dental Calculus
DENP-004	II	Li Tang	Palaeoproteomic evidence reveals dairying supported prehistoric occupation of the highland Tibetan Plateau
DENP-006	II	Eléa Gutierrez	New biomolecular methods for exploring vitamin D status in the past and a case study from Nunalleq, Alaska
DENP-007	I	Kyungcheol Choy	Reconstructing Viking diets in Aarhus, Denmark with compound-specific isotopic analysis of amino acids
DENP-008	II	Gunilla Eriksson	Island life before violent death - multi-isotopic analysis of plants, animals and humans from Sandby borg, Öland (Sweden)
DENP-009	I	Elissavet Ganiatsou	Assessing the weaning process of ancient individuals using machine learning and Bayesian modeling on stable isotope data of dentinal collagen
DENP-010	II	Alessandra Morrone	The Baltic Kindergarten: a multifaceted study of infant health and feeding practices in medieval and early modern Estonia through stable isotope analysis
DENP-012	II	Alejandro Serna	The function of the early Patagonian hunter-gatherer pottery (Argentina) explored through organic residue analysis
DENP-013	I	Kaur Kivirüüt	Metabolic adaptations reflect increased dependence on an aquatic diet in the Neolithic transition of Eastern Europe

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DENP-014	II	Kadir Toykan Özdoğan	Exploring consumption patterns during Roman period in Harelbeke, Belgium via sedaDNA analysis
DENP-015	I	Emrah Kırdök	Identification of oral pathogens and dietary components from three chewed pitch pieces from Huseby Klev
DOMP-001	I	Louis L'Hote	Tracking ancient livestock pathogens across the domestication process.
DOMP-003	I	Laura Botigué	Genomic analysis of ancient emmer wheat sheds light into the evolution of the first domestics
DOMP-004	II	Natalia Przelomska	Molecular clocks and archaeogenomics of a Late Period Egyptian date palm leaf reveal introgression from wild relatives and highlight the role of Economic Botany Collections
DOMP-005	I	Shuya Zhang	Archaeogenomics of maize evolution in the South American Andes
DOMP-006	II	Aurélie Manin	Diving into the genomic make-up of turkey (Meleagris gallopavo) domestication
DOMP-007	I	Laura Viñas Caron	The genetic history of sheep in the Iberian Peninsula over the last thousand years
DOMP-008	II	Markus Fjellström	Reconstructing reindeer grazing and mobility patterns in northern Fennoscandia – multi-isotope analyses of reindeer bones from the Piteå and Skellefteå River valleys in northern Sweden
DOMP-009	I	Colin Smith	Evidence for differences in amino acid carbon isotope values of domestic and wild fauna, but how do we explain them?
DOMP-010	II	Stephanie Dolenz	Home is where the herd is: Detection and analysis of domesticated mammals in houses from Bronze Age Slovakia through sedaDNA
DOMP-012	II	Danijela Popović	Tracing the early spread of domestic cat in Central Europe: Human-mediated dispersal or natural introgression?
DOMP-013	I	Eve Rannamäe	Genetic analysis of ancient and contemporary sheep in Estonia
DOMP-014	II	Valentina Rovelli	Paleogenetic analysis of cat mummies from ancient Egypt
DOMP-015	I	Aurélie Manin	Pig colonisation in the Pacific: A population genomic study
DOMP-016	II	Cristina Valdiosera	The Impact of Human Actions and Wild Introgression in the History of Domestic Cattle on the Iberian Peninsula
DOMP-017	I	Noémi Borbély	Genetic analysis of Late Copper Age to Bronze Age horses from the Carpathian Basin
DOMP-020	II	Deborah Diquelou	Ancient cattle genomics: domestication and the impact of Bronze Age migrations
DOMP-021	I	Jolijn Erven	Multi-proxy research shines light on the transition to animal husbandry in the Dutch wetlands
DOMP-022	II	Aine Halpin	Investigating the impact of human Steppe migrations on Neolithic and Bronze Age sheep populations

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FAUP-001	I	Marica Baldoni	Identification and characterization of Erysipelothrix rhusiopathiae in ancient cats remains
FAUP-002	II	Anne Kathrine Runge	Investigating prehistoric zoonotic disease reservoirs
FAUP-003	I	Amanda Gutiérrez Carbajal	Enamel proteome of Pleistocene Cave Bears from Sierra de Atapuerca Sites
FAUP-004	II	Florian Harking	De novo LC-MS/MS proteomics enables Elephantidae speciation using sequence variants in ivory proteins
FAUP-005	I	Johanna Krueger	Ancient proteins from Iberian equids in the light of ancient DNA
FAUP-006	II	Ryan Paterson	An Early Miocene enamel proteome of an early-diverging rhinocerotid from Canada’s High Arctic and a biomolecular phylogeny of Rhinocerotidae
FAUP-007	I	Arianna Weingarten	Horse mitochondrial genomes from the Middle Pleistocene open-air site of Schöningen
FAUP-008	II	Magdalena Krajcarz	Advances in single amino acid nitrogen isotopic analysis of carnivore trophic position
FAUP-009	I	Jan Laine	Ancient stickleback environmental genomes track adaptation across ecological transitions
FAUP-010	II	Edana Lord	Reconstructing collared lemming phylogenetic history using ancient and modern genomes
FAUP-012	II	Erika Rosengren	Systematic ancient DNA-based species identification of archaeological remains of large bovines (Bos primigenius and Bison bonasus)
FAUP-014	II	Maria Zicos	First insights into the population genomics of the extinct Darwin’s ground sloth (Mylodon darwinii) from Cueva del Milodón, Chile.
FAUP-015	I	Mateusz Baca	Ancient DNA clarifies the evolution of the field vole species complex
FAUP-016	II	Deon de Jager	Palaeogenomes of a lost world: Ancient bovids of the submerged Palaeo-Agulhas Plain of southern Africa
FAUP-017	I	Isabelle Feinauer	Tracking temporal changes in mitochondrial diversity in Scandinavian brown bears
FAUP-018	II	Alexandre Gilardet	Impact of Late and Middle Pleistocene climate change on the evolutionary genomics of megafauna at Denisova Cave
HDP-001	I	Emily Gaul	A Metagenomic Overview of The Lazzaretto Vecchio, Plague Hospital of Venice
HDP-002	II	Sarah Johnson	Oral metagenomes from ancestral Native American individuals highlight impact of European colonialism on bacterial strain diversity
HDP-003	I	Sterling Wright	Response of the ancient oral microbiome to urbanization in the Black Sea region

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HDP-004	II	Yoko Uchida-Fukuhara	Reconstruction of the oral environment of ancient Okhotsk people using palaeoproteomic analysis of dental calculus.
HDP-005	I	Biancamaria Bonucci	Metagenomics analysis of ancient dental calculus provide an insight into oral microbial ecology in an Anglo-Saxon population
HDP-006	II	Maria Lopopolo	Characterising the oral microbial make-up of Pre-Colonial human populations of the Southern Cone of the Americas
HDP-007	I	Nora Bergfeldt	Microbiomes and pathogens in Neolithic Scandinavia
HDP-009	I	Alina N. Hiss	A detailed analysis of Hepatitis B virus strains and implications for their transmission in early Medieval Eastern Central Europe
HDP-010	II	Hsiao-Lei Liu	Avian influenza viruses in formalin-fixed, ethanol-preserved historic North American bird specimens
HDP-011	I	Ian Light	Molecular evolution of Y. pestis using ancient and modern genomes
HDP-013	I	Zoé Pochon	Infectious diseases in the Late Viking Age town of Sigtuna
HDP-014	II	Shreya Ramachandran	Characterizing the cariogenic bacterium Streptococcus mutans in ancient Chile
HDP-016	II	Pooja Swali	Prehistoric Borrelia genomes provide insights into the evolutionary history of louse-borne relapsing fever
HDP-017	I	Kateřina Novotná	Complex analyses of ancient soil samples from burial context
HDP-018	II	Daniel Kolbe	Current allele distribution of the human longevity gene APOE in Europe can mainly be explained by ancient admixture
HGP-002	II	Eveline Altena	Community formation in the early medieval Netherlands; an integrated bioarchaeological case study in Nijmegen
HGP-003	I	Motahareh Amjadi	Genomic analyses of Seleucid and Parthian period population in North Iran
HGP-004	II	Ana Arzelier	Ancient DNA shed light on the funerary practices of a Late Neolithic collective burial in Southern France
HGP-005	I	Owyn Beneker	Genetic history and health in Medieval Europe with the Belgian town of Sint Truiden as a model
HGP-006	II	Emily M Breslin	The genomics of an Iron Age site in Fermo, Marche.
HGP-007	I	Selina Carlhoff	Investigating the occupation history and social structure at an early colonial site in Taiwan through archaeology, archaeothanatology, and archaeogenetics
HGP-008	II	Pablo Carrion	Disparate demographic impacts of the Roman and Visigothic presence in the Iberian Peninsula
HGP-009	I	Lorenza Coppola Bove	An archaeogenetic and paleopathological approach to reconstructing life in Early Medieval Iberia at La Olmeda (Spain, 6th – 11th c. CE)

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HGP-010	II	Nicolas Antonio da Silva	Exploring changes in immuno- and population-genetics in West Germany's Neolithic communities
HGP-012	II	Ábel Fóthi	An admixture of people conquered the Carpathian basin in the 10th century
HGP-014	II	Michał Golubiński	Y-chromosome analysis of Bronze Age populations from the territory of present-day Poland
HGP-016	II	Mogge Hajiesmaeil	A comprehensive picture of the genetic history of Iran
HGP-017	I	Kadri Irdt	Ancient birch tar as new source material for studying the human past in the Baltics
HGP-018	II	Dilek Koptekin	Human mobility patterns during the Holocene
HGP-019	I	Kim-Louise Krettek	Genetic Insights into the Demographic History of Colombia
HGP-020	II	Laura Lacher	Tracing ancestral shifts and migration patterns during the trasition from late antiquity to early middle ages - an archaeogenetic study on the Rhineland-
HGP-021	I	Martyna Molak	The crossroad of Europe. Ancient genomes from Poland tell the story of where the West meets the East
HGP-022	II	Aurore Monnereau	Genetic discontinuity in a Medieval Sicilian community
HGP-023	I	Alexandra Mussauer	Genetic study of ancient Egyptian human remains dating from the Predynastic Period to the early Islamic Period (ca. 4000 cal. BCE - 800 cal. CE)
HGP-024	II	Linda Ongaro	Investigating population structure and patterns of natural selection in Neolithic Europeans
HGP-025	I	Sanni Peltola	The Noaidi of Giggajávri (Fi. Kitka) - Life history of a Sámi shaman found in Kuusamo, Finland
HGP-026	II	Alise Pokšāne	Preliminary aDNA analysis of Viking Age collective grave in the Čunkāni – Dreņģeri cemetery from Latvia
HGP-027	I	Mélanie Pruvost	The Genetic Legacy of Ancient Gaul: Insights into Social Organization and Human Mobility during the Roman Empire
HGP-029	I	Francesco Ravasini	The Picenes and the Genetic Landscape of Central Adriatic Italy in the Iron Age.
HGP-030	II	Flavia Risi	Echoes from the last Green Sahara: a ghost population of cattle herders unveiled from joint whole modern genome analysis of Sahelian Fulani and ancient African individuals.
HGP-031	I	Xavier Roca-Rada	The genetic history of pre-Columbian Mesoamerica
HGP-033	I	Elina Salmela	The skull of a saint? A genetic analysis of the purported skeletal remains of Bishop Henry from the Cathedral of Turku, Finland

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HGP-034	II	Stefania Sasso	Ancient DNA perspective on the origins and structure of a Merovingian population in Belgium
HGP-035	I	Juliette Sauvage	When cultural insight of admixture does not match the genome ancestry: the case of the Cerny culture (Middle Neolithic, Northern France)
HGP-036	II	Oszkár Schütz	Preliminary genetic results about Sarmatians from the Carpathian Basin
HGP-037	I	Eleni Seferidou	Genetic research into pre-colonial Trinidad
HGP-038	II	Marina Silva	Genomic and isotopic evidence for a Sarmatian individual in Roman Britain
HGP-039	I	Kendra Sirak	Ancient Soqotri genomes over 1,000 years document a small, consanguineous, and genetically homogenous population with deep connections to the Arabian Peninsula
HGP-040	II	Angelos Souleles	Urbanization from a demographic and population history perspective in Thessaloniki between 300 BC and 1500 AD
HGP-041	I	Bea Szeifert	Analysis of genetic connections between the medieval communities of the Dniester Valley and the Carpathian Basin
HGP-042	II	Brina Zagorc	Integrating Multidisciplinary Methods to Investigate the Lives of Nonadults in Early Medieval Sites from North Eastern Croatia
HGP-043	I	Denisa Zlámalová	Archaeogenetic analysis of burials associated with Early Slavic state of Moravia, Czechia
HGP-044	II	Daniel Tabin	Mixed Turkic and Mongolic ancestry reveals complex history and origin of the Tu and other Chinese populations
HGP-045	I	Luca Traverso	East of the wall: aDNA in the Tisza region through the first phases of the Migration Period
HGP-046	II	Eugenia D'Atanasio	The dawn of Middle Age: a comprehensive archeogenetic analysis of the late antiquity site of Forum Sempronii in Central Italy.
HGP-047	I	Orhan Efe Yavuz	The Genetic Legacy of the Roman Imperial Rule in northern Italy
HGP-048	II	Nathalie Suarez Gonzalez	Paleo-Pathological Studies at Pachacamac, Peru: Challenges and Preliminary Results
KSSP-001	I	Perle Guarino-Vignon	Genome-wide analysis of a collective grave from Mentesh Tepe provides insight into the population structure of early neolithic population in the South Caucasus
KSSP-002	II	Xiaowen Jia	Archaeogenomic research of Kamenice, a prehistoric Albanian tumulus (1600-500 BCE)
KSSP-003	I	Juhyeon Lee	Genetic population structure of the Xiongnu Empire at imperial and local scales
KSSP-004	II	Ruairidh Macleod	Palaeogenomics of Stone Age Hunter-Gatherers at Lake Baikal

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KSSP-005	I	Iñigo Olalde	Demographic change and social interactions during the Early Islamic period in Northern Iberia: the case of the Plaza del Castillo Necropolis
KSSP-007	I	Sabine Reinhold	Two sides of kinship structure in Bronze Age burial mounds of the North Caucasian Bronze Age
METP-001	I	Jasmin Frangenberg	Assessing antimicrobial peptides, resistance genes, and functional gene clusters in ancient microbial DNA
METP-002	II	Guillermo Rangel-Pineros	µBiocodicology: studying ancient animal skin microbiomes through the analysis of historical parchment documents
METP-003	I	Yuejiao Huang	Benchmarking tools for the detection, reconstruction and phylogenetic analysis of ancient viral genomes
METP-004	II	Megan Michel	Leveraging High-Throughput Metagenomic Screening for the Identification of Human Parasitic Protozoa
METP-005	I	Jonas Niemann	Parasites lost: Parasite detection in ancient and modern metagenomic datasets
METP-006	II	Teresa Zeibig	Optimization of host and pathogen DNA recovery from archived tuberculosis wet tissue specimens
METP-007	I	Ragnheiður Diljá Ásmundsdóttir	The skeletal proteome: mapping proteome variation between cortical and trabecular bone
METP-008	II	Charllotte Blacka	Amelogenin sex determination: Developing mass spectrometric methods for rapid enamel-based palaeoproteomic sexing
METP-010	II	Yun Chiang	Going de novo? The suitability of de novo sequencing for ancient proteins
METP-011	I	Miranda Evans	Proteomic characterisation of the impact of cooking and burial on experimental food crusts and ceramics
METP-012	II	Claire Koenig	Fast and quantitative mass spectrometric assay for biological sex determination from dental enamel.
METP-013	I	Paula Kotli	A monk or a nun? The story of a partial dental element from an ascetic in-chain buried in a Christian Women's cemetery in Jerusalem area during Byzantine time
METP-014	II	Marlisa Mazzola	Potential of ancient proteins analysis of sheep and goats' bones to shed light on past human economy during the Italian Bronze Age
METP-015	I	Fazeelah Munir	Assessment of intra-crystalline enamel amino acid and proteins to understand enamel closed system model
METP-016	II	Fallen K.Y. Teoh	Comparison of magnetic beads (SP3), glass beads (SP4) and suspension trapping (S-trap) approaches for proteomics studies of ancient human dental calculus.
METP-017	I	Sierra Blunt	Ancient metagenomics and synchrotron microtomography of ancient dental calculus - an interdisciplinary approach to studying health and diet in archaeological populations

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METP-018	II	Helen Fewlass	Non-destructive screening of protein preservation in ancient bone
METP-019	I	Femke Reidsma	Fundamental Fire: laboratory-based chemical research into the effect of diagenesis on heated bone and its implications for the study of fire proxies and other biomolecules in the deep past.
METP-020	II	Alba Refoyo Martinez	Best practices for Neanderthal segment detection in time-series data using tree-sequence-based ancestry tracking
METP-021	I	Jiaqi Yang	New methods to detect archaic introgression in early modern human genomes with low-coverage data
METP-022	II	Matthew Williams	The Limits of Ancient DNA Analysis in Resolving Recent Human Genetic History
METP-023	I	Adrià Breu Barcons	Caution! Contents were hot: experiments exploring the suitability of novel high-temperature lipid biomarkers detected in Mediterranean neolithic pottery
METP-024	II	Jonica Ella Doliente	Increasing the sensitivity of cereal detection in pottery using LC-Q-Orbitrap MS
METP-025	I	Michael Campana	How do we construct a phylogeny when more than half the species are extinct? — A case study using the Hawaiian Honeycreepers
METP-026	II	Gülşah Merve Kılınç	Evaluation of genotype imputation of ancient human genomes from West Eurasia
METP-027	I	Roberta Davidson	Assessing the Daicel Arbor Biosciences Prime Plus enrichment bias: implications for the future of accessible ancient DNA research
METP-028	II	Marianne Dehasque	Duplicates, duplicates: Reducing ancient DNA sequencing cost by avoiding jumping DNA molecules
METP-029	I	Pavel Flegontov	Typical qpAdm protocols are not robust to false detection of genetic admixture
METP-030	II	Lei Huang	Exploring allele frequency dependencies of F4-statistics for investigating fine-scale population structure
METP-031	I	Maël Lefeuvre	A standardized comparative analysis of ancient DNA kinship estimation methods, using "BADGER" (Benchmark Ancient DNA GEnetic Relatedness): a high-fidelity ancient DNA pedigree simulations pipeline.
METP-032	II	Francesco Montinaro	Assessing ancestry through Principal component analysis
METP-033	I	Samuel Neuenschwander	Mapache: a flexible pipeline to map ancient DNA
METP-034	II	Joshua Rubin	HaploCart: Human mtDNA Haplogroup Classification Using a Pangenomic Reference Graph
METP-035	I	Clemens Schmid	Poseidon – Powerful and FAIR archaeogenetic genotype data management

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METP-036	II	Nicoletta Zedda	New data on Twist Bioscience's target enrichment efficiency on poorly preserved aDNA samples
METP-037	I	Nihan D. Dagtas	A comparison of DNA extraction methods to develop a rapid, on-site test for sedimentary ancient DNA
METP-038	II	Pere Gelabert	New methods for the discrimination and recovery of faunal taxa from sedaDNA libraries based on the study of Paleolithitic Sediments from El Mirón Cave, Spain.
METP-039	I	Louis Kraft	Benchmarking tools for ancient metagenome assembly - Current state and challenges
METP-040	II	Victoria Oberreiter	A new method of extract-pooling for sediment ancient DNA analyses
METP-041	I	Lucas Anchieri	Assessing ancient DNA sampling strategies for natural selection inference with time-series data
METP-043	I	Mikołaj Danielewski	Tracing changes in the human genome left by the process of adaptation
METP-044	II	Matthew Collins	A systematic review of database research engines using a controlled, degraded single protein
METP-045	I	Susanna Sawyer	Improved methylation detection in ancient DNA
METP-046	II	Ciarán O'Connor	Ancient Epigenomics of Cattle and Aurochs
NOVP-001	I	Maxime Borry	Reconstructing ancient microbial genomes from the wine ferments of the Roman biblical king Herod
NOVP-002	II	Remi Denise	Diversity of bacteriophages in the ancient human microbiome
NOVP-003	I	Abigail Gancz	Investigating the Ancient Oral Microbiome as a Marker of Frailty in Middle Eastern Populations Over Time
NOVP-005	I	Nikolay Oskolkov	aMeta:an accurate and memory-efficient ancient Metagenomic profiling workflow
NOVP-006	II	Piotr Rozwalak	Bacteriophages in ancient human gut metagenomes
NOVP-007	I	Anna White	Biomolecular perspectives on the uses of birch bark tar in prehistoric Europe
NOVP-008	II	Vincent Geyer	Exploring the temporal limits of RNA preservation in historical and ancient biological material
NOVP-009	I	Jessica Hendy	Ancient protein analysis of a Roman sealed jar: an intriguing palaeoproteomic case study
NOVP-010	II	Ioannis Patramanis	Using simulations to assess the power and limits of evolutionary inference based on ancient protein sequences.
NOVP-011	I	Liam T. Lanigan	Multi-omic analyses of palaeofaeces from Viking Age Ribe, Denmark
NOVP-012	II	Keith Thomas	Out of the Bottle: Bioarchaeology of recovered beverages.

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NOVP-013	I	Rachel Winter	Collagen sequencing and peptide mass fingerprinting for the marine historical ecology of groupers (Epinephelidae) in the eastern Mediterranean.
NOVP-014	II	Fei Yang	The impact of taphonomy on post-translational modifications on the Middle Palaeolithic assemblages of Hohle Fels: a combined ZooMS and zooarchaeological study
NOVP-015	I	Tziona Ben-Gedalya	A Complex Blend of West and East: An Organic Residue Analysis Study of Wine Manufacturing in Judea of the Early Roman Period
NOVP-017	I	Isabel Wiltshire	Using a multi-pronged approach to the analysis of absorbed lipid residues to investigate chronological trends in pottery use from the Neolithic to the Iron Age in Saxony
NOVP-018	II	Judith Ballesteros	Genomic exploration of private American diversity and its effect on ancient DNA analysis
NOVP-019	I	Alice Cao	An experimental approach: Exploring DNA preservation on archaeological ground stones
NOVP-020	II	Niall Cooke	Complex analyses of ancient soil samples from burial context
NOVP-021	I	Toni de Dios	Potential use of bone-adhered soil as a novel source of host and environmental ancient DNA
NOVP-022	II	Rikai Sawafuji	Ancient human DNA from archaeological sediments: insights from sediments surrounding human bones and in settlements
NOVP-023	I	Kelsey Moreland	Ancient DNA from the Upper Paleolithic Mammoth Ivory of Hohle Fels, Germany
NOVP-024	II	Aleksandra Laura Pach	A Comparative Study of Taxonomic Assignment Methods for Palaeodietary Reconstruction using Shotgun Metagenomics
NOVP-027	I	Gillian Taylor	Biochemical Preservation of Roman Leather Shoes
NOVP-028	II	Selina Brace	Large-scale quantification of the DNA preservation in insects from natural history collections
ODAP-001	I	Martina Farese	Exploring class and time influence on the oral microbiome through ancient DNA analysis of Classical and post-Classical Italian populations
ODAP-002	II	Ingrid Bertin	Proteomic analyses applied to consolidated prehistoric wooden artifacts: how to overcome perturbations by polyethylene glycol and acrylic resin ?
ODAP-004	II	Sarah Sandron	Combining biomolecular, osteological analysis and historical research for the characterization of a post-medieval monastic community in northern Italy
ODAP-005	I	Alessia Monticone	Biomolecular archaeology as a tool for reconstructing site biographies: the case of the 1980s rescue excavations at Chiomonte-La Maddalena, Western Alps

POSTER PROGRAMME

Posters will be placed across the entire accessible part of the Museum.
Posters will be on display throughout the conference in the order listed below (provided the presenter has provided them by the start of the conference) but presenters will only be available in the listes poster session.

Poster Code	Poster Session	Presenter	Abstract title
ODAP-006	II	Anne-Mai Ilumäe	Human and language migration to the shores of the Gulf of Finland during the Iron Age - Finnic languages, tarand burial culture and climate anomalies.
ODAP-007	I	Jack Sharpen	Assessing Biomolecular Degradation using a multi-omic approach
ODAP-008	II	Carlo Cocozza	A Bayesian high-resolution osteo-biography of an unknown individual found in a Roman camp in Brno, Czech Republic
PLEP-001	I	Palesa Madupe	Paranthropus robustus first dental enamel proteome
PLEP-002	II	Diyendo Massilani	The high-coverage genome of a male Neandertal
PLEP-003	I	Elena Zavala	New genetic and chronological data from the oldest Upper Paleolithic Burial in Poland
PLEP-004	II	He Yu	Palaeogenomics of European hunter-gatherers across the LGM: insights from the Italian peninsula

Abstracts
Keynote Speakers
&
Invited Speakers

KEYNOTE LECTURE 1

PROF. ANNE STONE
Arizona State University, USA

Ancient DNA research since the first ISBA conference

Abstract:

Since the first ISBA meeting in 2013, ancient DNA research has flourished, benefitting from new and/or improved laboratory protocols, sequencing technologies, and bioinformatic analyses. These have resulted in a flood of studies not only about the evolutionary history of humans and other animals, but also about ecological (and microbiome) communities and pathogens. Over the past ten years, ancient DNA research has extended our knowledge back further in time, even past previous estimates of DNA preservation, to reveal insights into past ecosystems and mammoth evolutionary history. While these discoveries were from cold environments, warmer environments have also yielded ancient DNA data, including from sites in Africa, the Caribbean and Polynesia. The avalanche of ancient DNA data also includes many studies of archaic humans that illuminate their interactions with modern humans and with each other. Analyses of modern human population history, particularly in western Eurasia has become increasingly fine-grained, improving our understanding of migrations and adaptations as well as social structure. Ancient DNA research has also provided insight into the process and spread of human domesticates both plant and animal. Ancient microbial DNA analyses have shown how pathogens affected us and our domesticates, as well as how the structure of microbial communities in our microbiomes has changed over time. In this presentation, I will review the highlights of the last ten years as well as attempt to predict the future of the field.

Feat.
Moderators
Ian Barnes
Oliver Craig

KEYNOTE LECTURE 2

DR. CARL HERON

The British Museum, UK

Biomolecular archaeology and museums: History, curation and engagement

Abstract:

From newsletters to Nobel Prizes and, in terms of ISBA symposia, from Amsterdam to Tartu, biomolecular archaeology has reached a prominent position in the study of the human past. Research activities span significant themes, including evolution, migration, status, gender, diet, disease, climate and technology. Many of the findings continue to attract interest and spark debate in scholarly contexts and in wider public arenas.

The first page or two of ‘Neanderthal Man: In search of lost genomes’ (Pääbo 2014) underlines the role, importance and challenges of museum collections citing ‘a small piece of a Neanderthal arm bone held at the Rheinisches Landesmuseum Bonn’, ‘permission to remove a small section’ and ‘(p)erhaps someone had used glue produced from cow hide to treat the bones at some point.’

The rapid pace of methodological development, including sample throughput, and application breadth presents challenges for museums and archives in balancing information gained through research with the care of the collection. Nevertheless, the opportunities are immense and the benefits can work both ways. Biomolecular research can help to disentangle the complex histories of Museum collections and help to create datasets that can translate into museum galleries and exhibitions. In this presentation, I highlight briefly some moments in the history and development of the field before turning to the relationships between biomolecular archaeology and museums in the broadest sense, from collections and curation, to access and sampling, and to galleries and exhibitions.

INVITED SPEAKER 1

Melanie Roffet Salque

University of Bristol, UK

Advancing the application of lipids in archaeological and palaeoenvironmental reconstruction

Abstract:

It was realised in the 1970s that archaeological pottery vessels preserve abundant biochemical residues of natural products, mainly derived from foods, absorbed within the porous fabric of vessel walls. The predominant compounds are hydrophobic lipids, e.g. fats and waxes, with their molecular and isotopic characteristics providing the basis for their use in wide-ranging archaeological investigations.

The last two decades have seen organic residue studies expand from single vessels to those involving tens, hundreds or even thousands vessels to provide insights at the site, regional and even continental levels. The diagnostic capacity of lipids is enhanced through their use with other archaeological proxies, especially zooarchaeological and palaeobotanical remains. Consequently, the scope of lipid residue analyses now goes far beyond pottery function to reveal subsistence practices, facilitate palaeoecological reconstruction, provide calendrical dates, while the H isotope signal of lipids holds potential as a novel precipitation-driven climate proxy. These new avenues of applications are underpinned by a number of technological advances in analytical methods and instrumentation.

The increasing robustness and value of lipids as a unique source of archaeological and palaeoenvironmental proxy information is benefitting from the capability to derive absolute dates at high precision and accuracy by accelerator mass spectrometry. This methodological breakthrough has opened and number of new avenues of investigation, including the effects of freshwater and marine 14C reservoirs on dates, and has paved the way for the dating of new classes of compounds present in archaeological and environmental matrices. Complementary to this, the opening of a new analytical window has been made possible through the use high-resolution mass spectrometry. The application of this state-of-the-art analytical method is currently allowing the detection of biomarkers at hitherto unattainable sensitivity and specificity, leading to new possibilities for investigating aquatic resource exploitation and plant use (millet and cereals) through pottery residues. Of vital importance in expanding the scale and scope of applications is the need to support archaeological interpretations based on molecular and isotopic proxy validation through extensive experimentation, feeding studies, database assembly and authentication of residues.

INVITED SPEAKER 2

Giedrė Motuzaitė Matuzevičiūtė

Vilnius University, Lithuania

A biomolecular approach to millet journey across time and space

Abstract:

The past dispersal of various crop species across the world drove an important set of transformations in human lifeways. Crop domesticates with different geographical origins, such as wheat and barley from southwest Asia or broomcorn millet and buckwheat from East Asia, compose a unique mosaic of culinary heritage which has undergone continuous transformation as new crops have joined our cuisines. However, we have a remarkably thin understanding of how new crops moved over time, were integrated as staple foods among past populations, and why certain crops were never accepted or later abandoned.

A multi-faceted investigation of a pioneering crop in Eurasian food globalization - broomcorn millet (Panicum miliaceum) - can help to answer many of these questions, as it stands out from all the other cereals due to its unique and traceable biochemical properties.

In my talk I will hypothesize that by applying biomolecular analyses to the unique biochemistry of millet in tandem with other novel methods, the distribution of millet consumers could be both geographically and chronologically traced with respect to human culture, culinary preferences, demographic categories of sex and age, social status, individual mobility history and palaeoclimates. This knowledge could lead not only to identifying the key mechanisms involved in the adoption, exploitation and eventual rejection of millet cultivation and consumption by past societies, but also to develop a better understanding of the patterns of agricultural dispersal as a whole – one of the most important transformations in human history.

INVITED SPEAKER 3

Benjamin Vernot

Max Planck Institute for Evolutionary Anthropology, Germany

Metagenomics Reveals the Past

Abstract:

Metagenomic studies in biomolecular archaeology have emerged as a powerful tool for understanding ancient environments, human history, and the interactions between humans and their microbial counterparts. By analyzing the genetic material extracted from archaeological samples, such as bones, teeth, and sediments, researchers can reconstruct the composition and functions of ancient communities, shedding light on the past. These communities may give insights into the environments in which humans and other animals were living, the microbes that lived on our bodies, or even pathogens or diseases which infected us.

Most metagenomic approaches in biomolecular archaeology involve high-throughput DNA sequencing technologies coupled with advanced bioinformatics tools. These tools typically compare the sequenced DNA to a set of reference genomes, and either place each read with a particular taxonomic group (species, genus, etc), or directly estimate the relative abundances of various taxonomic groups. In some cases, researchers recover sufficient DNA from single individuals or organisms, enabling a more detailed study of a subset of the whole community.

Here I will discuss the state-of-the-art of metagenomic studies in biomolecular archaeology, reviewing the latest work and summarizing the most commonly used methods. I will conclude by discussing new avenues in metagenomics, with a special focus on recent population genetics studies from environmental samples such as archaeological sediments.

INVITED SPEAKER 4

Beatrice Demarchi
University of Turin, Italy

Ancient proteins in archaeology

Abstract:

The survival of old proteins in the 'fossil' record is old news. In 1954 Abelson reported that amino acids, the building blocks of proteins, were found in biominerals millions of years old. This discovery came three years after the α-helix and β-sheet structures were proposed. It was immediately clear to scientists that proteins - ubiquitous, tissue-specific biomolecules, which preserve a phylogenetic signal encoded in their amino acid sequence from DNA - would be an excellent resource for studying the molecular evolution of extant and extinct organisms as well as the relationship between people and their environment. In the new millennium, mass spectrometry-based approaches have unlocked that potential and revealed that intact peptide sequences are able to resist the inexorable passing of time well beyond the limits of DNA.

The development of increasingly sophisticated methods for protein recovery, data generation and analysis is driving the present flourishing of the discipline. Applications are as varied as the sources of ancient proteins, and most studies have been characterised by an “exploratory mode” of enquiry: well-defined issues have been tackled by specific approaches - by varying extraction techniques, sample preparation, instrumentation, protein/proteome characterisation/quantification. As a result, palaeoproteomics has been providing important and sometimes unexpected insights into many aspects of evolution, ecology, paleontology, cultural heritage, and archaeology.

This talk will focus on the relationship between ancient protein studies and archaeology, highlighting key achievements in addressing issues related to minimal sample size, extent of protein degradation, data authentication, dissemination and interpretation within disciplinary or interdisciplinary disciplinary frameworks. While trying to envisage possible future directions for the discipline, I will explore how palaeoproteomics can fruitfully engage with the array of developments in archaeological thought over the last two decades.

INVITED SPEAKER 5

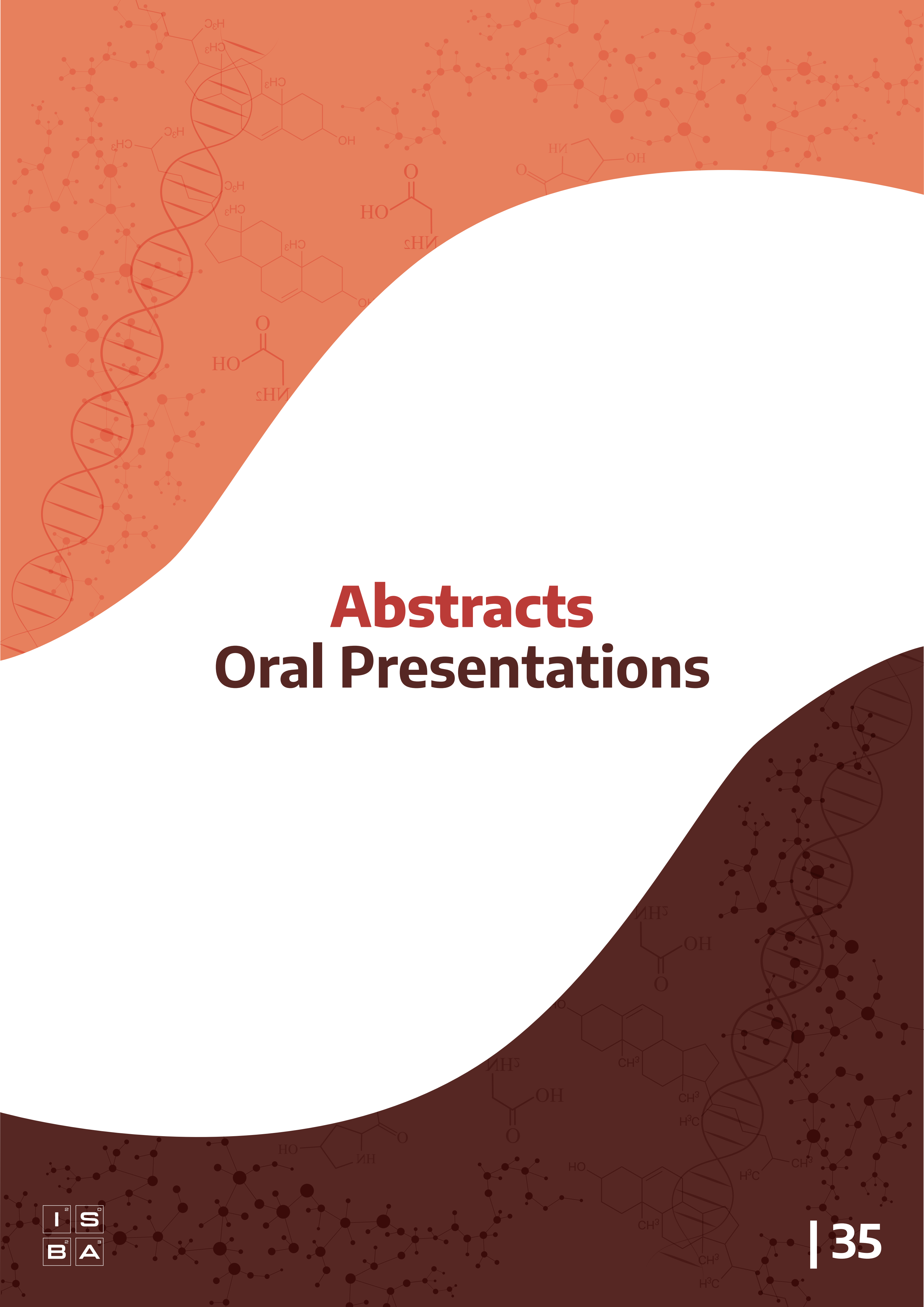
Martin Petr

University of Copenhagen, Denmark

Charting ancient past through modern genomics

Abstract:

Over the last decade, we have seen an astonishing rise in the number of published ancient genomes, resulting in an ever-increasing density of geographical and temporal sampling of sequenced genomes across the world. This has, on the one hand, allowed a detailed characterisation of dramatic, continental-scale migration events, as well as the identification of many examples of biological adaptation—processes which have both had a profound impact on the global distribution of genomic variation we observe today. On the other hand, the increased density of sampling has unlocked the possibility to study the residence patterns and kinship on a much more localised scale, sometimes down to the level of individual settlements and their social dynamics across just a few generations. Many of these exciting discoveries have been facilitated by several recent developments in bioinformatics and population genomics, such as imputation of ancient genomes, detection of identity-by-descent segments, and statistical modelling of geographical distribution of genetic variation in a spatially-explicit manner. In this talk I will highlight a few of these important developments and point to some of the most exciting avenues of ongoing and future research. In particular, I will discuss the possibilities of recent advances in the study of ancestral recombination graphs and tree sequences, the promise they hold for the reconstruction of complex historical spatio-temporal population dynamics carried by each genome, and the potential of integrating large-scale ancient genomic data with other sources of information about ecological and cultural processes across space and time.



Abstracts
Oral Presentations

ABSTRACT AF1-001

Widen the perspectives: expanding the range of identifiable content in African pottery

Speaker: **Léa Drieu**
Université Côte d'Azur, France; Cultures et Environnements Préhistoire, Antiquité, Moyen Âge, France

Co-authors: Martine Regert[1,2], Pauline Debels[3], Julien Vieugué[4], Anne Mayor[3]

[1] Université Côte d'Azur, France
[2] Cultures et Environnements Préhistoire, Antiquité, Moyen Âge, France
[3] University of Geneva, Swiss
[4] Technologie et Ethnologie des Mondes Préhistoriques, France

Abstract:

While organic residue analyses have become standard analyses for studying the economy and diet of ancient populations, it remains difficult to interpret data from African pottery. The molecular composition of many foods that can be consumed on the continent has been little studied, and the molecular signal that is likely to be absorbed and preserved in the ceramic walls has been barely investigated. Amongst typical African commodities, biomarkers have only been identified for palm kernel oil and cowpea. In this talk, we will present the results of the search for potential biomarkers of two fermented beverages still consumed in West Africa: palm wine and cashew wine. In order to document the molecular composition of these two types of fermented beverages, we used a methodology involving the analysis of both lipids and short-chain hydrophilic organic acids. Using ethnographic pottery collected during ethnoarchaeological work in southern Senegal, we studied the molecular composition of palm wine and cashew wine. We also investigated how these molecules are absorbed into the walls during the use of vessels for storing, serving and consuming fermented beverages. Control vessels, used to process and consume other foodstuffs, were analysed to verify the presence/absence of compounds of interest and to ensure the reliability of our interpretations. Finally, we will present an attempt to use these new findings to interpret the contents of West-African archaeological pots.

ABSTRACT AF1-002

Investigating the adoption of rice and millet by hunter-gatherer-fishers of central Japan using organic residue analysis

Speaker: **Jasmine Lundy**
University of York, UK

Co-authors: Manon Bondetti[1], Alexandre Lucquin[1], Helen M. Talbot[1], Natsuki Murakami[2], Eiko Endo[3], Seiji Nakayama[4], Motoki Harada[5], Miho Suzuki[2], Simon Carrignon[6], Enrico R. Crema[6], Oliver E. Craig[1], Shinya Shoda[1,2]

[1] University of York, UK
[2] Nara National Research Institute for Cultural Properties, Japan
[3] Meiji University, Japan
[4] Teikyo University, Japan
[5] Aichi Asahi Site Museum, Japan
[6] University of Cambridge, UK

Abstract:

The adoption of agriculture by hunter-gatherer-fisher communities is a key topic in archaeological research. It has been established that rice and millet arrived in Western Japan from Korea around 3000 years ago and spread eastwards across the archipelago in the next 700 years. However, the extent to which agriculture transformed traditional Jomon hunter-gatherer-fisher communities is debated. Notably, the arrival of Yayoi cultural artefacts post-dates the appearance of agriculture. Here, we examine the use of pottery by final Jomon and early to middle Yayoi communities in two regions of Chubu, Central Japan, using lipid residue analysis. GC-MS and GC-c-IRMS analysis were undertaken on 246 vessels from 6 sites. Here, we compared the lipid residue data with evidence of cereal impressions on pottery and stable isotope analysis of human remains. We show that pottery use did not radically change in response to the arrival of farming despite clear changes in pottery style. Carbon isotope values of residues from Yayoi pottery, alongside the presence of alkylphenyl alkanoic acids (APAAs), clearly indicates the processing of marine and freshwater fish in several vessels. There was no clear evidence for ceramic artefacts dedicated for processing rice as has been previously hypothesised. Although the identification of specific biomarkers for rice remains elusive, differences in isomeric distribution of C18APAAs with the arrival of rice and millet indicates a potential change in plant processing. We were also able to identify biomarkers for millet (miliacin) in both final Jomon and Yayoi pottery that was probably mixed with wild hunted and foraged foods. We conclude that it is unlikely that the early stages of rice and millet agriculture in central Japan marked a radical departure from traditional dietary and culinary habits.

ABSTRACT AF1-003

Regional differences in stone cooking in the Japanese Palaeolithic as revealed by lipid residues

Speaker: **Shinya Shoda**

Nara National Research Institute for Cultural Poperties, Japan; University of York, UK

Co-authors: Natsuki Murakami[1], Yasuo Hosaka[2], Helen M. Talbot[3], Alexandre Lucquin[3], Oliver E. Craig[3]

[1] Nara National Research Institute for Cultural Properties, Japan

[2] Minobuyama University, Japan

[3] University of York, UK

Abstract:

Lipid residue analysis has been mainly conducted on pottery because of its porous nature which entraps organic residues within their matrices and its direct connection with their cooking activities. However, this method can be applied only to the period when pottery exists, and to the context in which they used pottery. Here, this paper first presents the results of lipid residue analysis for cooking stones excavated from Japanese Paleolithic sites (ca. 28k – 13k years BP), located at both ends of the country. We have extracted lipids from 40 samples from the Kagoshima prefecture in southern Japan and 23 samples from the Hokkaido prefecture in northern Japan, applying the existing method for pottery lipid residue analysis (acidified methanol extraction method) with six times more sample mass. As a result, a striking contrast between the north and south has been highlighted: while terrestrial animal resources were mainly processed in the former, aquatic resources were dominantly processed in the latter. This study extends the potential for lipid residue analysis to culinary artefacts beyond the arrival dates for pottery.

ABSTRACT AF1-004

Investigating the use of broomcorn millet (P. miliaceum) in culinary activities across East Kazakhstan throughout the Bronze Age

Speaker: Edward Standall

Nara National Research Institute for Cultural Properties, Japan

Co-authors: Paula Dupuy[1], Michael Frachetti[2], Zhanargul Kalieva[3], Aidyn Zhuniskhanov[1], Shinya Shoda[4]

[1] Nazarbayev University, Kazakistan
[2] Washington University in Saint Louis, USA
[3] Institute of Archaeology named after A. Kh. Margulan, Kazakistan
[4] Nara National Research Institute for Cultural Properties, Japan

Abstract:

From its domestication in present day China, to its translocation across Eurasia, broomcorn millet (Panicum miliaceum) has enabled, and perhaps promoted, economic and cultural change among diverse communities. However, archaeological evidence for the impact that the introduction of this cereal had on Central Asian agropastoral communities, which already possessed SW Asian domesticated cereals, is scarce. Previous research in Central Asia has identified early evidence for the use of P. miliaceum as animal fodder at Dali and Begash (ca. 2700 BC) and observed its presence in funerary contexts at Begash (ca. 2300 BC). However, contemporary evidence for the processing of P. miliaceum for human consumption has not presently been identified. The incorporation of P. miliaceum into culinary activities may be identified and understood via molecular and isotopic analysis of ceramic-absorbed organic residues, presenting an opportunity to elucidate the role and significance of the cereal in past economies and cultures. This study presents a spatiotemporal investigation of over 100 ceramic-absorbed residues from three multi-period, Bronze Age sites in East Kazakhstan, including Dali and Begash, situated in the Inner Asian Mountain Corridor (IAMC), and Koken, situated in the Eurasian Steppe. The data obtained in this study indicates localised approaches to the use of P. miliaceum in the IAMC, where the cereal was not consistently consumed by humans from its introduction. In addition, a later and substantially smaller introduction of P. miliaceum into culinary activities in the Eurasian Steppe highlights regional approaches to the cereal and perhaps the limited role that this region played in the dispersal of P. miliaceum across Eurasia. Finally, this study demonstrates the inclusion of P. miliaceum into diverse subsistence strategies and culinary activities practiced throughout East Kazakhstan during the Bronze Age.

ABSTRACT AF1-005

From Dates to Hens: Exploring Lipid Biomarkers for Novel Commodities in Roman Britain.

Speaker: **Rachel Vykukal**
Friedrich-Alexander-University, Germany

Co-authors: Anastasia Gabiger[1], Lucy Cramp[2], Martin Pitts[3], Simon Hammann[1]

[1] Friedrich-Alexander-University, Germany
[2] University of Bristol, UK
[3] University of Exeter, UK

Abstract:

Considerable work remains in identifying lipid biomarkers that can adequately discriminate between foods absorbed in pottery. The consumption of certain commodities, especially those that are lipid poor, may continue to be underestimated in archaeological residue results without further experimentation into diagnostic compounds. This is of particular importance to the study of Roman Britain. The Romans were known to have imported foods into Britain in the first to third centuries CE, such as dates and lentils, (Cool, et al. Cambridge University Press 2006; Van der Veen, et al. Environ. Archaeol. 2008), and yet the extent to which the local Britons adopted these foods and how foodways changed in response to a foreign population influx remain debated. As part of the larger Roman Melting Pots project, which explores cultural diversity and integration through culinary practices, we investigate potential biomarkers of some important, yet difficult to identify commodities eaten in the Romano-British world. Fourteen foodstuffs, such as chicken, figs, eggs, and turnips, were selected based on archaeological and literary sources and cooked repeatedly in replica cooking pots and dishes to produce lipid signatures. Extracted residues were analyzed with liquid chromatography coupled with high-resolution mass spectrometry (LC-HRMS), as well as gas chromatography coupled with mass spectrometry (GC-MS). The combination of GC-MS in archaeological residue research with the less established LC-HRMS allows for higher biomarker screening power and critical exploration of differential coverage and discrimination potential between the techniques. Characteristic differences in the lipid profiles of the commodities tested and the potential for these compounds to serve as biomarkers will be discussed.

ABSTRACT AF2-001

Palaeodietary reconstruction from chewed birch pitch using shotgun metagenomics

Speaker: **Aleksandra Laura Pach**
University of Copenhagen, Denmark

Co-authors: Jonas Niemann[1], Theis Zetner Trolle Jensen[1], Hannes Schroeder[1]

[1] University of Copenhagen, Denmark

Abstract:

Defining dietary changes of past peoples and tracking introductions of domesticates are often based on studies of available archaeological remains. Through the study of ancient metagenomic data extracted from substrates like ancient mastics (Jensen, et al. Nat. Commun. 2019) it is possible to obtain information about specific species consumed in a recent meal. Although the analysis of such data is not without its challenges. Databases are often contaminated or incomplete and genomes comprise many regions of high similarity between different species. These issues result in false positive results of the taxonomic assignment of the source of multi loci shotgun sequencing data (Mann, et al. Quat. Int. 2020). In order to minimize those, here we propose a workflow to properly classify most possible species alongside criteria for different thresholds for parameters determining the certainty of authentication. The following workflow has been tested on metataxonomic aDNA data from pieces of pitch collected from Alpine excavation sites and Scandinavian slotted bone points. Between the two sites at least 24 different eukaryotic taxa were identified where fifteen of those belong to Viridiplantae and seven to Bilateria. Mistletoe was detected in all samples from Scandinavia revealing novel information about utilization of the plant for hunting. Taxa from currently domesticated crops were found in different distributions in the samples from Alpine sites, further refining knowledge about introduction of domesticates in this region. These results help unravel previously unavailable cultural information about the different sites, and further highlight chewed birch pitch as a possible source of aDNA. Additionally, as the material has been found at multiple locations in Northern Europe and is not uncommonly found at sites around the Alps, this can broaden the perception at which archaeological materials are deemed as useful for aDNA analysis, especially at excavation sites where no human remains are found.

ABSTRACT AF2-002

Recovering proteins from foodcrust, biased from the start

Speaker: **Joannes Dekker**
University of York, UK; University of Copenhagen, Denmark

Co-authors: Matthew Collins[1,2], Jessica Hendy[3]

[1] University of Copenhagen, Denmark
[2] University of Cambridge, UK
[3] University of York, UK

Abstract:

Charred foodcrusts on ceramic vessels have proven a valuable source of dietary information (Dolbunova, et al. Nat. Hum. Behav. 2023). They have been mainly targeted for their lipid content, but recently efforts have been made to analyse the protein preserved in the foodcrusts. However, the recovery of proteins from foodcrusts is often limited to only a handful and a framework for their interpretation is missing (Hendy, et al. Proc. Biol. Sci. 2018; Shevchenko, et al. PLoS ONE 2018). Limiting our ability to effectively analyse foodcrust proteins is our lack of understanding of the formation of foodcrusts and the biases that affect the incorporation and preservation of proteins in them. To remedy this gap in our knowledge we performed a cooking experiment, heating a mixture of a protein-rich, carbohydrate-rich and lipid-rich foodstuffs in varying proportions in ceramic vessels for one hour at a fixed temperature nine times and subsequently burying the vessels for 52 days. Samples were taken for palaeoproteomic analysis after the first, fifth and ninth cooking event and after burial in order to highlight the effect of successive heating on protein preservation. The volume of foodcrust formation was also quantified by 3D scanning the samples after the final cooking event. Results show clear differences in the number of recovered proteins between both the different cooking events and the different food mixtures. Additionally, we also observe large variation in the volume of foodcrust formed depending on the composition of the mixture of foodstuffs. Although proteomic analysis will be biassed towards protein-rich foods in its identification of foodstuffs, it appears that mixtures of protein-rich foodstuffs with lipid- and carbohydrate-rich foodstuffs allow for higher protein recovery than foodcrusts formed from only protein-rich food. These results demonstrate that in the interpretation of proteomic analysis we must be mindful of proteomically less-visible foodstuffs as well, even though their direct detection remain

ABSTRACT AF2-003

Biomolecular and macro-botanical evidence sheds light on millet consumption in Late Bronze Age Central Germany

Speaker: **Eleftheria Orfanou**
Max Planck Institute for Evolutionary Anthropology, Germany; Friedrich-Schiller University Jena, Germany; Max Planck Institute for Geoanthropology, Germany

Co-authors: Barbara Zach[1,2], Mary Lucas[2,3], Adam B Rohrlach[4,5], Enrico Paust[1], Florian N. Schneider[1], Peter Ettel[1], Taylor Hermes[4], Wolfgang Haak[4], Robert Spengler[2], Patrick Roberts[2]

[1] Friedrich-Schiller University Jena, Germany
[2] Max Planck Institute for Geoanthropology, Germany
[3] UiT-the Arctic University of Norway, Norway
[4] Max Planck Institute for Evolutionary Anthropology, Germany
[5] University of Adelaide, Australia

Abstract:

Recent archaeobotanical research employing direct 14C dating indicates that East Asian broomcorn millet spread to Europe by ca. 1550 BCE and became widespread over two centuries. However, the extent of the adoption of millet and its particular uses are still not agreed upon in many areas of central Europe. By employing multi-isotopic analysis on human and animal bone collagen and tooth enamel, accompanied by 14C dating, archaeobotanical analysis of millet seeds, and human ancient DNA, we investigated the dietary patterns and genetic affinities of people at the LBA sites of Esperstedt and Kuckenburg in Central Germany, representing a period in which inhumations were rare and cremation was the dominant mortuary practice. Our results show that human individuals did not consume millet before the Middle-Late Bronze Age (ca. 1600 BCE). During the earlier phase of the LBA (1300-1100 BCE), we find that people consumed millet, in often-significant quantities, but then they seem to return to a diet solely based on C3 plants during the later phase of the LBA (1000-800 BCE), even though carbonized seeds of millet were still found at the site. The genetic results indicate that the LBA individuals consuming millet had a similar ancestry profile to people from the Early Bronze Age in the same region. Hence, this is likely a case of local adoption and consumption of millet, and not linked to the arrival of new people. Together, our data highlight that millet was an important crop by the beginning of the Late Bronze Age in Central Germany. Whether the adoption of millet was linked to trade and exchange, changing environmental conditions, or cultural reasons, it formed part of a dynamic, adaptive system to local ecologies.

ABSTRACT AF2-005

The make-up of skeletons to make-up a city

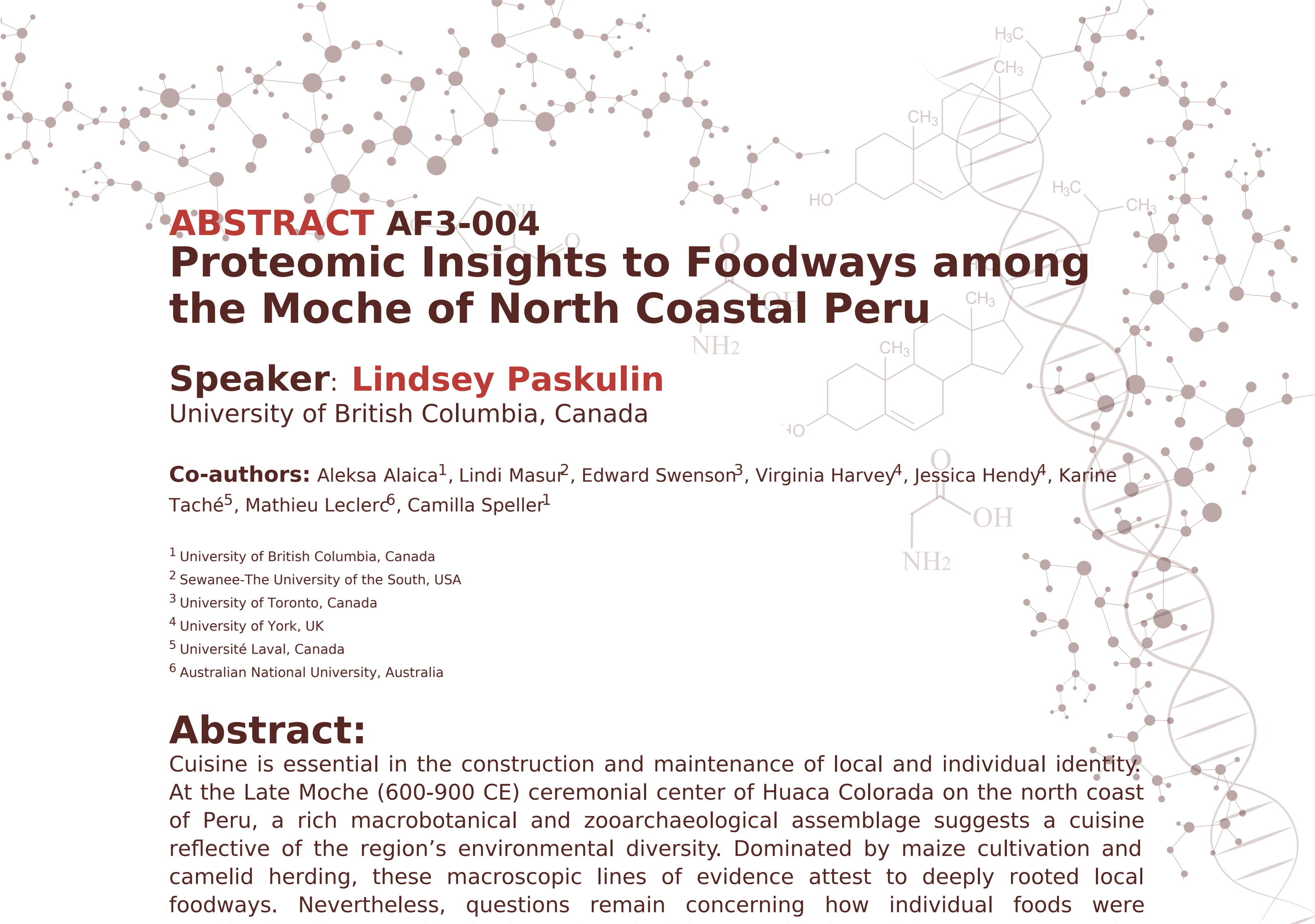
Speaker: **Rachèl Spros**
Vrije Universiteit Brussel, Belgium

Co-authors: Elisavet Stamataki[1], Veronica Jackson[1], Bart Lambert[1], Barbara Veselka[1], Christina Cheung[2], Philippe Claeys[1], Steven Provyn[1], Thyl Snoeck[1], Christophe Snoeck[1]

[1] Vrije Universiteit Brussel, Belgium
[2] The Chinese University of Hong Kong, China

Abstract:

During the high medieval period (12th-13th c.), the city of Ypres in present-day Belgium turned into one of the largest in North-western Europe, benefiting from the success of its cloth industry and international trade relations. Yet, what was the composition of its population remains poorly documented. In this period, the city experienced challenges including a rapidly expanding number of inhabitants, the political unrest of popular revolts, and natural disasters like pandemics and famines. Multi-isotope analyses on human remains have been used for decades to understand the human past and provide information on people’s environment, health, movements, and social interactions. However, possible behavioural changes following these factors are missed as multi-intra-skeletal sampling is not often done on larger groups of individuals from a single population, which is needed before conclusions can be made at the scale of a population. Especially since the comparison of isotope values obtained from different skeletal elements is sometimes debated, resulting in a limitation of intra- and interindividual comparisons. How do we link information between different bones and teeth, and how can this information be applied in order to not just understand this population, but also to improve future sampling strategies to best answer historical questions? To overcome these limitations, over 1,200 analyses for carbon, nitrogen, oxygen, and strontium isotopes are measured on 150 individuals from high medieval Ypres. Additionally, statistical analyses made intra- and interindividual comparisons possible, providing answers to a larger variety of questions ranging from the more methodologically oriented, like the existence of intra-tissue differences, to historical ones; for example sex based divisions in mobility in medieval Ypres. The implications of these findings are not only relevant for the medieval population of Ypres, but also for isotope analyses studies in general.



ABSTRACT AF3-004

Proteomic Insights to Foodways among the Moche of North Coastal Peru

Speaker: **Lindsey Paskulin**
University of British Columbia, Canada

Co-authors: Aleksa Alaica[1], Lindi Masur[2], Edward Swenson[3], Virginia Harvey[4], Jessica Hendy[4], Karine Taché[5], Mathieu Leclerc[6], Camilla Speller[1]

[1] University of British Columbia, Canada
[2] Sewanee-The University of the South, USA
[3] University of Toronto, Canada
[4] University of York, UK
[5] Université Laval, Canada
[6] Australian National University, Australia

Abstract:

Cuisine is essential in the construction and maintenance of local and individual identity. At the Late Moche (600-900 CE) ceremonial center of Huaca Colorada on the north coast of Peru, a rich macrobotanical and zooarchaeological assemblage suggests a cuisine reflective of the region's environmental diversity. Dominated by maize cultivation and camelid herding, these macroscopic lines of evidence attest to deeply rooted local foodways. Nevertheless, questions remain concerning how individual foods were combined and prepared in the formation of cuisine. Considering cuisine as one expression of identity, our research seeks to reconstruct past recipes through the analysis of ancient proteins preserved in ancient cooking pots (ollas). We apply shotgun proteomics – a method of ancient protein analysis – for the identification of plant and animal food-derived proteins in pottery residues from Huaca Colorada. First, we tested the efficiency of two extraction techniques — single-pot solid-phase-enhanced (SP3) and gel-aided (GASP) sample preparation— in yielding proteins from an assemblage of experimental pottery. We then applied the optimized technique to ceramic residue and matrix samples from Huaca Colorada. As a complement to other forms of analysis, including archaeobotany and zooarchaeology, proteomics has potential to contribute to understandings of cuisine through interpretations of food preparation and cooking.

ABSTRACT CE1-001

Researchers' perspectives on the ethics of human remains research: from tissue to biomolecules

Speaker: **Rita Peyroteo Stjerna**
Linnaeus University, Sweden

Co-authors: Liv Nilsson Stutz[1]

[1] Linnaeus University, Sweden

Abstract:

Ancient human remains are highly prized research subjects because of the wealth of information they can provide about past lives, which otherwise would be difficult to uncover. In recent years, the astonishing development of biomolecular techniques such as residue and stable isotope analyses, proteomics, and the breakthrough of the next generation sequencing of ancient DNA, propelled Biomolecular Archaeology to a leading field of research, crossing major disciplinary boundaries between the Humanities and the Natural Sciences. While the study of human remains is just one portion of the vast tool kit of biomolecular research, its rapid development aggravated a number of already existing challenges and underlined the ethical entanglements of research using human remains in a highly unregulated field.To give researchers a voice in this debate, and to disentangle the multiple ethics of biomolecular research on human remains, we conducted semi-structured interviews with researchers and technical staff carrying out ancient DNA and other biomolecular research on human remains from archaeological, ethnographic, or medical-anthropological collections in museums and other institutions. This paper reports the preliminary results of these conversations. At ISBA10, we would like to concentrate on the biomolecular dimensions of human remains in research, how researchers approach this legacy, and how it differs from handling hard or soft tissue. By focusing on this aspect, we aim to highlight that biomolecular archaeologists not only have unique responsibilities, but also are exceptionally positioned to lead the debate forward.This study is part of a larger research project - Ethical Entanglements: The Care for Human Remains in Museums and Research, which seeks to strengthen the competence and awareness, among museum professionals and researchers of the complex ethical dimensions of research and curation of human remains.

ABSTRACT CE1-002

Building a community-based consensus for ancient sequencing data metadata reporting with MInAS

Speaker: **James Fellows Yates**
Leibniz Institute for Natural Product Research and Infection Biology, Germany; Max Planck Institute for Evolutionary Anthropology, Germany

Co-authors: SPAAM Community[1], Antonio Fernandez-Guerra[2]

[1] SPAAM Community
[2] University of Copenhagen, Denmark

Abstract:

Ancient DNA (aDNA) is a rich resource of information, both in time and diversity. Such information could be utilised by a wide range of researchers in biology, anthropology, and other fields, however such ancient samples are often rare and precious, and there is a need to maximise the (re-)usage of aDNA data. While having been previously touted as a poster child for the sharing of raw sequencing data, palaeogenomics needs to continue building on this leadership by improving the findability of such data.The metadata of ancient sequencing data on public sequencing archives are currently very variable when it comes to the level of detail and formats, making it difficult to rapidly identify potentially useful data for re-use. Other domains of biology have already developed standardised reporting guidelines to improve data discoverability. Such checklists already exist for modern (meta)genomics, and are required for upload to repositories such as the EBI's ENA and NCBI's SRA.In this talk I will present the 'Minimum Information about an Ancient Sequence' (MInAS) project (https://mixs-minas.org/), which aims to develop a core set of standardised metadata in a checklist specifically for ancient DNA sequences. Critically, this project will require the input and agreement of the broader palaeogenomics, archaeology- and biological-related communities to ensure adoption and integration with domain-specific databases. We wish to identify more stakeholders to get involved in the development of the checklist, therefore I will also discuss ways in which the research field can contribute to the project to develop a community-consensus.

ABSTRACT CE1-003

Biomolecular archaeology meets ocean conservation in biodiversity hotspots

Speaker: **Andre Carlo Colonese**
Universitat Autonoma de Barcelona, Spain

Co-authors: Thiago Fossile[1], Krista Michelle McGrath[1], Dannieli Firme Herbst[1], Leopoldo Cavaleri Gerhardinger[1], Marjolein Admiraal[2], Oliver E Craig[2]

[1] Universitat Autònoma de Barcelona, Spain
[2] University of York, UK

Abstract:

Anthropogenic impacts on tropical and subtropical coastal environments are increasing at an alarming rate compromising ecosystem functions, structures and services. Understanding the scale of marine population decline and diversity loss in these regions requires a long-term perspective that incorporates information from a range of sources, including ancient biomolecules from archaeological records. Here we will bring together zooarchaeological and biomolecular (ORA, ZooMS and stable isotopes) analyses of fauna, human and artefact remains to reconstruct marine animal diversity, changes in subsistence economy and diet in coastal Brazil over the last 6000 years. The results reveal how collaborative research efforts involving molecular archaeologists, historians and marine ecologists can productively advance our understanding of long-term change in coastal ecosystems in the southwestern Atlantic Ocean and contribute to conservation debates. The work is part of TRADITION, an ERC-Consolidator Grant funded research project (European Commission) that is currently assessing the long-term development of small-scale fisheries in Brazil.

ABSTRACT CE1-004

Metagenomic perspectives on traditional beer brewing: New insights from Scandinavian yeast rings

Speaker: **Oya Inanli**
University of York; University of Copenhagen, Denmark

Co-authors: Anna E. White[1,2], Jonas Niemann[2], Yuejiao Huang[2], Michael Dondrup[3], Atle Ove Martinussen[4], Hans Geir Eiken[5], Nathan Wales[1], Hannes Schroeder[2]

[1] University of York, UK
[2] University of Copenhagen, Denmark
[3] University of Bergen, Norway
[4] Western Norway Cultural Academy, Norway
[5] Norwegian Institute of Bioeconomy Research, Norway

Abstract:

The introduction of pure cultured yeast strains in the 19th century led to the industrialisation of beer production. Despite these large-scale changes, traditional forms of beer production have survived in some parts of the world. In Western Norway, traditional ‘kveik’ brewing involves the use of ornate pieces of wood known as yeast rings or yeast logs. Although the rings are no longer in use, “kveik” yeasts are still used in traditional farmhouse brewing in Norway today. However, the origins of kveik yeast are debated, and it is unclear to what extent the strains being used today reflect past diversity. In this project, we explore the potential of recovering ancient yeast strains from historical Norwegian yeast rings and fermentation barrels. We tested DNA extraction methods previously used on ancient plant and herbarium specimens to maximise DNA yields. We recovered several Saccharomyces cerevisiae genomes from different artefact types using shotgun sequencing. The amount of damage in the DNA fragments is consistent with the age of the samples. In addition, we examined the phylogenetic relationships between past and modern S. cerevisiae strains in Western Norway. Our analyses highlight the potential of ancient DNA analyses for studying historical and archaeological artefacts to expand our understanding of traditional brewing practices and the evolution of fermentation microbiomes.

ABSTRACT CE1-005

Tracing touch through time: Ancient human DNA recovered from a Palaeolithic pendant

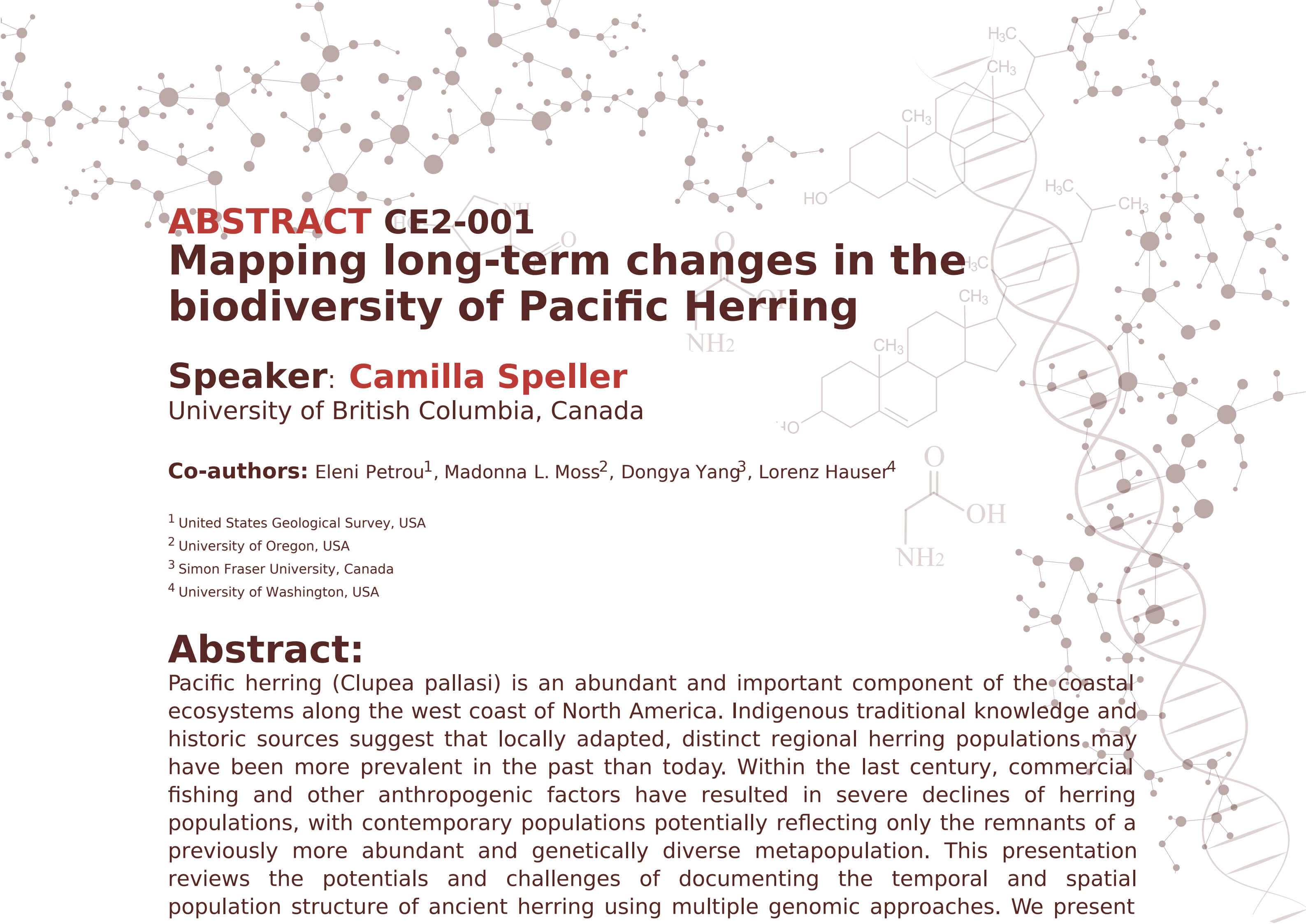
Speaker: **Elena Essel**
Max Planck Institute for Evolutionary Anthropology, Germany

Co-authors: Elena I. Zavala[1,2], Ellen Schulz-Kornas[3], Maxim B. Kozlikin[4], Helen Fewlass[1,5], Benjamin Vernot[1], Michael V. Shunkov[4], Anatoly P. Derevianko[4], Katerina Douka[6], Ian Barnes[7], Anna Schmidt[1], Merlin Szymanski[1], Tsenka Tsanova[8], Nikolay Sirakov[9], Elena Endarova[10], Jean-Jacques Hublin[1,11], Janet Kelso[1], Svante Pääbo[1], Mateja Hajdinjak[1,5], Marie Soressi[12], Matthias Meyer[1]

[1] Max Planck Institute for Evolutionary Anthropology, Germany
[2] San Francisco State University, USA
[3] University of Leipzig, Germany
[4] Russian Academy of Sciences, Russia
[5] The Francis Crick Institute, UK
[6] University of Vienna, Austria
[7] Natural History Museum, UK
[8] University of Tübingen, Germany
[9] National Institute of Archaeology with Museum Bulgarian Academy of Sciences, Bulgaria
[10] National Museum of History, Bulgaria
[11] Collège de France, France
[12] Leiden University, Netherlands

Abstract:

Palaeolithic artefacts provide important insights into human behaviour in the Pleistocene. However, in the absence of burials, no direct inferences are possible as to who made/used them. To determine if it is possible to identify the maker/user of artefacts by traces of DNA they may have left behind, we developed a non-destructive DNA extraction method using serial incubation in phosphate buffer for temperature controlled DNA release. We applied this method to eleven previously excavated osseous artefacts from Quinçay Cave (France) and recovered ancient mammalian mitochondrial DNA from two of them. However, all artefacts also released large amounts of contaminating modern human DNA, making it impossible to determine whether ancient human DNA was preserved. To overcome the problem of human DNA contamination, we applied the method to four freshly excavated artefacts, collected using measures for contamination prevention: three from Bacho Kiro Cave (Bulgaria) and one from Denisova Cave (Russia). All artefacts yielded ancient mammalian DNA sequences matching their morphological identification, and noticeably less present-day human DNA contamination. In addition, we recovered large quantities of ancient human DNA from the Denisova Cave artefact, a pierced cervid tooth. Genetic dating of the cervid and human mitochondrial DNA estimated the age of the pendant at approximately 19,000 to 25,000 years, and nuclear DNA analysis identified its presumed maker/wearer as a female individual with strong genetic affinities to a group of Ancient North Eurasian (ANE) individuals. Our study establishes Palaeolithic osseous artefacts as a previously unrecognized source of ancient human DNA and opens new possibilities for establishing direct links between the cultural and genetic records of the past. Follow-up studies are planned to determine which types of artefacts are most suitable for genetic investigations and to develop strategies to further reduce modern human DNA contamination.



ABSTRACT CE2-001

Mapping long-term changes in the biodiversity of Pacific Herring

Speaker: **Camilla Speller**
University of British Columbia, Canada

Co-authors: Eleni Petrou[1], Madonna L. Moss[2], Dongya Yang[3], Lorenz Hauser[4]

[1] United States Geological Survey, USA
[2] University of Oregon, USA
[3] Simon Fraser University, Canada
[4] University of Washington, USA

Abstract:

Pacific herring (Clupea pallasi) is an abundant and important component of the coastal ecosystems along the west coast of North America. Indigenous traditional knowledge and historic sources suggest that locally adapted, distinct regional herring populations may have been more prevalent in the past than today. Within the last century, commercial fishing and other anthropogenic factors have resulted in severe declines of herring populations, with contemporary populations potentially reflecting only the remnants of a previously more abundant and genetically diverse metapopulation. This presentation reviews the potentials and challenges of documenting the temporal and spatial population structure of ancient herring using multiple genomic approaches. We present two case studies assessing ancient population diversity of herring in Washington and Alaska, respectively. We apply SNPs capture to elucidate the use of herring from different spawning groups in Puget sound by Coast Salish people for over 900 years. In Alaska, we quantify changes in genetic diversity over several hundred years by analyzing whole genome sequencing data recovered from two Tlingit archaeological sites: Craig Administrative Site (2360-2120 cal BP) and Starrigavan (650-550 cal BP). We highlight the importance of collaborations between Indigenous communities, modern fisheries scientists and archaeologists for advancing research on this culturally and ecologically important forage fish.

ABSTRACT CE2-002

Historical ecology and species diversity of Mediterranean marine apex predators

Speaker: **Elisabetta Cilli**
University of Bologna, Italy

Co-authors: Fausto Tinti[1], Valentina Crobe[1], Maria Vittoria Iacovelli[1], Federico Lugli[1,2], Alexia Mazzini[1], Martina Pasino[1], Valentina Brombin[3], Paola Iacumin[4], Alessia Cariani[1]

[1] University of Bologna, Italy
[2] University of Modena and Reggio Emilia, Italy
[3] University of Ferrara, Italy
[4] University of Parma, Italy

Abstract:

The Mediterranean Sea has played a crucial role for the development and socio-economic progress of the civilizations that have inhabited it for millennia and exploited its marine resources, determining a strong competition for habitat and food between humans and apex predators such as large epipelagic fish (sharks, tuna) and marine mammals (seals, whales, dolphins). To date, the undeniable decline of most of them has led conservationists to consider the knowledge of natural/anthropogenic drivers of this decrease as a key-target for protection. We multidisciplinary analyzed the historical biodiversity of three dolphin species and five species of elasmobranchs, the great white shark and four locally extinct sawfish species, using more than 500 historical osteological specimens (skulls, rostra, jaws, vertebra and teeth from 19th-21st centuries) provided by a network of more than 30 museums and private collections in the Mediterranean region. We combined traditional and geometric morphometry species identification with ancient DNA and multi-element stable isotope analyses to assess biocomplexity spatio-temporal shifts, identify the drivers of such changes and whenever possible assess historical baselines of biodiversity. Main goals we achieved are 1) a full representation of the pre-extinction species diversity of the Mediterranean sawfish apparently greater than that expected from sightings and anecdotal/documental records; 2) relative species frequency shifts of dolphins in the Italian seas with the identification of putative historical interspecific hybrids and 3) ecological shifts for habitat preferences and for feeding and reproductive behavior in the historical and contemporary Mediterranean white sharks. Knowledge of the pristine baseline of large predator populations is useful for the comparison with the current levels of biocomplexity and related human impacts, assuming crucial relevance both in scientific knowledge of nature and in conservation management.

ABSTRACT CE2-003

Exploring Degradation of Arctic Heritage through metagenomics

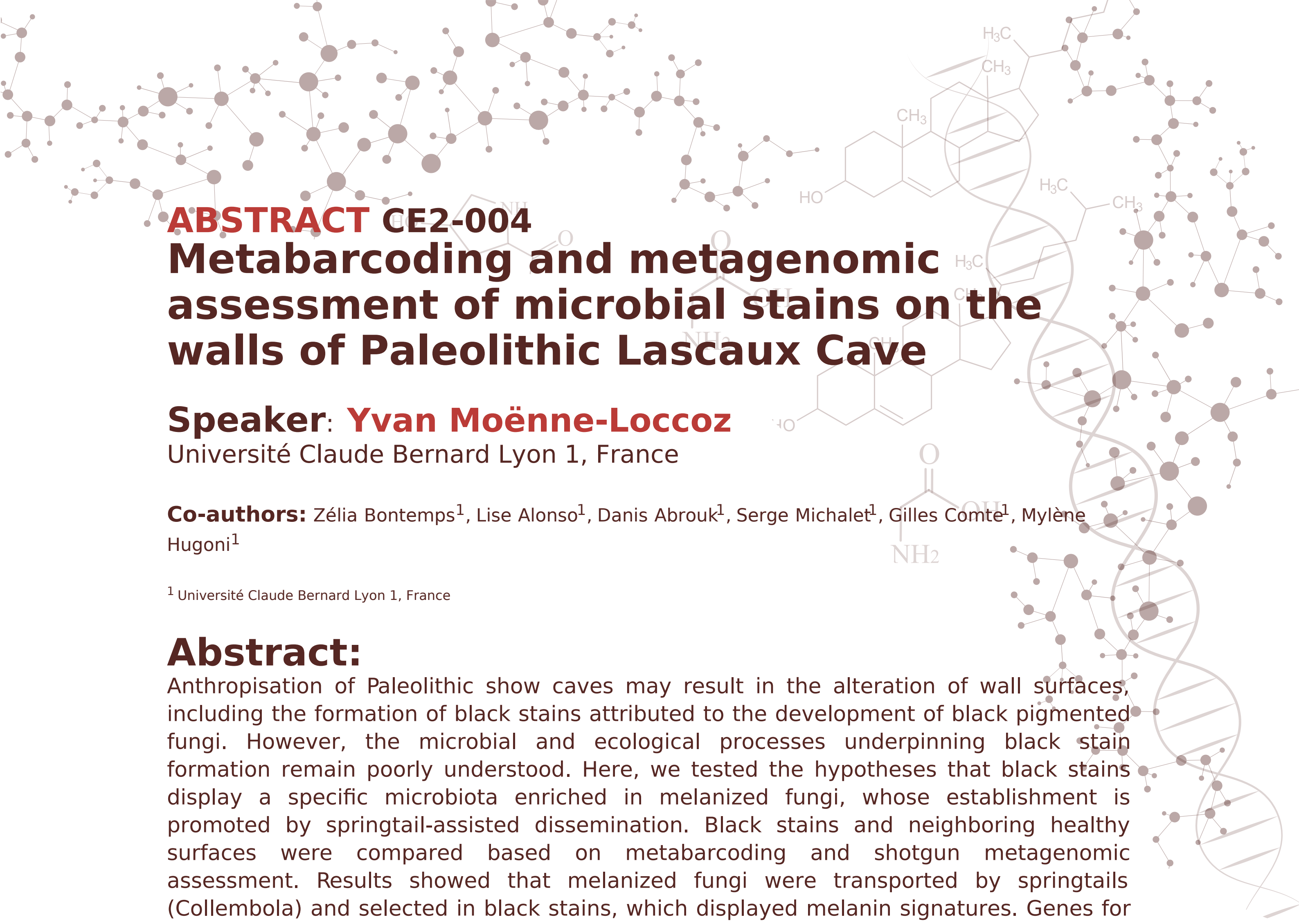
Speaker: **Anne Marie Høier Eriksen**
National Museum of Denmark, Denmark

Co-authors: Henning Matthiesen[1], Frederik Seersholm[2], Mikkel Winther Pedersen[2], Juan Antonio Rodriguez[2], Anne Birgitte Gotfredsen[2], Bjarne Grønnow[1]

[1] National Museum of Denmark, Denmark
[2] University of Copenhagen, Denmark

Abstract:

As part of the project Activating Arctic Heritage (AAH) we have explored five Norse, Inuit and colonial period archaeological sites located within the two UNESCO World Heritage areas, Kujataa in South Greenland and Aasivissuit-Nipisat in West Greenland. The main focus has been to understand the environmental dynamics around the archaeological sites and to study the preservation conditions in culture layers through a multiproxy analytic method using among other techniques sedaDNA from the middens as well as aDNA from excavated caribou ribs. One of our focuses has been on the state of preservation of the animal bones from the midden layers at the site of Aasivissuit. Aasivissuit, an Inuit summer caribou hunting site located close to the Ice sheet in West Greenland and settled by the Inuit in different periods mainly during the last millennium, offers a unique set of data as this site was partly excavated in 1978. In order to study the degree of decay of the bones in the culture layers, the same excavation trench was opened again in 2021 as part of the AAH project. We analyzed shotgun metagenomic data from 33 caribou ribs equally distributed between the two excavation periods giving a new perspective on the preservation both at the site of Aasivissuit over a period of 43 years but also of the degradation processes happening in the museum collections. Our preliminary results suggest a significant difference in both DNA fragment lengths and amount of preserved endogenous DNA between the two excavation periods. However, we found signs of degradation in both batches, as there was a high C-T deamination at the first position in all samples. We will explore this data in more detail and correlate with histological analysis, assessment of the microbial shotgun metagenomic data, as well as environmental data from the archaeological site and the museum storage.



ABSTRACT CE2-004

Metabarcoding and metagenomic assessment of microbial stains on the walls of Paleolithic Lascaux Cave

Speaker: **Yvan Moënne-Loccoz**
Université Claude Bernard Lyon 1, France

Co-authors: Zélia Bontemps[1], Lise Alonso[1], Danis Abrouk[1], Serge Michalet[1], Gilles Comte[1], Mylène Hugoni[1]

[1] Université Claude Bernard Lyon 1, France

Abstract:

Anthropisation of Paleolithic show caves may result in the alteration of wall surfaces, including the formation of black stains attributed to the development of black pigmented fungi. However, the microbial and ecological processes underpinning black stain formation remain poorly understood. Here, we tested the hypotheses that black stains display a specific microbiota enriched in melanized fungi, whose establishment is promoted by springtail-assisted dissemination. Black stains and neighboring healthy surfaces were compared based on metabarcoding and shotgun metagenomic assessment. Results showed that melanized fungi were transported by springtails (Collembola) and selected in black stains, which displayed melanin signatures. Genes for synthesis of melanin and carotenoid pigments were more prevalent in black stains than unstained surfaces and were identified in several reconstructed genomes (MAGs). They were evidenced not only in fungi (as expected) but also in bacteria. The presence of genes involved in the degradation of aromatic compounds and presumably of biocides used in the cave was also evidenced, strengthening that previous chemical treatments could have selected melanin-producing microorganisms as well as melanin synthesis. These findings confirm previous predictions regarding microbial alterations in anthropized Lascaux Cave ecosystem, by documenting the range of microorganisms involved, potential biotransformations taking place, and key fauna-microbe interactions accounting for black stain formation. This microbial functioning needs to be taken into account for the development of sustainable conservation strategies for underground Paleolithic art. References: Alonso, et al. Microbiome 2018 Alonso. et al. Env. Microbiol. Rep. 2023

ABSTRACT CE2-005

Deciphering climate change impacts on Arctic marine mammals using sedimentary ancient DNA

Speaker: **Lennart Schreiber**
University of Copenhagen, Denmark

Co-authors: Heike Zimmermann[1], Sofia Ribeiro[1]

[1] Geological Survey of Denmark and Greenland, Denmark

Abstract:

The Arctic Ocean is one of Earth’s most fragile ecosystems and the scale of change taking place due to warming and loss of sea ice cover is overwhelming. Reliable data are imperative for making informed predictions and decisions concerning the conservation of Arctic marine mammal species, but there is a paucity of long-term data on the response of these species to climatic perturbations. Palaeo-archives such as sediment cores are invaluable for the reconstruction of past environmental changes and biological processes. However, most research has focused on resolving dynamics of physical parameters and obtaining proxy time-series from organisms at the base of the food web, whereas the limited fossil record has made it challenging to study higher trophic levels. Our project aims at characterizing the histories of marine mammals in the Arctic region. For this purpose, ancient DNA extracted from marine sediment cores covering the last ~10,000 years was analysed using a hybridization panel which captures mitogenomic reads of Arctic marine mammals such as beluga whales, narwhals, bowhead whales, ringed seals, bearded seals and polar bears. The enriched libraries were sequenced to characterize species histories both by providing information on the presence in a specific location and time, but also by inferring phylogeographic placements of past populations. We integrated our findings with proxy data that document the timing and magnitude of environmental changes, as well as community structure and abundance of lower trophic levels. This allows for a holistic perspective on the processes that cause spatial and temporal variability in marine mammals, which will also aid answering the question whether demographic changes in marine mammals were driven by bottom-up ecosystem processes or anthropogenic pressure such as whaling.

ABSTRACT DEN-001

Detection of protein malnutrition using amino acid isotopic tracers

Speaker: **Carlo Cocozza**

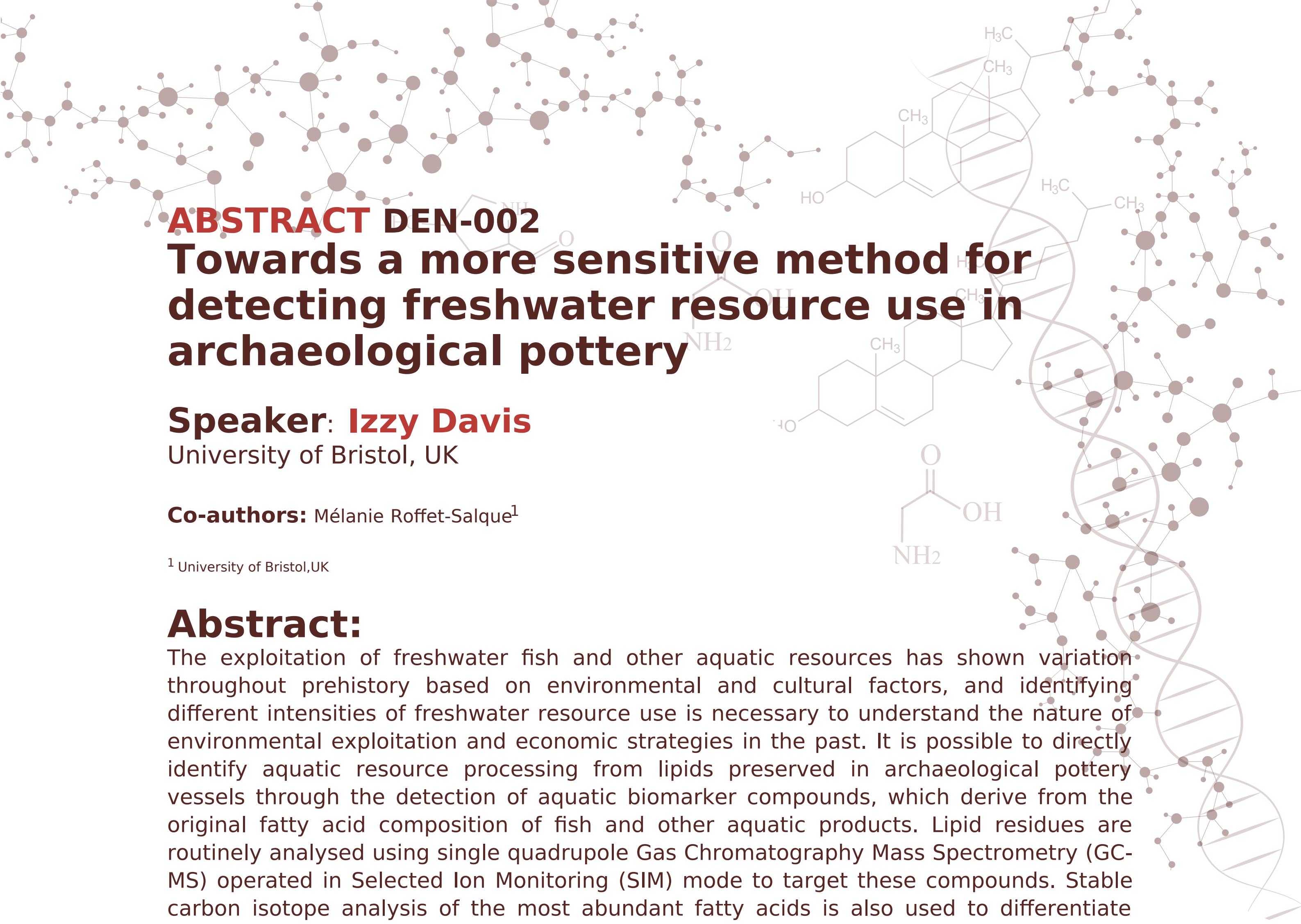
Max Planck Institute for Geoanthropology, Germany; Ludwig-Maximilians-Universität München, Germany; Università degli studi della Campania "Luigi Vanvitelli", Italy

Co-authors: Ricardo Fernandes[1,2,3]

[1] Max Planck Institute for Geoanthropology, Germany
[2] University of Oxford, UK
[3] Masaryk University Brno, Czech Republic

Abstract:

Understanding metabolic routing mechanisms is crucial for comprehending how food nutrients are integrated into consumer tissues. Relevant information can be acquired through controlled feeding experiments and suitable tracers. Stable isotope studies have provided valuable insights, but certain aspects remain unexplored, such as the precise quantification of the relative contribution of different macronutrients to consumer tissues and the impact of malnutrition on consumer isotopic values. To address these issues, it is beneficial to employ multi-proxy approaches that combine bulk and compound-specific analysis using various isotopic tracers. Feeding experiments were conducted on omnivorous mammals, and stable isotope measurements (C, N, S) were performed on bulk tissues (e.g., bone collagen, hair keratin, bioapatite) and single amino acids from food and consumer tissues. Experimental setups encompassed a wide range of food and macronutrient types with contrasting isotopic values, as well as foods with varying protein contents to assess isotopic detection of protein malnutrition. The results enabled the quantification of elemental contributions from food macronutrients (proteins, carbohydrates, lipids) to consumer tissues. The implications of these findings for the study of nutrition physiology and the application of isotopic methods for dietary reconstruction will be further discussed.



ABSTRACT DEN-002

Towards a more sensitive method for detecting freshwater resource use in archaeological pottery

Speaker: **Izzy Davis**
University of Bristol, UK

Co-authors: Mélanie Roffet-Salque[1]

[1] University of Bristol,UK

Abstract:

The exploitation of freshwater fish and other aquatic resources has shown variation throughout prehistory based on environmental and cultural factors, and identifying different intensities of freshwater resource use is necessary to understand the nature of environmental exploitation and economic strategies in the past. It is possible to directly identify aquatic resource processing from lipids preserved in archaeological pottery vessels through the detection of aquatic biomarker compounds, which derive from the original fatty acid composition of fish and other aquatic products. Lipid residues are routinely analysed using single quadrupole Gas Chromatography Mass Spectrometry (GC-MS) operated in Selected Ion Monitoring (SIM) mode to target these compounds. Stable carbon isotope analysis of the most abundant fatty acids is also used to differentiate aquatic and terrestrial sources, but this method is limited for identifying freshwater resources, particularly low contributions, due to the variation exhibited between freshwater species and environments.Here we present a novel method for aquatic lipid biomarker detection using high-resolution GC-quadrupole-time-of-flight-MS (GC-qTOFMS). We show that this method offers increased analytical selectivity, sensitivity, and full mass-spectrum capabilities compared to GC-MS in SIM mode, allowing the simultaneous detection of aquatic biomarkers (isoprenoid fatty acids, dihydroxy fatty acids, and ω-(o-alkylphenyl)alkanoic acids) in complex mixtures using a non-targeted approach, thus enabling us to study low intensity aquatic resource use. This novel method is applied to lipids extracted from pottery vessels from early Neolithic settlements located next to freshwater environments, to investigate the exploitation of these resources by the first farming populations in central Europe.

ABSTRACT DEN-003

New determination of C, N, O and S stable isotopes Trophic Enrichment Factors in bone collagen and apatite of carnivorous mammals from Białowieża Forest (Poland)

Speaker: **Dorothée Drucker**
Senckenberg Centre for Human Evolution and Palaeoenvironment, Germany;
University of Tübingen, Germany

Co-authors: Magdalena Krajcarz[1], Maciej Krajcarz[2], Emilia Hofman-Kamińska[2], Rafał Kowalczyk[2], Chris Baumann[3], Hervé Bocherens[1]

[1] University of Tübingen, Germany
[2] Polish Academy of Sciences, Poland
[3] University of Helsinki, Finland

Abstract:

An increasing number of studies uses stable isotope tracking to reconstruct ecological interactions among terrestrial mammals, including predatory relationships. Refined models have been developed based on Bayesian approaches to reconstruct the diet composition of human and animal predators. All of them involve the use of Trophic Enrichment Factors (TEFs) whose values were partly defined based on controlled diet studies. Most of these feeding experiments consider the isotopic spacing between tissues, often not including bone, and the whole diet, whose controlled composition may be quite different from the natural one. In past ecosystems, bone and teeth are the only body parts available for isotopic measurement from both predators and potential preys (e.g. Baumann et al., Quaternary Science 2020). Fossils may contain, however, several biogenic fractions, each providing a specific isotopic tracking of the diet. There is thus a need to define the isotopic spacing between bone collagen and bioapatite fractions of the predators and those of their preys in their natural environment (e.g. Bocherens & Drucker, International Journal of Osteoarchaeology 2003; Krajcarz et al., Rapid Commun. Mass Spectrom. 2019). Białowieża Forest (Poland) provides a very favorable context of free-ranging large mammal species whose dietary behavior is well monitored. It is home of two large predators, one canid wolf and one felid lynx, which prey preferences, especially among the cervids red deer and roe deer, are well studied. In this paper, we present the results of TEFs in carbon, nitrogen, sulfur and oxygen stable isotopes in bone collagen and bioapatite for both predatory species. The obtained TEFs values, sometimes different from those currently accepted, can be used as references for the study of modern and ancient predator dietary preferences and will contribute to refine our understanding of trophic interactions in past ecosystems.

ABSTRACT DEN-004

The potential of Sequential Thermal Desorption/Pyrolysis-Gas Chromatography-Mass Spectrometry in the analysis of human dental calculus: a case study from the Bronze Age Aegean.

Speaker: **Cynthianne Spiteri**
University of Turin, Italy; Eberhard Karls University of Tübingen, Germany

Co-authors: Stephen Buckley[1], Robert C. Power[2], Stefanie Eisenmann[3], Joann Fletcher[1], Birgitta Hallager[4], Joseph Maran[5], Maria Andreadaki-Vlazaki[6], Photini J. P. McGeorge[7], Michael Schultz[8], Philipp W. Stockhammer[9,10]

[1] University of York, UK
[2] University College Dublin, Ireland
[3] Humboldt Universität zu Berlin, Germany
[4] The Swedish Institute at Athens, Greece
[5] University of Heidelberg, Germany
[6] Excavation House "Sevach", Greece
[7] The British School at Athens, Greece
[8] University Medical School Göttingen, Germany
[9] Ludwig Maximilian University Munich, Germany
[10] Max Planck Institute for Evolutionary Anthropology, Germany

Abstract:

Sequential Thermal Desorption/Pyrolysis-Gas Chromatography-Mass Spectrometry (TD/Py-GC-MS) is still an underutilised methodology in the field of biomolecular archaeology. Here we present new data showcasing the potential of this technique when applied to human dental calculus. Our paper reports the earliest archaeometric evidence for the use of lignite (brown coal) in Europe and sheds new light on the use of combustion fuel in the 2nd millennium BCE Eastern Mediterranean. We analysed dental calculus from 67 individuals from sites in the Aegean, Egypt and the Near East using TD/Py-GC-MS and Polarizing Microscopy. Scant evidence for the use of combustion markers in the calculus from Egypt was identified, but clear evidence for the burning of Pinaceae wood, hardwood (e.g. oak and olive), and dung was found in all of the other individuals tested. Furthermore, individuals from the Palatial Period at the Mycenaean citadel of Tiryns and the Cretan harbour of Chania showed evidence for the inhalation of smoke from lignite. Significantly, lignite here appears a thousand years prior to the mention of its use by Theophrastus (374/369 – 288/285 BC) in his work, On Stones. Based on the scientific evidence we obtained, we suggest that lignite had been exploited at the time in connection with the manufacture of crafts production including metals, ceramics and glass, which were important and highly traded resources during the Bronze Age. Our results further showed that the inhalation of lignite was evident in both males and females, suggesting that both biological sexes were involved in crafts production.

ABSTRACT DEN-005

Bioarchaeological record reveals millenia-long use of North African seagrass meadows by endangered green turtles

Speaker: **Willemien de Kock**
University of Groningen, Netherlands

Co-authors: Meaghan Mackie[1], Max Ramsøe[1], Morten E. Allentoft[1,2], Annette C. Broderick[3], Julia C. Haywood[3], Brendan J. Godley[3], Robin T. E. Snape[3,4], Phil J. Bradshaw[3], Hermann Genz[5], Matthew von Tersch[6], Michael W. Dee[7], Per J. Palsbøll[7,8], Michelle Alexander[6], Alberto J. Taurozzi[1], Canan Çakirlar[7]

[1] University of Copenhagen, Denmark
[2] Curtin University, Australia
[3] University of Exeter, UK
[4] Society for the Protection of Turtles, North Cyprus
[5] American University of Beirut, Lebanon
[6] University of York, UK
[7] University of Groningen, Netherlands
[8] Center for Coastal Studies, USA

Abstract:

‘Protect and restore ecosystems and biodiversity’ is the second official goal of the current UN Ocean Decade (2021-2030) calling for the identification and protection of critical marine habitats. However, data to inform policy are often lacking altogether or confined to recent times preventing the establishment of long-term baselines. For the first time, we employ the unique insights gained from combining bioarchaeology (palaeoproteomics, stable isotope analysis of δ13C, δ15N, δ34S) with contemporary data (from satellite tracking technology) to identify vulnerable sea turtle habitats in the eastern Mediterranean over a five millennia period. Our analysis of archaeological green turtle (Chelonia mydas) bones revealed they likely foraged on the same North-African seagrass meadows as their modern-day conspecifics; evidence of site-fidelity to the same foraging habitat for several millennia . Quantitative methods enabled us to establish site fidelity at the generational level, uncovering habitat significance over time scales beyond the Anthropocene. This study highlights the opportunities, and potential pitfalls, of combining modern and bioarchaeological data to draw conclusions about habitat use through time. By accessing the bioarchaeological archive, we generated results which demonstrate the long-term use of Egyptian and West-Libyan coastal seagrass beds by the endangered green turtle. Protecting these areas would not only be important for species conservation in the Mediterranean, it would also conserve an ancient heritage.

ABSTRACT DOM-001

Mixed diets at the Mesolithic-Neolithic transition? Bulk and compound-specific isotope evidence for the interaction between hunter-gatherers and farmers at Grotta dell’Uzzo (Sicily)

Speaker: **Marcello Mannino**
Aarhus University, Denmark; Max Planck Institute for Evolutionary Anthropology, Germany

Co-authors: Geert Van Biesen[1], Benjamin T. Fuller[2,3], Sahra Talamo[4,5], Antonio Tagliacozzo[6], Carmine Collina[7], Rosaria Di Salvo[8], Vittoria Schimmenti[8], Michael P. Richards[5,9], Vaughan Grimes[1]

[1] Memorial University of Newfoundland, Canada
[2] Observatoire Midi Pyrénées, France
[3] Aarhus University, Denmark
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Abstract:

Biomolecular investigations on Grotta dell’Uzzo (Sicily) demonstrated that the cultural changes that took place at this cave in the early Holocene correspond with changes in the genomes of its Mesolithic and Neolithic occupants (Yu, et al. 2022 iScience). Late Mesolithic humans, producers of Castelnovian-like lithic industries, carried ~20% ancestry originating from northern and/or eastern European hunter-gatherers, and most of them relied heavily on marine resources, including stranded cetaceans. Conversely, bulk carbon (δ13C) and nitrogen (δ15N) isotope data from the earliest phase of the Neolithic show that humans of farming ancestry relied heavily on terrestrial resources and marginally on marine protein. Some early Neolithic domestic animals at Grotta dell’Uzzo, including a few ovicaprids and numerous cattle specimens, have very high δ13C values, unlike earlier and later terrestrial mammals at the site. Based on the δ13C, δ15N, and sulphur (δ34S) bulk isotope values, the most likely explanation for this is that some early Neolithic cattle fed mainly on plants within the C4 photosynthetic pathway. Compound-specific δ13C analyses on the amino acids of the same collagen samples confirm that some of the cattle consumed C4 plants heavily. The bulk and compound-specific data show that the occupants of Grotta dell’Uzzo adapted to rapid climate-driven environmental changes in the late Mesolithic, adopted mixed subsistence strategies at the Mesolithic-Neolithic transition, and relied increasingly on domesticates after the earliest stages of the Neolithic. Uniquely for the Mediterranean, our study supports the original interpretation that foragers interacted with incoming farmers (who brought cattle with them), albeit for a short time, as is compatible with the limited genetic evidence for interaction on Sicily.

ABSTRACT DOM-002

Exploring the domestication of Agave - Preliminary results from the Tehuacán Valley Caves in central Mexico

Speaker: **Marcela Sandoval-Velasco**
Smithsonian National Museum of Natural History, USA

Co-authors: Elsa Peters[1], Abisaí García-Mendoza[2], Norma Anzures[3], Alejandro Casas[2], María Ávila-Arcos[2], Logan Kistler[1], Daniel Piñero[2]

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Abstract:

Plant domestication was crucial for the rise of civilizations and even though it is a long-studied subject we still lack fundamental understanding about many aspects of human-plant relationships and the origins of cultivation, especially outside the range of staple crops. Agaves are one of the most culturally and historically important groups of plants in the Americas and have been extensively and continuously used by humans for thousands of years (HS Gentry, 1982). Archaeobotanical remains of agaves are present to such an extent in the archaeological record, that it has been suggested they may be one of the earliest domesticated plants from Mesoamerica and that their cultivation may have laid cultural and ecological groundwork for the domestication of other crops (CE Smith, 1967). A continuous record of agave usage was recovered from the Tehuacán Caves located in central Mexico. These caves are considered unique in the world since they represent an uninterrupted history covering the period between the first human occupation until the Spanish conquest. Aiming to describe the mechanics, location and timing of the processes driving cultivation and domestication, we extracted aDNA from 150 archaeobotanical remains of agaves across an extensive time series comprising 10,000 years of continuous human use. We generated both nuclear shotgun palaeogenomic data and whole cpDNA genomes to identify at the species level the agaves from the archaeological assemblages over time and the existence of selected traits that allow us to reconstruct their cultivation and domestication history. The rich record of preserved agaves constitutes a genomic archive of their use and evolution in human landscapes. Understanding when, why, and which species were domesticated, will shed light on how their cultivation impacted the domestication of other Mesoamerican crops, offering an opportunity to improve our understanding of the processes resulting in plant management and landscape modification.

ABSTRACT DOM-003

The genetic identity of Europe’s first dogs

Speaker: Anders Bergström

University of East Anglia, UK

Co-authors: Anja Furtwängler[1], Erika Rosengren[2], Abagail Breidenstein[3], Thomas Booth[4], Sarah Johnston[4], Jesse McCabe[4], Jessica Peto[4], Mia Williams[4], Monica Kelly[4], Kyriaki Anastasiadou[4], Alexandre Gilardet[4], Isabelle Glocke[4], Alexander Herbig[1], Kay Prüfer[1], Saskia Pfrengle[5], Joscha Gretzinger[5], Tatiana R. Feuerborn[5], Ella Reiter[5], Chris Baumann[6], Hervé Bocherens[5], Susanne C. Münzel[5], Verena J. Schuenemann[7], Johannes Krause[1], Pontus Skoglund[4]

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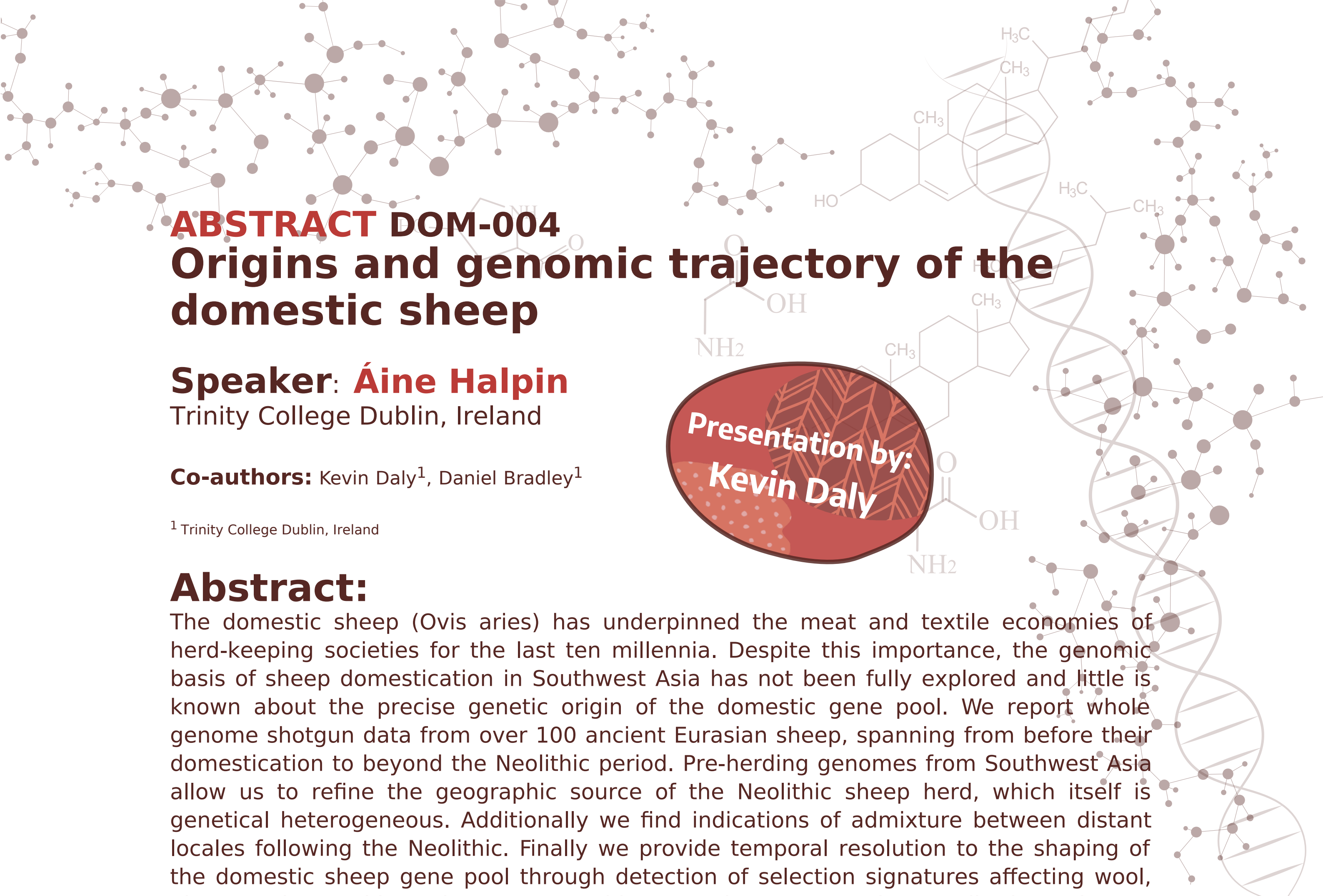
Abstract:

Some of the earliest morphologically identifiable dogs have been found in central Europe, dating back to ~14,000 years ago. Despite this, genomes from Late Pleistocene European wolves suggest that these wolves were not the source of dogs, as present-day and available ancient dog genomes instead show stronger affinities to wolves in eastern Eurasia. Neolithic and later European dogs additionally have a minority fraction of ancestry from a second wolf source of western Eurasian, likely Near Eastern, origin. However, the lack of genomic data from European dogs predating the Neolithic means that the genetic identity and origin of the earliest dogs in the region remains elusive. We applied capture of ~500,000 genome-wide SNPs, as well as shotgun sequencing, to various early European dog remains. We find that one of the earliest European dogs, from the Magdalenian site Kesslerloch cave in Switzerland, shares at least some of the eastern-related ancestry that unites all known later dogs, implying it was not independently domesticated from local European wolves. We also find that Mesolithic dogs from southern Sweden show affinity to early dogs in Karelia and Siberia, without detectable contributions from the second, western-related wolf source. Overall, our results suggest that dogs who had likely originated further east had reached Europe already prior to the onset of the Neolithic.



ABSTRACT DOM-004

Origins and genomic trajectory of the domestic sheep

Speaker: **Áine Halpin**
Trinity College Dublin, Ireland

Co-authors: Kevin Daly[1], Daniel Bradley[1]

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Presentation by:
Kevin Daly

Abstract:

The domestic sheep (Ovis aries) has underpinned the meat and textile economies of herd-keeping societies for the last ten millennia. Despite this importance, the genomic basis of sheep domestication in Southwest Asia has not been fully explored and little is known about the precise genetic origin of the domestic gene pool. We report whole genome shotgun data from over 100 ancient Eurasian sheep, spanning from before their domestication to beyond the Neolithic period. Pre-herding genomes from Southwest Asia allow us to refine the geographic source of the Neolithic sheep herd, which itself is genetical heterogeneous. Additionally we find indications of admixture between distant locales following the Neolithic. Finally we provide temporal resolution to the shaping of the domestic sheep gene pool through detection of selection signatures affecting wool, pigmentation, and horn development. This research represents the contributions of many collaborators who will be acknowledged during the presentation of this work.

ABSTRACT DOM-005

Paleogenomics of European wild and domestic cats

Speaker: **Marco De Martino**
University of Rome “Tor Vergata”, Italy

Co-authors: Valentina Rovelli[1], Bea De Cupere[2], Tullia Di Corcia[1], Francesca Alhaique[3], Eugenio Cerilli[4], Emanuela Ceccaroni[5], Sonja Vuković[6], Cleia Detry[7], Idoia Grau[8], Lluís Lloveras[9], Jacopo De Grossi Mazzorin[10], Claudia Minniti[10], Marta Moreno[11], Jordi Nadal[12], Vedat Onar[13], Vera Pereira[14], Nicolai Spassov[15], Barbara Wilkens[4], Joris Peters[16], Wim Van Neer[2], Claudio Ottoni[1]

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Abstract:

Zooarchaeological and genetic evidence from the last two decades demonstrated that domestic cats originated from the North African and Near Eastern wildcat, Felis silvestris lybica. The commensal relationship between humans and cats most likely started 11 thousand years ago (kya) in the Neolithic Levant. More recently, ancient mitochondrial DNA (mtDNA) evidence suggested that domestic cats spread to Southeast Europe as early as 4400 BC, however their dispersal to the rest of Europe is controversial due to the paucity of data. Furthermore, complex scenarios of admixture between domestic and wild populations (e.g., the European wildcat F. s. silvestris and the Asian wildcat F. s. ornata) may have taken place across time, thus leaving a mtDNA-based reconstruction unsatisfactory. Here we show the preliminary results of our paleogenomic investigation from more than 150 cat remains from European archaeological sites dated from 15 kya to the 18th century AD, with a peculiar focus on the Mediterranean area. By screening the samples for endogenous cat DNA content, we provide a framework of ancient DNA preservation in cat remains across time and space. Furthermore, by generating complete mtDNAs and low-coverage nuclear genome data (ranging from 0.2- to 1.4-fold), we were able to refine the chronology of cat dispersal in the Mediterranean region, and to address questions around potential admixture patterns between wild and domestic cat populations. Our paleogenomic dataset lay the foundations for future and more in-depth analyses aimed at understanding the factors determining the evolutionary success of the domestic cat.

ABSTRACT FAU-001

A systematic evaluation of hominin and faunal DNA preservation in Pleistocene sediments

Speaker: **Merlin Szymanski**
Max Planck Institute for Evolutionary Anthropology, Germany

Co-authors: Viviane Slon[1,2], Louisa Jauregui[1], Kseniya Kolobova[3], Andrey Krivoshapkin[3,4], Zenobia Jacobs[5], Richard G. Roberts[5], Janet Kelso[1], Matthias Meyer[1], The Sediment DNA Analysis Consortium[6]

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[6] The Sediment DNA Analysis Consortium

Abstract:

Recent years have seen an increase in the use of sedimentary DNA analysis to infer the past presence of species at Pleistocene archaeological sites, including hominins such as Neandertals, Denisovans and modern humans. However, there has been a lack of systematic investigation of the success rate at which hominin and faunal DNA can be recovered from archaeological sediments and of the factors that contribute to long-term DNA preservation in sediment. To address this, we collected over 800 sediment samples from 148 Middle and Late Pleistocene sites in Europe, Asia, and Africa, including caves, rock shelters, and open-air sites, and tested them for the presence of ancient mammalian DNA. DNA libraries were prepared from each sample and enriched for human and mammalian mitochondrial DNA by hybridization capture. We developed a computational pipeline to optimize the assignment of retrieved sequences to biological families (and in some cases specific species or populations) and to evaluate their ancient origin based on the presence of ancient DNA damage patterns. Tests performed on simulated data show that this pipeline outperforms previously published approaches in both accuracy and speed. Our preliminary findings indicate that ancient DNA is best preserved in sediments from caves, followed by rock shelters and open-air sites. Temporal and geographical limits of DNA preservation closely match those previously observed in the analysis of ancient skeletal remains. We also identified ancient hominin DNA in sediments at sites and in archaeological layers for which no hominin genetic data was previously available. A particularly exciting discovery is new evidence for the presence of Denisovans in the Altai Mountains in places other than Denisova Cave. We hope that the empirical data presented here will help to devise optimal sampling strategies for future studies, especially with regards to the number of samples and the contexts that are most promising for DNA analysis

ABSTRACT FAU-002

Reconstructing faunal diversity from the last Glacial period in northern Norway using zooarchaeology and bulk-bone metabarcoding

Speaker: **Aurélie Boilard**
University of Oslo, Norway

Co-authors: Samuel J. Walker[1], Trond Lødøen[2], Mona Henriksen[3], Henriette Linge[2], Thijs van Kolfschoten[4,5], Stein-Erik Lauritzen[1,2], Liselotte Takken Beijersbergen[2], Anne Karin Hufthammer[2], Sanne Boessenkool[1]

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Abstract:

Northern Europe experienced extreme topographical, environmental and climatic changes during the last interglacial-glacial cycle. High-latitude, fossil faunal records are, however, almost non-existent due to the Late Pleistocene erosion and removal of sediments by flushing meltwater from the massive glaciers that covered extensive parts of the northern temperate regions. The effects of the dramatic Quaternary climatic changes on animal distributions in Fennoscandia therefore remain largely unresolved. The Storsteinshola cave system (68°50’N) in Kjøpsvik, northern Norway, is an exception, with one of the sections of this large karst cave system containing an extra-ordinary bone-rich sediment deposit preliminary dated to 70 000 - 120 000 years BP. We exploit the exceptional opportunity of this deposit for the comparative, interdisciplinary analyses of a high-latitude faunal record from the last interglacial-glacial cycle. Following two large-scale excavations, we combined morphological identification with bulk-bone metabarcoding to maximise taxonomic identification of the highly fragmented, recovered bone material. Through these analyses over 40 taxa were identified, including a diverse range of mammals (e.g. bear Ursus sp., reindeer Rangifer tarandus, bowhead whale Balaena mysticetus), birds (e.g. king eider Somateria spectabilis, ptarmigan Lagopus sp., common murre Uria aalge) and fish (e.g. Atlantic cod Gadus morhua, golden redfish Sebastes marinus, salmonids Salvelinus). Our results highlight the power of combining ancient DNA with traditional, zooarchaeological methods to broaden taxonomic identification of fragmentary material that is otherwise difficult or even impossible to identify. Moreover, chronology established using a diversity of dating methods together with sedimentological analyses provide a framework for palaeo-environmental interpretations of the exhaustive faunal record that is reconstructed.

ABSTRACT FAU-003

A Ghost on the Coast: Lessons from the Extinction of the Sea Mink (Neogale macrodon) and Conservation Implications for the American Mink (Neogale vison)

Speaker: **Courtney Hofman**
University of Oklahoma, USA

Co-authors: Bonnie Newsom[1], Torben C. Rick[2], Karissa Hughes[3], Olivia Olson[4], Lilly Parker[3], Victoria Paige[3], Chris Abin[3], Donald Soctomah[5], Arthur E. Spiess[6], Linda Welch[7], Alexis Mychajliw[4]

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Abstract:

The presence of ghosts in our world is palpable: the evidence of lost species interactions and ecological functions now punctuates landscapes globally. Yet, reckoning with these ghosts is crucial for detecting the natural range of variation in ecological systems and for setting attainable restoration and reintroduction goals in the context of changing climates and human populations. To examine these processes, we explore the fates of two coastal fur-bearing mammals in the Gulf of Maine: the extant American mink (Neogale vison), and a ghost, the sea mink (Neogale macrodon). The sea mink or “shell heap” mink was first scientifically described after its presumed extinction by Prentiss (1903), but is called supeqi-ciyahkehsu by the Wabanaki people. Based on fragmentary documents from early 20thcentury, the sea mink was a large, reddish mink that foraged in the intertidal zone and fed exclusively on marine resources prior to its disappearance by 1910. While there are no known historic specimens of the sea mink pelage, faunal assemblages of bones from shell midden archaeological localities around the Gulf of Maine reveal that the species was harvested for millennia by Wabanaki families. By combining diverse datasets from paleogenomics, archaeology, paleoecology, and present-day ethnography, we reconstruct biocultural history of extinct sea mink and its extant cousin, the American mink and generate conservation lessons for the harvest of modern furbearing mammals. We assess whether the American mink has become a suitable ecological, economic, and cultural surrogate for the lost sea mink, providing a case study of relevance for extinct and extirpated species globally.

ABSTRACT FAU-004

Exploring question-oriented mass sampling strategies to integrate ZooMS into zooarchaeological analyses of prehistoric faunal collections

Speaker: **Geneviève Pothier-Bouchard**
Université Laval, Canada; Université de Montréal, Canada

Co-authors: Julien Riel-Salvatore[1], Michael Buckley[2], Karine Taché[1]

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Abstract:

ZooMS (Zooarchaeology by Mass Spectrometry) collagen fingerprinting is increasingly applied to prehistoric faunal collections – especially highly fragmented and/or altered ones – to tackle questions regarding diet, subsistence, and hunting strategies. When mass sampling archaeological bones (i.e., hundreds of bone fragments), ZooMS is a powerful tool to improve overall taxonomic identification of the indeterminate fraction of faunal assemblages. However, sampling many bone fragments at random entails certain risks regarding methodological biases and collagen preservation for such specialized analysis. Question-oriented sampling strategies can help refine specific dimensions of our reconstructions about past subsistence behaviours. In addition, in collections showing poor collagen preservation, using a portable FTIR instrument can be an effective and cost-efficient in-field pre-screening method for ZooMS. We present here two case studies from contrasting contexts (i.e., NE North American Woodland open-air site and NW Italian Paleolithic rockshelter site) to explore how to develop sampling strategies adapted to different research questions and archaeological contexts.

ABSTRACT FAU-005

Spondylus Palaeoproteomics: tracing the iconic shell of prehistory

Speaker: **Jorune Sakalauskaite**
Vilnius University, Lithuania; University of Turin, Italy; University of Burgundy-Franche-Comté, France; University of Copenhagen, Denmark

Co-authors: Beatrice Demarchi[1], Frédéric Marin[2], Matthew Collins[3,4], Daniel J. Jackson[5], Hala Alarashi[6,7], Meaghan Mackie[3,8,1], Alberto Taurozzi[3], Solange Rigaud[9], Claire Manen[10], Monique de Cargouët[11], Nicolas Potier[11], Maria A. Borrello[12], Felipe Cárdenas-Arroyo[12], Elena Sarropoulou[13], Christian Carøe[3], Max Ramsøe[3]

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Abstract:

Spondylus, the thorny oyster, is the most iconic shell of prehistoric times. The mediterranean species S. gaederopus was widely used in Europe during the Neolithic and was crafted into ornaments, beads, bracelets and figurines. While native to the Mediterranean sea, many prehistoric Spondylus artefacts are found all across Europe: from the southeast to the west and reaching as far as northern France, Germany and Poland. Archaeological research on Spondylus has a lot of potential - its artefacts may encode information on exchange and trade routes, or shared symbolic rituals and traditions. However, we are hampered by the difficulty to identify Spondylus. When heavily worked and/or fragmented, it has often been mistaken for shells of similar properties, such as the marine clams Tridacna and Glycymeris. Our group has been working on collecting a comprehensive biomolecular Spondylus shell database, to securely identify it using palaeoproteomics. Spondylus proved to be challenging - unknown protein sequences, absence of its genome and difficulty to get live modern specimens. Only thanks to the collaborative efforts of scientists in biomineralization, transcriptomics, palaeoproteomics, archaeology and the marine biology research consortium Assemble+, we were finally able to decipher the Spondylus shell proteome. We found that its shell proteins are distinct from other shell sequences, including those from its phylogenetically closest neighbour, Pecten. Some of the proteins are intracrystalline, and they are stable over archaeological timescales, proved also by artificial ageing experiments. More importantly, characteristic Spondylus proteins allow to securely identify the raw material, even from small prehistoric samples. Our data brings an important contribution to the field of archaeomalacology and we hope that Spondylus research will expand to other continents, such as South America, where this shell also played a phenomenal role in pre-columbian societies.

ABSTRACT HD1-001

Contrasting evolutionary and adaptive histories revealed for three oral pathobionts recovered from Bronze Age Irish remains

Speaker: **Iseult Jackson**
Trinity College Dublin, Ireland

Co-authors: Marion Dowd[1], Linda Fibiger[2], Lara M Cassidy[3]

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Abstract:

The development of ancient genomic techniques has allowed the exploration of both host genomes and the genomes of commensal and pathogenic microbes. Teeth provide a particularly rich substrate: as well as endogenous host DNA, they are a source of DNA from both bloodborne pathogens and the oral microbiota. We carried out metagenomic screening of a dataset of 344 published tooth and calculus samples from diverse prehistoric, Medieval and early modern contexts. This identified two teeth from a limestone cave (Killuragh, Co. Limerick, Ireland) with exceptional preservation of oral pathobiont species. Both were found to belong to a single Early Bronze Age individual (2343-2036 cal BC). Given the large quantities of pathobiont DNA recovered, novel ancient genomes could be assembled de novo for two species, Streptococcus mutans and Treponema denticola, while a third, Tannerella forsythia, was reconstructed through reference alignment. An additional 38 T. denticola and 18 T. forsythia ancient genomes were reconstructed from published samples in the literature. This dataset provided unprecedented resolution on the evolutionary histories of these three pathobionts. Contrasting phylogenetic patterns were observed, with a very recent adaptive radiation observed for T. forsythia in the early modern period and deep divergences within modern S. mutans diversity, some pre-dating the branch leading to Killuragh. Comparative analysis also revealed differences in the functional repertoires of oral pathobionts. Changes in the presence of key virulence factors in the species' pangenomes correlates with changes in human behaviour, such as dairying, industrialisation and the widespread use of antibiotics. The timing of these changes appears to differ between species, suggesting differences in the factors affecting these pathobionts' co-evolution with their human hosts.

ABSTRACT HD1-002

Down syndrome in ancient societies

Speaker: **Kay Prüfer**

Max Planck Institute for Evolutionary Anthropology, Germany

Co-authors: Adam Benjamin Rohrlach[1], Maïté Rivollat[1], Patxuka de-Miguel-Ibáñez[2], João C. Teixeira[3], Xavier Roca-Rada[4], Javier Armendáriz-Martija[5], Kamen Boyadzhiev[6], Yavor Boyadzhiev[6], Bastien Llamas[4], Anthi Tiliakou[1], Angela Mötsch[1], Jonathan Tuke[4], Päivi Onkamo[7], Ulla Moilanen[8], Anne-Mari Liira[8], Philipp W. Stockhammer[1], Henrike O. Heyne[9], Johannes R. Lemke[10], Roberto Risch[11], Stephan Schiffels[1], Johannes Krause[1], Wolfgang Haak[1]

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Abstract:

More than 1/1000 infants in present-day industrialized societies are born with Down syndrome, a condition that is mostly caused by the presence of an additional full copy of chromosome 21. Down syndrome is associated with congenital, physical and neurodevelopmental symptoms and individuals with the syndrome rarely survive up until birth. However, modern medical treatments have increased the average life-expectancy for those born with the condition from approximately 10 years in the 1960s to around 60 years, today. Here, we investigate ancient cases of Down syndrome to learn more about individuals with the condition in the past. We screened genetic data from approximately 10,000 individuals, dating from a few hundred to several thousands of years ago, using a novel Bayesian method designed to detect evidence of three copies of chromosome 21 from as few as 1000 ancient DNA sequences. Five cases of Down syndrome dating to prehistoric times (>2000 years of age) and one case dating to the 17th or 18th century were detected. All cases were from perinatal to infant individuals. Although osteological evidence is not diagnostic for Down syndrome, we observe skeletal markers on some of the remains that are consistent with the condition. We observed a frequency of cases among our tested individuals that was lower than the modern prevalence. This difference could be explained by an average younger age of mothers in the past since the age of mothers is positively associated with Down syndrome risk. However, we cannot exclude a sampling bias in the remains collected for ancient DNA sequencing as an alternative explanation. Finally, for all time periods and geographical regions the six individuals were either buried according to standard or, in some cases, distinguished practices, acknowledging them as part of their community.

ABSTRACT HD1-003

High-coverage genomic data of ancient treponemal bacteria allow multifaceted analyses on the evolution and adaptations of Treponema pallidum

Speaker: **Kerttu Majander**
University of Vienna, Austria

Co-authors: Marta Pla-Díaz[1,2], Gülfirde Akgül[3], Martyna Molak[4,5], Louis du Plessis[6,7], Hanna Panagiotopoulou[5], Karolina Doan[5], Wiesław Bogdanowicz[5], Paweł Dąbrowski[8], Maciej Oziembłowski[9], Joanna Grzelak[8], Natasha Arora[3], Fernando González-Candelas[1,2], Verena J. Schuenemann[3,10]

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Abstract:

Syphilis, yaws and bejel, caused by three subspecies of Treponema pallidum bacteria, are globally re-emerging diseases that have threatened human health for centuries or more. Although modern genetics have helped characterize the causative agents; the origin, evolution and spread routes of these diseases are still largely unknown. Ancient pathogen genomics can reveal aspects of these pathogens' past, unretrievable from modern data alone. Here we analyze the high-coverage genomes of several T. pallidum lineages from ancient human remains, and demonstrate the potential of combining modern and ancient data sources. All available previously published ancient data, along with a novel high-coverage genome of the syphilis-causing agent, T.p. pallidum, recovered from the archaeological context of 17th-century Wroclaw, Poland; Akgül, et al. bioRxiv 2023), are being used to trace hitherto unknown recombination events and positive selection in the putatively virulence-associated genes of T. pallidum. Furthermore, the exclusion of the recombining regions is observed to affect the phylogeny of T. pallidum, especially for the endemic treponematosis subspecies, T.p. pertenue and T.p. endemicum, insinuating the importance of recombination in their divergence. Finally, molecular clock dating, assessing the historical times and the possible order of these divergences is generated through a combined dataset of ancient and modern treponeme genomes. Overall, our results shed light on so far poorly understood evolutionary adaptations, and help illuminating the emergence and early connections of treponemal subspecies.

ABSTRACT HD1-004

Recent increase in allele frequency of the common norovirus-protective FUT2 variant

Speaker: **Richard Ågren**
Karolinska Institutet, Sweden

Co-authors: Johan Nordgren[1], David Hu[2], Marie Hagbom[1], Lennart Svensson[1,2], Hugo Zeberg[2]

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Abstract:

Background Fucosyltransferase 2 (FUT2) encodes an enzyme that mediates the synthesis of antigens on the gastrointestinal mucosa. Individuals with a non-functional FUT2 enzyme are less susceptible to noro- and rotaviruses. Several FUT2 variants are known, with the most common inactivating mutation (c.G428A, rs601338) introducing a premature stop at position 154 in the encoded protein. This variant has an allele frequency of 30-50% in most present-day populations. The widespread prevalence of this loss-of-function FUT2 variant suggests evolutionary selection. Methods The Allen Ancient DNA Resource (v54.1) was used to map rs601338-A temporospatially. Clinical associations of rs601338-A were investigated using the UK Biobank and FinnGen, totalling ~700,000 individuals of European descent. Results We identify the FUT2 rs601338-A variant in a 43,100 years old genome from the Bacho-Kiro cave in present-day Bulgaria. The allele frequency of this variant was ~10% ~10,000 years before present, evolving to a frequency of 30-50% in modern genomes. Compared to other G>A substitutions on the same chromosome, which show similar modern allele frequencies, the FUT2 c.G428A variant has increased the most, suggesting selection. In modern-day biobanks we find a clinical association between rs601338-A and protection against viral enteritis (odds ratio [95% confidence interval] = 0.87 [0.85-0.90], p = 3.3 x 10^-15). However, this variant is also associated with increased risk of gallstone disease (OR = 1.07 [1.05-1.08], p = 1.4 x 10^-18) and duodenal ulcers (OR = 1.12 [1.08-1.16], p = 8.2 x 10^-10). Conclusions The inactivating FUT2 rs601338-A variant conferring protection to viral gastroenteritis has increased dramatically over the last 10,000 years. This increase coincides with the transition from hunting and gathering to settled agriculture. However, whereas it confers protection to viral gastroenteritis, it is also associated with an increased risk of other gastrointestinal diseases.

ABSTRACT HD1-005

The evolutionary path of the Salmonella enterica Para C lineage

Speaker: **Gunnar Neumann**
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Abstract:

Salmonellosis, caused by the bacterial pathogen Salmonella enterica, is one of the most common food-borne diseases world-wide. Most of the ~2600 different S. enterica serovars can infect a wide variety of host species and predominantly lead to self-limiting gastro-enteric disease when transmitted to humans. However, a small number of serovars is strictly human-adapted and causes enteric fever. Of these, Paratyphi C forms the so-called Para C lineage together with the swine-specific Typhisuis and the human/swine-adapted Choleraesuis. Previous aDNA studies have shown that host-adaptation on this lineage through gene gain and loss as well as pseudogenization could be linked to the Neolithization process (Key, et al. Nat. Ecol. Evol. 2020). Here, we present a temporal and geographic transect of new ancient S. enterica subsp. enterica genomes ranging from 5000-500 years BP across Eurasia. Most genomes from between 5000-3000 BP form a distinct phylogenetic subclade that lacks any modern representatives suggesting it most likely went extinct. The other genomes dated to the last 2700 years position along the ParatyphiC and Choleraesuis branches. Their successive distribution allows for the in-depth investigation of host adaptation both through the acquisition of genomic loci and through gene pseudogenization. Ancient DNA data is particularly helpful in reconstructing the timing or order of such events. For example, our results show that the Salmonella pathogenicity island SPI-7 was gained before the tcfABCD operon of SPI-6 was lost for ParatyphiC. These insights will help in characterizing the evolutionary path and process of host-adaptation of the S. enterica Para C lineage and how its changing genetic structure altered its virulence.

ABSTRACT HD2-001

An ancestral recombination graph for the hepatitis B virus

Speaker: Arthur Kocher

Max Planck Institute for Geoanthropology, Germany

Co-authors: Ariane Weber[1], Timothy G Vaughan[2], Johannes Krause[3], Denise Kühnert[1]

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Abstract:

The hepatitis B virus (HBV) has been infecting humans for millennia and remains an important global health problem. In recent years, the reconstruction of numerous ancient HBV genomes dated to the last 10,000 years has provided major insights into the past genetic diversity of this virus and the origin of modern HBV strains. Furthermore, the phylogeographic history of HBV is tightly linked to that of its human hosts. Phylogenetic analyses of ancient HBV genomes have unveiled patterns reflecting well-known aspects of human history as well as some pointing to yet unidentified events. However, HBV undergoes genetic recombination. Therefore, classic phylogenetic methods which do not consider horizontal genetic transfers can, at best, provide partial representations of HBV evolutionary history. Instead, genetic recombination can be explicitly modelled within ancestral recombination graphs, but these are notoriously difficult to estimate. Here, I will present our work towards reconstructing the first ancestral recombination graph of HBV, which together with newly reconstructed ancient HBV genomes, allows revisiting some important aspects of this virus' phylogeographic history.

ABSTRACT HD2-002

Atherosclerotic cardiovascular disease in mummies - A polygenic risk score based on a genetic enrichment approach

Speaker: **Christina Wurst**
Eurac Research - Institute for Mummy Studies, Italy

Co-authors: Frank Maixner[1], Alice Paladin[1], Guido Valverde[1], Randall Thompson[2], Albert Zink[1]

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Abstract:

Atherosclerotic cardiovascular disease (ASCVD) results in heart attack, stroke, and peripheral vascular disease and is one of the main causes of death worldwide. Until recently, ASCVD was generally considered to be a modern disease and connected to an unhealthy lifestyle. However, recent studies show growing evidence for the presence of atherosclerosis in ancient human remains. In addition, genetic predisposition is becoming increasingly important in understanding the development of ASCVD. Nevertheless, genetic data concerning the prevalence of the disease associated single nucleotide polymorphisms (SNPs) in our ancestors is scarce. Here, we present a weighted polygenic risk score (PRS) for ASVCD in human remains based on 87 SNPs in 56 genes that were associated with ASCVD in genome-wide association studies. We analysed ancient human genomes (N=22) of various geographic origins and time periods, including mummies from South America, Australia, Egypt, and Europe. Next-generation sequencing methods were applied, including a novel enrichment approach specifically designed to capture SNPs associated with ASCVD. A correlation of the calculated PRSs to scores obtained from contemporary people shows that the ancient individuals passing all filter steps, cover the complete range of PRSs acquired from modern individuals. Furthermore, their genetic results reflect the phenotypic results, as the only two mummies showing calcified atherosclerotic arterial plaques on computed tomography scans are the ones also exhibiting the highest calculated PRSs. Our study provides further insights into the presence and possible changes of genetic risk factors in our ancestors. Comparing the PRS to the different lifestyles in the past has the potential to lead to a better understanding of the interaction between environmental and genetic influences on the development of ASCVD. In future studies, this could also help to understand the evolution of antagonistic pleiotropy.

ABSTRACT **HD2-003**

Investigating the ecological suicide (“ecocide”) theory in Rapa Nui with ancient DNA data

Speaker: **Bárbara Sousa da Mota**
University of Lausanne, Switzerland

Co-authors: J. Víctor Moreno-Mayar[1], Tom Higham[2], Signe Klemm[1], Moana Gorman Edmunds[3], Francisco Torres Hochstetter[4], Martin Friess[5], Jesper Stenderup[6], Miren Iraeta Orbegozo[6], Diana I. Cruz Dávalos[7], Véronique Laborde[5], Evelyne Heyer[5], Morten E. Allentoft[8], Hannes Schroeder[6], Olivier Delaneau[7], Anna-Sapfo Malaspinas[7]

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Abstract:

Rapa Nui (Easter Island) is a speck of land in the Pacific Ocean, at the easternmost vertex of the Polynesian triangle. Rapa Nui is famous for its stone statues, the moai, and as an example of ecological suicide (“ecocide”). Many believe that the Rapanui cut all trees to sustain their way of living, resulting in famine, war, and population collapse in the 1600s. While it is established that deforestation took place, there is a growing body of evidence against a population collapse before the slave raids in the 1860s.Here, we investigate the “ecocide” theory by analyzing ancient DNA and conducting extensive simulations. To do so, we sequenced and studied the DNA of 15 ancient Rapanui, carbon-dated to the beginning of the 1800’s. We found no close relatives among these and estimated very low amounts of inbreeding. Although a large proportion of their genomes were in runs of homozygosity (ROH), none had ROH longer than 16Mb, suggesting limited inbreeding and a small population. Our reconstruction of the effective population size through time shows that the Rapanui population was small (maximum ~2,000 individuals) and steadily grew after peopling the island. We found no evidence of a second strong bottleneck occurring between peopling and European contact, as postulated by the “ecocide” theory. Altogether, these results add to the existing evidence that the Rapanui history should be considered an example of human resilience and ingenuity in the face of limited resources and environmental changes, as opposed to an example of self-inflicted collapse.

ABSTRACT HD2-004

Optimising sampling and analysis strategies for detecting epidemic-driven selection: a simulation-based tool.

Speaker: **Cindy Gilda Santander**
University of Copenhagen, Denmark

Co-authors: Ida Moltke[1]

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Abstract:

Across the span of history, epidemics have devastated populations across multiple species, such as the cases of Rinderpest in African Cape buffalo (~80% mortality) and the Black Death in humans (~30% mortality). While it seems tempting to hypothesise that at least some of these have led to strong selection on certain genetic variants, few if any clear examples of this exist. This could at least in part be because current selection scan methods are not well powered for the type of selection an epidemic is bound to induce, i.e. very short term selection on standing variation. Here we present a simulation framework that allows you to explore under what circumstances it is possible to detect epidemic-driven selection using multiple standard selection scan methods like FST, joint site frequency spectrum, and iHS. This includes varying what time points you have samples available from and how many samples you have while allowing users to take into account the demographic history of the population under study. We also present an example to illustrate how the framework can be used, emphasising the limitations of current methods, and potential opportunities regarding study design. Our hope is that this framework will help improve future studies of epidemic-driven selection thus improving our understanding of the role that such selection has played in the evolutionary histories of several species.

ABSTRACT HD2-005

Ancient chicken remains reveal the origins of virulence in Marek’s disease virus

Speaker: **Aurélie Manin**
University of Oxford, UK

Co-authors: Steven R. Fiddaman[1], Evangelos A Dimopoulos[1,2], Ophélie Lebrasseur[3,4], Louis du Plessis[5,6], Bram Vrancken[7,8], Sophy Charlton[1,9], Ashleigh F. Haruda[1], Kristina Tabbada[1], Patrik G. Flammer[1], Stefan Dascalu[1], Nemanja Marković[10], Hannah Li[11], Gabriella Franklin[12], Robert Symmons[13], Henriette Baron[14], László Daróczi-Szabó[15], Dilyara N. Shaymuratova[16], Igor V. Askeyev[16], Olivier Putelat[17], Maria Sana[18], Hossein Davoudi[19], Homa Fathi[19], Amir Saed Mucheshi[19], Ali Akbar Vahdati[20], Alison Foster[21], Naomi Sykes[22], Gabrielle Cass Baumberg[1], Jelena Bulatović[23], Arthur O. Askeyev[16], Oleg V. Askeyev[16], Marjan Mashkour[19,24], Oliver G. Pybus[1,25], Venugopal Nair[1,26], Adrian L Smith[1], Greger Larson[1], Laurent A. F. Frantz[27,28]

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Presentation by:
Greger Larson

Abstract:

The dramatic growth in livestock populations since the 1950s has altered the epidemiological and evolutionary trajectory of their associated pathogens. For example, Marek’s disease virus (MDV), which causes lymphoid tumors in chickens, has experienced a marked increase in virulence over the last century. Today, MDV infections kill >90% of unvaccinated birds and controlling it costs >US$1bn annually. By sequencing MDV genomes derived from archaeological chickens, we demonstrate that it has been circulating for at least 1000 years. We functionally tested the Meq oncogene, one of 49 viral genes positively selected in modern strains, demonstrating that ancient MDV was likely incapable of driving tumor formation. Our results demonstrate the power of ancient DNA approaches to trace the molecular basis of virulence in economically relevant pathogens.

ABSTRACT HG1-001

Comparing demographic and cultural histories of Brazilian Sambaqui societies

Speaker: **Cosimo Posth**
University of Tübingen, Germany

Co-authors: Tiago Ferraz[1], Suarez Villagran[1], Kathrin Naegele[2], Tábita Hünemeier[1], André Strauss[1]

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Abstract:

Shellmound societies, also known as Sambaqui societies, are one of the most important archaeological phenomena in pre-colonial South America, existing for around 7,000 years across 3,000 km of the region’s Atlantic coast. Archaeological similarities over hundreds of shellmounds along the Brazilian coastline led to the question whether Sambaqui societies represented a genetically homogeneous population. However, little is known about their genomic diversity and links with inland hunter-gatherer and horticultural groups. Here, we report genome-wide data of 34 ancient individuals spanning the last 10,000 years from eleven archaeological sites in Brazil. We reveal that early Holocene hunter-gatherers from eastern South America did not genetically contribute to subsequent coastal groups. Moreover, contrary to the similarity expressed in the archaeological record, we discover genetic heterogeneity among contemporaneous Sambaqui societies from the southern and southeastern Brazilian coasts. From around 2,000 years ago onwards, we find evidence of genetic contacts with inland horticulturalists, much before the spread of ceramics in the region, albeit corresponding to a previously described cultural shift in Sambaqui societies. This study highlights the importance of more regionally and thematically focused studies, for directly comparing demographic and cultural histories of ancient South American populations.

ABSTRACT HG1-002

Genetic history of the Altai Population 4th-14th centuries

Speaker: **Yusuf Can Özdemir**
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Co-authors: Balázs Gyuris[1,2], Kristóf Jakab[1], Gergely Csiky[1], Tamás Szeniczey[2], Balázs G. Mende[1], Alexey Tishkin[3], Anna Szécsényi-Nagy[1]

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Abstract:

The Altai region of East Eurasia is a mountainous area which separates Western and Eastern steppes but also acts as a crossroads between these two regions. For a long time, the Altai population was ruled by various nomadic polities that had similar military and political structures. The Medieval era of East Eurasia is understudied from population genetics aspects, therefore a novel study has been initiated. We present over 100 genomes from the 4th-14th centuries of the Altai region that shed light on complex population histories of the highly mobile Medieval communities in that area. Preliminary results show that the Medieval period inhabitants of the Altai had a heterogeneous genetic profile, being variously related to ancient and modern North Asian, East Asian and Eurasian steppe populations. The results indicate multiple population movement and admixture events, which happened possibly along the political changes in Central Asia. Bearing high Ancestral North Eurasian ancestry, the Samoyed-affiliated population of the Odintsovo culture was formed by an admixture between their genetically more northern ancestors and the nomadic Bulan-Koby people of the Altai, later assimilating and integrating various other steppe groups. The new data from the Bulan-Koby population, archaeologically connected with the nomadic empires Xiongnu, Xianbei and Rouran, suggest genetic connections with the proposedly Iranian-speaking Saka people. Early Turkic culture developed upon the Bulan-Koby culture in the study area. The data shows that Bronze and Iron Age steppe and East Eurasian precursor populations had genetic influences on later Turkic groups. East Eurasian ancestry increased significantly in the Altai region in the period after the establishment of the Turkic Khaganate. The collapse of the Second Turkic Khaganate heralded new population movements, saw the formation of the Turkic-related Srostki culture and accelerated the Turkification of Samoyedic people of Western Siberia.

ABSTRACT HG1-003

In the pursuit of CNVs in palaeogenomes

Speaker: **Mehmet Somel**
Middle East Technical University, Turkey

Co-authors: Arda Söylev[1], Eren Yüncü[2], Dilek Koptekin[2], Sevim Seda Çokoğlu[2], Mevlüt Köz[2], Dila Nur Çakal[2], Nergis Yasav[2], Utku Gürs[2], Safa Kerem Aydın[2], Mehmet Emre Özkan[2], Elif Dönmez[2], Kanat Gürün[2]

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Abstract:

Estimating copy number variation from low-coverage and short-read-based genomes and using technically heterogeneous data sources is a significant challenge. We recently developed CONGA, an algorithm for genotyping CNV events in low-coverage shotgun paleogenomes. In simulations, CONGA can accurately genotype deletions of size >1kb at down to 0.5x coverage. In actual human ancient genome data, we find that deletion detection can be considerably compromised by technical variation linked to laboratories of origin. We can nevertheless call deletion frequencies with confidence from the majority of shotgun genomes analysed. We show that deletions thus called from Eurasian paleogenomes with at least 0.5x coverage display expected patterns of drift and negative selection. We further investigate two measures for improving CNV detection in ancient DNA: alignment using graph genomes, and multidimensional normalisation approaches to account for inter-library variation in genome-wide coverage distributions, apparently caused by technical factors as well as GC content and chromatin state. Finally, we investigate CONGA-typed deletion loads over time and space in human populations over the last 15,000 years and compare these with SNV mutation loads. Our results highlight the growing potential for evolutionary CNV analyses using paleogenomes, especially as the production of shotgun-sequenced paleogenomes and the publication of raw FASTQ data becomes more widespread.

ABSTRACT HG1-004

Northwest African Neolithic ignited by migrants from Iberia and Levant

Speaker: **Luciana G. Simões**
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Abstract:

In northwestern Africa, lifestyle transitioned from foraging to food-production ~7,400 years ago, but what sparked that change remains unclear. Archaeological data supports conflicting views: that migrant European Neolithic farmers brought the new way of life to North Africa (Linstädter, et al. Quat. Int. 2012), or that local hunter-gatherers adopted technological innovations (Mulazzani, et al. Quat. Int. 2016). The latter is also supported by archaeogenetic data (Fregel, et al. PNAS 2018). Here, we fill key chronological and archaeogenetic gaps for the Maghreb, from Epipalaeolithic to Middle Neolithic, by sequencing the genomes of nine individuals (to between 45.8 and 0.2× genome coverage). Remarkably, we trace 8,000 years of population continuity and isolation from the Upper Palaeolithic via the Epipaleolithic, to some Maghrebi Neolithic farming groups. However, remains from the earliest Neolithic contexts showed mostly European Neolithic ancestry. We suggest that farming was introduced by European migrants and then it was rapidly adopted by local groups. During the Middle Neolithic, a new ancestry from the Levant appears in the Maghreb, potentially associated with the arrival of pastoralism in the region, and all three ancestries blend together during the Late Neolithic. Our results reveal ancestry shifts in the Neolithization of northwestern Africa that likely mirrored a heterogeneous economic and cultural landscape, in a more multifaceted process than observed in other regions.

ABSTRACT HG1-005

The peopling of the Canary Islands

Speaker: **Javier G Serrano**
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Abstract:

The Canary Islands are an archipelago located 100 km from the North African Atlantic coast, initially settled by peoples with cultural, social, and linguistic traits related to Berber communities from the Maghreb. Hence, the analysis of the Canarian indigenous peoples provides both a window into the past of North Africa and a unique model to explore the effects of isolation, migration, and adaptation to a new environment. We have analyzed 50 indigenous samples, including 40 new genomic data from individuals from the seven islands dated between the 3rd and 16th centuries CE. We identify that the Canarian natives show genetic signatures related to Bronze Age expansions in Eurasia and trans-Saharan migrations into North Africa, along with components already present in the Neolithic populations from the Maghreb. The genetic composition of the Canarian natives was not homogeneous, showing the effect of a strong genetic drift process where every island experienced a unique evolutionary path. The lack of gene flow between the islands and the constant or decreasing effective population sizes suggest that populations after the initial settlement were isolated. While some island populations maintained relatively high genetic diversity, with the only detected bottleneck coinciding with the colonization time, other islands with fewer natural resources show a strong effect of isolation. Finally, we detected genetic differentiation between eastern and western islands, reinforcing the idea of a heterogenous colonization process in the archipelago.

ABSTRACT HG2-001

Living on the edge: 5,000 years of human occupation of Portugal

Speaker: **Xavier Roca-Rada**
The Australian National University, Australia

Co-authors: Sofia Tereso[1,2], Ana Maria Silva[1], Vítor Matos[1], Yassine Souilmi[3], Rebecca Anne MacRoberts[4], Anne France Mauer[4], Teresa Fernandes[4], Pedro Carvalho[1], Bastien Llamas[3], João C Teixeira[3]

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Abstract:

The Iberian Peninsula is a geographically isolated region located at the westernmost edge of continental Europe. Iberia is a unique setting to contrast ancient traces of human migration as measured by the flow and arrival of human genes with the structure and stability of local population networks. The importance of Iberia for human evolution was recently evidenced by the discovery of local refugia for hunter gatherer populations during the last glacial maximum. Over the last few years, several ancient DNA studies attempted to uncover large-scale demographic events in the history of the Iberian Peninsula by mostly focusing on Spanish populations. To date, however, only a handful of whole-genome sequences were published for Portugal, a country that covers most of the western Atlantic coast of Iberia. Here, we provide preliminary whole-genome analyses of the largest collection of ancient Portuguese human samples to date, consisting of a total of 90 samples across 18 archaeological sites and spanning a 5,000 year transect, from the Late Neolithic to the contemporary historical period. These newly-generated ancient genomes were sampled from across Portugal and cover several important periods of cultural transition, including the Late Neolithic, the Bronze Age, as well as Roman, Visigoth, Islamic and Christian Medieval periods. By combining archaeological, historical, anthropological and genetic data this transdisciplinary research opens new avenues on human evolution and population dynamics in Iberia over the last 5,000 years.

ABSTRACT HG2-002

Post-Lapita human genomes provide insights on 2,000-years of genetic history in Fiji

Speaker: **Michal Feldman**

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Co-authors: Rita Radzeviciute[1], Selina Carlhoff[1], Kathrin Naegele[1], Elia Nakoro[2], David V. Burley[3], Patrick D. Nunn[4], Simon Best[5], Sepeti Matararaba[2], Hallie R. Buckley[6], Rebecca L. Kinaston[7], Adam Powell[1], Johannes Krause[1], Cosimo Posth[8]

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Abstract:

Landmass between Vanuatu and Polynesia and its cultural and linguistic diversity, make it a key region for understanding the settlement history of Remote Oceania. Present-day Fijians derive the largest single portion of their gene pool from a Papuan-related ancestry, but the source of this ancestry and the timing of its arrival are poorly understood. While previous ancient genomic studies have successfully addressed such questions in other Oceanian regions, no ancient Fijian genomes have been sequenced to date. Here we report human genomic data, spanning the last two millennia, obtained from skeletal remains of 45 individuals excavated in western Fiji. These data revealed that Papuan-related ancestry reached Fiji in at least two distinct waves, genetically dated to circa 2,000 and 1,200 years before present, respectively. Interestingly, the earlier wave was centuries later than the first evidence of Papuan-related ancestry in Vanuatu, suggesting a slower expansion process compared to the initial, Lapita-associated one. In addition, we find that the earlier Papuan-related gene flow stemmed from a population with higher genetic diversity whereas the later one was likely contributed by a bottle-necked group. Both admixture pulses were sex-biased with a substantially higher male contribution of Papuan-related ancestry, as previously observed for other Pacific regions. Finally, we integrated estimations of genetic sex, genealogy and consanguinity, with archaeological information from our most sampled archeological site to address local aspects of social structure and funerary practices. Our results provide new insights into post-Lapita genomic transformations in Remote Oceania as well as a zoomed-in perspective on the socio-cultural organization of past Fijian societies.

ABSTRACT HG2-003

Inferring IBD segments in ancient DNA - What next?

Speaker: **Harald Ringbauer**

Max Planck Institute for Evolutionary Anthropology, Germany

Co-authors: Yilei Huang[1], Shai Carmi[2]

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Abstract:

Recently developed methods can robustly identify long identical DNA sequences shared between pairs of ancient humans. These segments provide an ideal genomic signal for studying recent genealogical connections, as they must be co-inherited from a recent common ancestor, with recombination pruning the segments and thus acting as a rapid clock. Population genetic studies based on IBD segments have inferred the recent demographic history of present-day populations, including population size dynamics and geographic mobility. With the growing availability of aDNA samples, the study of IBD segments in ancient humans can offer an equally powerful opportunity to investigate past demography. To realize this potential, we present new computational tools designed to make demographic inferences from IBD segments in time-stratified aDNA data, allowing us to estimate population size dynamics, cross-coalescence rates between ancient groups, and geographic mobility patterns. We showcase the utility of our tools through a series of example applications to ancient DNA data. For instance, we infer that a strong population bottleneck occurred in early Bronze Age Western Eurasia, followed by rapidly growing effective population sizes. Moreover, we infer the intensities and time depths of genetic connections between various important ancient Bronze Age cultural groups such as Yamnaya, Corded Ware, and Bell Beakers. Our findings demonstrate that our tools can generate new demographic insights into human population history.

ABSTRACT HG2-004

A test of pretreatment and DNA extraction methods for uncovering endogenous content in Neolithic human remains from the Near East

Speaker: **Kelly Blevins**
Durham University, UK

Co-authors: Jo-Hannah Plug[1], Jessica Pearson[1], Miquel Molist[2], Anna Bach[2], Eva Fernández Domínguez[1]

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Abstract:

The Near East was a critical region where major human subsistence and behavioral changes emerged 10,0000 years ago, such as the adoption of sedentary lifestyles and development of agriculture. Ancient DNA (aDNA) studies offer high-resolution insights into how this major inflection point in human history affected social organization through the analysis of individuals from intra-site mortuary contexts. The Near East, however, is characterized by alternating dry, hot, and wet seasons, which are suboptimal for DNA preservation, resulting in low aDNA recovery rates, often below 20%. In standard genomic workflows, aDNA libraries undergo a shallow shotgun sequencing run to assess the presence of authentic endogenous DNA prior to target enrichment. Poorly preserved samples that fall below an acceptable screening threshold are discarded and remain unused in labs. To improve detection of endogenous content by reducing the exogenous signal, we compared three DNA extraction methods to the standard Dabney et al. 2013 extraction protocol using pars petrosa samples from five individuals from Tell Halula, a pre-pottery Neolithic B site in the Middle Euphrates, Syria (7550 BCE) that had previously not met the threshold for target enrichment. We employed a combination of pre-treatment wash, varying lengths of demineralization and digestion, and treatment with surfactants and reducing agents. All extracts (n = 20) were built into double stranded libraries and sequenced to approximately five million reads. We found that a pre-treatment wash with two overnight demineralization and digestion incubations at different temperatures results in a two-fold increase in endogenous human DNA content. In research groups where data generation is financially constrained and for projects in geographic regions where DNA preservation is poor, these low-cost modifications during DNA extraction can significantly increase project success rate by allowing for informed sample selection for enrichment.

ABSTRACT HG2-005

Genomes from Pastoral Neolithic Sahara reveal ancestral north African lineage

Speaker: **Nada Salem**
Max Planck Institute for Evolutionary Anthropology, Germany

Co-authors: Marieke van de Loosdrecht[1,2], Arev Pelin Sümer[1], Stefania Vai[3], Alexander Hübner[1], Kay Prüfer[1], Raffaela Bianco[1], Marta Burri[4], Mary Anne Tafuri[5], Giorgio Manzi[5], Harald Ringbauer[1], David Caramelli[3], Savino di Lernia[5,6], Johannes Krause[1]

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Abstract:

Known as one of the most arid areas on the planet today, the Sahara Desert was, in fact, a green savannah in the Holocene, dotted by forests and water bodies that promoted human occupation and fostered pastoralism. Due to the present-day climatic conditions, ancient DNA does not preserve well in the region, resulting in limited knowledge of the Sahara’s demographic past. Here, we report the first ancient human genome-wide data from the Saharan Pastoral Neolithic. We obtained genomic data from two ca. 7000-year-old female pastoralists buried in the Takarkori rock shelter at the heart of the Tadrart Acacus massif in southwestern Libya, which was used as a burial ground by pastoral communities. We find that the majority of the Takarkori individuals’ ancestry stems from a previously unknown lineage that appears to have remained isolated for most of its existence. Both individuals are most closely related to the preceding 15,000-year-old foragers from Morocco associated with the Iberomaurusian techno-complex, whereas both Takarkori and Iberomaurusian individuals are distantly related to sub-Saharan African lineages. The quality of one of the genomes from Takarkori is sufficient to detect prospective Neandertal ancestry and we find evidence for few segments of ancestry that sum to a total comparable to that detected in the genomes of sub-Saharan Africans. Our results therefore support a model of cultural diffusion, rather than human migration, for the emergence of pastoralist subsistence in the Sahara region.

ABSTRACT KSS-001

Ancient DNA-based large pedigrees and haplotype-IBD networks provide unprecedented insights into the social structure of steppe descent Avar period communities

Speaker: **Guido Alberto Gnecchi-Ruscone**
Max Planck Institute for Evolutionary Anthropology, Germany

Co-authors: Zsófia Rácz[1], Levente Samu[1], Tamás Szeniczey[1], Luca Traverso[2], Tivadar Vida[1,3], Johannes Krause[2], Zuzana Hofmanová[2,4]

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Abstract:

Recent archaeogenomic studies showed that during the Avar Khaganate (6th to 9th centuries CE) there was an influx of people from the Eurasian Steppe, that settled in the Carpathian Basin for the ~250 years of Avar dominion in the region. These people and their descendants carried varying mixtures of ancestries components found in the preceding or contemporary populations from across the Eastern to the Western Eurasian steppe and coexisted with people carrying European ancestries traceable to pre-Avar local populations. Here we analyzed four complete Avar period cemeteries with archeological contexts associated to these steppe communities located in present day Hungary. We were able to obtain genome-wide high-quality data for 424 individuals across these four sites. We found that the majority of the individuals were first or second degree related to someone else within each site. This allowed us to reconstruct large pedigrees, the largest being composed of 146 individuals spanning up to 9 generations and ~250 years. These pedigrees reveal a very strict patrilineal descent system consistent with strong pattern of patrilocality and female exogamy. We also identified cases of levirate unions, i.e. closely related males having offspring with the same female, and a high number of multiple partners, some possibly traceable to polygamic practices. Together with a complete absence of consanguinity these features inform us that biological relationship was known and unions between relatives was intentionally avoided. There were no close relatives between sites but we found a large number of haplotype-IBD shared between the four and other Avar period sites revealing more distant relatedness. The reconstruction of networks of IBDs allowed us to infer relations between communities as well as detected patterns linked to genetic differences and possibly to differences in social status.

ABSTRACT KSS-002

An Outbreak of the Stone Age Plague in a Large Extended Family

Speaker: **Frederik Seersholm**
University of Copenhagen, Denmark

Co-authors: Karl-Göran Sjögren[1], Julia Koelman[2], Emma M. Svensson[2], Jacqueline Staring[3], Thomaz Pinotti[4], Tony Axelsson[1], Torbjörn Ahlström[5], Kristian Kristiansen[4], Mattias Jakobsson[2], Helena Malmström[2], Martin Sikora[4]

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Abstract:

In Northern Europe, the period between 5,300 and 4,900 BP is characterized by decreasing population sizes, and is often termed the Neolithic decline. The cause of this population collapse is still widely debated, and several factors have been put forward as possible explanations, including the spread of an early variant of Yersinia pestis, the etiologic agent of the plague. Here we analyse ancient DNA from 112 Scandinavian individuals from the period immediately before and during the Neolithic decline. We correlate biological relations within multiple megalithic graves, with patterns of pairwise IBD sharing and genetic reconstructions of the most common human pathogens detected. We reconstruct three large pedigrees, the largest of which consists of 23 individuals spanning five generations. Furthermore, we find that Yersinia pestis was surprisingly abundant in the population, detected in 19% of all individuals analysed, and present in all three extended families. Taken together, our findings suggest the presence of widespread ancient plague epidemic at the Neolithic decline spanning a wide geographical area from Zealand, Denmark to north of Gothenburg in Sweden.

ABSTRACT KSS-003

The Genetic Legacy of African Americans from Catoctin Furnace

Speaker: Éadaoin Harney

23andMe, Inc., USA; Harvard University, USA

Co-authors: Steven Micheletti[1], Karin S. Bruwelheide[2], William A. Freyman[1], Katarzyna Bryc[1], Ali Akbari[2,4], Ethan Jewett[1], Elizabeth Comer[5], Henry Louis Gates Jr.[3], Linda Heywood[6], John Thornton[6], Roslyn Curry[1,3], Samantha Ancona Esselmann[1], Kathryn G. Barca[2], Jakob Sedig[3,4], Kendra Sirak[3,4], Iñigo Olalde[4,7], Nicole Adamski[4], Rebecca Bernardos[4], Nasreen Broomandkhoshbacht[4], Matthew Ferry[4], Lijun Qiu[4], Kristin Stewardson[4], J. Noah Workman[4], Fatma Zalzala[4], Shop Mallick[4,8], Adam Micco[4,8], Matthew Mah[4,8], Zhao Zhang[4], 23andMe Research Team[1], Nadin Rohland[4], Joanna Mountain[1], Douglas W. Owsley[2], David Reich[2,4,8]

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Abstract:

Few African Americans can trace their family histories to their earliest enslaved African ancestors in the United States. Genetic analysis of historical individuals and identification of present-day close relatives has the potential to restore this knowledge. We analyze 27 individuals buried in Maryland's Catoctin Furnace African American Cemetery during the 18th–19th centuries, and identify identical by descent DNA segments documenting 41,799 relatives among consenting research participants in 23andMe, Inc.'s genetic database of ~12.8 million people. One of the largest geographic concentrations of close relatives is in Maryland, revealing that some descendants of the enslaved and free African Americans at Catoctin Furnace stayed in the area after records indicate their removal from the ironworks, a finding not demonstrable through genealogical analysis alone. We show that many Catoctin individuals likely derived their ancestry from a small number of African groups, specifically the Wolof and Kongo, and that some carried risk factors for Sickle Cell anemia and G6PD deficiency, genetic diseases common in African Americans today. These analyses provide the first direct look at the genome-wide genetic ancestry of enslaved people in the United States, and demonstrate the power of joint analysis of DNA from historical individuals and the extremely large datasets generated through direct-to-consumer ancestry testing.

ABSTRACT KSS-004

Ancient DNA and kinship analysis at the Iron Age cemetery of Wetwang Slack, East Yorkshire, UK

Speaker: **Ian Armit**
University of York, UK

Co-authors: Lindsey Büster[1,2], Claire-Elise Fischer[1], Iñigo Olalde[3], Tom Booth[4], David Reich[5]

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Abstract:

Wetwang Slack is the largest excavated Iron Age cemetery in Britain, containing around 450 inhumations, mostly buried under small square barrows. It belongs to the so-called 'Arras Culture' of East Yorkshire which is well-known for its dense distribution of inhumation cemeteries (highly unusual in a British context) and occasional chariot burials that share characteristics with La Tène rites in parts of Continental Europe. As part of the ERC-funded COMMIOS project (https://commiosarchaeology.com/) we conducted genome-wide ancient DNA analysis of several hundred individuals within the Wetwang Slack cemetery, including three chariot burials. Our results indicate that many individuals from the cemetery are close biological relatives. One pedigree, for example, contains seven generations of a 'family' group which appears to show descent through the female line, with a marked predominance of mother-daughter relationships indicative of matrilocal marriage patterns. Evidence from mitochondrial DNA further suggests repeated inter-marriage between two descent groups. Our results are especially interesting in relation to wider evidence for female power in the region, exemplified by the numerical dominance of female burial, the repeated occurrence of rich female chariot burials, and later literary references to female rulers in northern and eastern Britain. Despite the evident patterning in the data, however, there is a degree of variability that demonstrates the complexity and 'messiness' of kinship practice as it was played out within a living community. Biological relatedness cannot be straightforwardly equated with kinship, and we must consider various forms of social institution, such as adoption and fosterage, particularly in societies where many died young leaving parentless children. This paper examines the aDNA results from the Wetwang Slack cemetery and considers their implications for the interpretation of kinship structure and practice in this Iron Age community.

ABSTRACT KSS-005

Investigating the population history of present-day Georgia using diachronic archaeogenomic data

Speaker: Eirini Skourtanioti

Max Planck Institute for Evolutionary Anthropology, Germany

Co-authors: Xiaowen Jia[1], Nino Tavartkiladze[2], Angela Mötsch[1], Raffaela Angelina Bianco[1], Nikoloz Tushabramishvili[3], Ramaz Shengelia[4], Liana Bitadze[2], Sturla Ellingvåg[5], Philipp W. Stockhammer[1], Johannes Krause[1], Harald Ringbauer[1]

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Abstract:

The South Caucasus was a hub of cultural innovations within West Eurasia throughout prehistory, with a lot of interest placed on its population history from the Early Holocene to the Bronze Age. However, in the following historical periods starting around 1000 BCE, significant societal changes led to language diversification and the formation of the first states of Colchis and Iberia kingdoms in the region of present-day Georgia. Throughout this period, foreign contacts through the Greek colonies established on the Black Sea, the Persian Median empire, and the early Christianization of Iberia have been suggested. Later, during the migration period of the Early Middle Ages, the presence of various groups from Inner Asia and East Europe is attested, e.g. by the occurrence of artificial skull elongations. To understand how various modes of gene flow shaped the population of present-day Georgia, we generated aDNA from 200 individuals spanning the Early Bronze to the Early Middle Ages. With this dense archaeogenetic dataset from the historical Caucasus, we document a remarkably high degree of genetic continuity throughout more than three millennia. However, from the early Christianization period of the Iberia kingdom to the migration period, we identify gene flow from Anatolia and the presence of individuals of Central Asian origin. Artificially elongated skulls in their majority belonged to individuals of local ancestry, corroborating to a cultural practice often carried genealogically and through imitation from Central Asian ethnic groups. In addition, by estimating the sharing of identical-by-descent segments, we establish higher levels of biological relatedness among individuals from rural areas buried a few kilometers apart, compared to large urban centers like Samtavro, close to the capital of Iberia kingdom. Thereby, this study showcases how fine-scale population dynamics inferred archaogenetically can contribute new insights to well-studied historical contexts.

ABSTRACT MET-001

euka - Robust characterisation of eukaryotic taxa from sedimentary ancient DNA with pangenome graphs

Speaker: **Nicola Alexandra Vogel**
Technical University of Denmark

Co-authors: Joshua Daniel Rubin[1], Mikkel Swartz[1], Juliette Vlieghe[1], Peter Wad Sackett[1], Anders Gorm Pedersen[1], Mikkel Winther Pedersen[2], Gabriel Renaud[1]

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Abstract:

Sedimentary ancient DNA (sedaDNA) has opened a new way of understanding past environments and studying ancient populations. However, sedaDNA samples are difficult to analyse due to their ancient DNA characteristics as well as problems arising from environmental DNA, including the correct identification of eukaryotic taxa and their respective abundances. Current sedaDNA methods focus on the alignment against reference genomes and taxonomic binning. Only a few methods provide additional analysis on abundance estimations. However, they are slow and imprecise.We present euka, a tool to robustly and rapidly identify tetrapodic and arthropodic taxa in sedaDNA samples. We use a taxa-based mitochondrial pangenome graph for mapping and an ancient-aware maximum-likelihood framework to evaluate the alignments. Combined with our test for a minimum breadth of coverage, we could minimise the effects of spurious alignments and provide accurate abundance estimation of detected taxonomic groups.euka exceeds current methods in detecting taxonomic groups and estimating their abundances. On simulated data, we outperform existing methods in accurate taxa detection, regardless of the filtering set. Notably, euka is more robust to to-low-abundance data, common in sedaDNA analysis, compared to other methods. We have also demonstrated that euka produces results consistent with competing tools when tested on empirical data. Additionally, euka is about ten times faster than existing quantification tools. euka has been built to deal with the unique challenges of sedaDNA samples, providing a streamlined and efficient alternative to existing methods.

ABSTRACT MET-002

Investigation of protein degradation using LC-MS/MS, MALDI-MS, and Amino Acid Racemization: A case study with Beta-lactoglobulin

Speaker: Bharath Anila Bhuvanendran Nair

University of Copenhagen, Denmark

Co-authors: Meaghan Mackie[1], Tina Ravnsborg[2], Samantha Presslee[3], Alberto Taurozzi[4], Kirsty Penkman[5], Jesper V. Olsen[4], Ole Nørregaard Jensen[2], Carsten Wiuf[4], Matthew Collins[4,6]

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Abstract:

Palaeoproteomics, the study of ancient proteins, lies at the interface between molecular biology, archaeology, biochemistry, palaeontology, and history and aims to recover sufficient sequence information to identify the source proteins. Many proteins, such as -lactoglobulin (BLG), are source-specific but show variation between species and can therefore be used to explore questions as diverse as diet and evolution. Unfortunately, many of the most recovered proteins (such as milk proteins) are also found in lists of common laboratory contaminants. This is compounded by a lack of approved standards for the authentication of ancient proteomes. Over time, long-lived proteins undergo alteration in their chemical composition due to diagenesis. Therefore, it is essential to study the diagenetic pathways and patterns of ancient proteins to discriminate authentically old proteins from modern contaminants. Herein, we explored the degradation patterns of the model protein BLG underacidic (pH 3), basic (pH 11), and neutral (pH 7) conditions for 128 days. We characterised the thermal degradation products of BLG using liquid chromatography-tandem mass spectrometry (LC-MS/MS) and reverse phase-high performance liquid chromatography (RP-HPLC). We propose a new model to estimate the kinetic parameters of peptide bond hydrolysis using the LC-MS/MS data. We also investigated the extent of amino acid racemization using RP-HPLC data. It is shown that high-temperature kinetic experiments can accelerate diagenesis, and analysing degradation products at various time points using mass-spectrometry-based proteomics and amino acid racemization can advance our understanding of protein/peptide degradation. This talk reports our findings on protein degradation pathways and patterns within BLG as a model system.

ABSTRACT MET-003

Using ancient and modern DNA from relatives to reconstruct a missing genome

Speaker: **Théo Cavinato**
University of Lausanne, Switzerland

Co-authors: Simone Rubinacci[1], Olivier Delaneau[1], Anna-Sapfo Malaspinas[1]

[1] University of Lausanne, Switzerland

Abstract:

Inference of the genetic kinship between individuals from an archeological site allows pedigree reconstruction and improves our knowledge on past social structures. However, the genomes of several pedigree members are often unavailable, limiting the applicability of current kinship-based methods in this context. We developed a method that relies on the available genetic information and the pedigree to reconstruct the genotypes of a missing parent. Our approach relies on Mendelian rules and IBD sharing between relatives to reconstruct the missing genotypes. We implement our method for the case where the genomes of one parent and its children are available while the other parent could not be sequenced. We assess the accuracy of our approach on simulated data and show that we can reconstruct more than half of the missing genomes under some conditions. We then use our reconstructions to refine pedigree inference with other family members. Furthermore, we quantify how features specific to ancient DNA such as low coverage and DNA damages can impact our approach. Finally, we apply our method to mass grave data and discuss cases where we can widen the pedigree reconstruction.

ABSTRACT MET-004

Extensive diversity of unnamed Anaerolineaceae taxa in ancient dental calculus revealed through de novo genome assembly

Speaker: **Irina M. Velsko**
Max Planck Institute for Evolutionary Anthropology, Germany

Co-authors: Alexander Hübner[1], Christina Warinner[2]

[1] Max Planck Institute for Evolutionary Anthropology, Germany
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Abstract:

The bacterium Anaerolineaceae bacterium oral taxon 439 (Abot439) is highly abundant in ancient dental calculus. This organism is difficult to culture and study in vitro, and only a single reference genome has been published to date. Therefore little is known about the diversity of this organism in dental biofilms, or about its physiology or evolutionary history. Phylogenetic reconstructions of this species recovered by mapping ancient calculus against its reference genome suggest geographic structuring, yet high SNP heterogeneity indicates the presence of multiple strains or closely related species in many samples, possibly confounding phylogenetic reconstructions. We assembled 261 medium- and high-quality metagenome-assembled genomes (MAGs) annotated as Abot439 from 222 ancient and 9 modern dental calculus samples, and performed analyses to explore the genomic diversity in this species through space and time. Genomic clustering grouped the MAGs into 10 distinct species encompassing 73 unique strains, and the majority of MAGs (200/262, 76%) fell in a single species clade along with the reference genome. Mapping ancient dental calculus samples against representative genomes of these species identified substantial heterogeneity in the presence and abundance of these organisms, which until now has been undetected due to a lack of representation in genome databases. A strain assembled from a sample from Ethiopia and dated to ~4500 BP was ubiquitous and abundant across all ancient calculus samples, while other strains were found only in a handful of samples. Here we show the utility of bacterial genome reconstruction from ancient dental calculus to reveal as-yet undescribed taxa, improve species diversity estimates, clarify phylogenetic reconstruction, and perform genomic analysis of otherwise difficult-to-study microorganisms.

ABSTRACT MET-005

Imputation of ancient dog genomes informs on their inbreeding history since the onset of domestication

Speaker: **Katia Bougiouri**
University of Copenhagen, Denmark

Co-authors: Evan K. Irving-Pease[1], Alberto Carmagnini[2,3], Tatiana R. Feuerborn[4], Sophy Charlton[3], Heidi Parker[4], Alex Harris[4], Greger Larson[5], Shyam Gopalakrishnan[1], Elaine A. Ostrander[4], Laurent Frantz[2,3], Fernando Racimo[1]

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Abstract:

As the first domesticated species, dogs have been a popular study system for population genetics, addressing questions related to domestication, admixture, selection, and parallel evolution with humans. While ancient DNA (aDNA) has provided a unique resource to elucidate these processes, the low quality inherent to it still restricts the questions that can be confidently approached using this resource. To circumvent this issue, we implemented a novel imputation pipeline utilising a large canid reference panel. We benchmarked the method’s accuracy by comparing the concordance between down-sampled imputed samples with their high coverage counterparts, as well as assessing the imputation’s impact on principal component analyses (PCA) and runs of homozygosity (ROH). Our results showed that we can confidently impute samples as low as 0.5x. In addition, imputation showed no significant bias when assessing the placement of down-sampled imputed samples relative to the high coverage ones in PC space. Based on these results, we then imputed a worldwide dataset of more than 100 ancient dogs and wolves and further assessed inbreeding patterns in the form of ROHs over space and time. Ancient populations showed various inbreeding patterns specific to geographic location and time periods, with most significant temporal changes observed in Europe. Overall, the imputation of ancient dog genomes constitutes a promising approach into the study of dog evolution by permitting the application of methods, previously confined to high quality datasets.

ABSTRACT NOV-001

Community signatures of past human lifestyles are preserved within faecal concretions

Speaker: **Eleanor Green**
University of York, UK

Co-authors: Sam Presslee[1], Jessica Hendy[1], Helen Whelton[2], Lara González Carretero[1], Camilla Speller[3], Nathan Wales[1]

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[3] University of British Columbia, Canada

Abstract:

Faecal concretions are amorphous masses of cemented material which, under favourable conditions, form via phosphatization in cesspits. Their potential biomolecular content is most similar to archaeological sediment. In this project, faecal concretions from Coppergate, York, UK, were analysed using a range of bioarchaeological techniques, including archaeogenetics, palaeoproteomics, lipidomics and microscopy. Results from ancient metagenomic analysis demonstrate that these samples contain a plethora of ancient DNA relating to the human diet, human waste and the local environment. Unlike coprolites (distinct faecal samples), the concretions give a mixed host DNA signature. Nevertheless, we hypothesised that these samples were likely to be human-derived given that they were found in formal waste pits. We performed a hybridization capture of 1240k SNPs, resulting in six of the ten concretions covering over 10,000 SNP positions. Palaeoproteomic analysis using LC-MS/MS yielded a low number of peptides, whereas RP-HPLC analyses revealed a high concentration of bound amino acids in these samples, alluding to some peptide survival. Characterisation of the concretions using lipidomics reflects the mixed signature in the metagenomic results, although viewing these two analyses together is a beneficial way of determining the majority contributor to a sample. Microscopic investigations have revealed evidence of cereal and fruits embedded within the concretions. Again, comparisons of microscopic and metagenomic data provide unexpected insights into ancient DNA authentication methodologies. With further development, the analysis of concreted masses could present a new bioarchaeological opportunity to assess human health, subsistence and environment at a community level.

ABSTRACT NOV-002

New spatiotemporal tools for the meta-analysis of stable isotope measurements from organic tissue

Speaker: **Rowan McLaughlin**
Maynooth University, Ireland

Co-authors:

Abstract:

This paper introduces a set of free and open-source backwards modelling tools for inferring patterns in datasets of measurements of stable isotopes. The particular focus is on measurements taken from archaeological samples of organic tissue, especially bone collagen. Like much archaeological data, stable isotope measurements are often associated with considerable chronological uncertainty, even for those samples directly associated with radiocarbon measurements. This makes it difficult to detect or model any diachronic trends inherent to these data. Through the application of Monte Carlo simulation and Bayesian modelling, here I introduce timeseries and spatial methods for exploring emergent patterns in ensembles of hundreds or thousands of individual stable isotope measurements from a given region. In a case study from Ireland, the application of these new methods has revealed significant spatial and temporal patterns in stable carbon and nitrogen isotope data, which can be interpreted in terms of the the changing inter-relationships between human economic practices, demography or settlement density, soil evolution, and cultural change. These analysis revel how 'big' datasets of isotopic measurements can generate new insight into the human relationship with the physical environment, and address predictions about changing intensities of resource use made via the meta-analysis of other strands of archaeological data.

ABSTRACT NOV-003

Palaeoproteomic approaches for identifying avian remains from archaeological sites: current potential and future possibilities

Speaker: **Maria Codlin**
University of Turin, Italy

Co-authors: Josefin Stiller[1], Lisa Yeomans[1], Beatrice Demarchi[2]

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[2] University of Turin, Italy

Abstract:

The avifauna recovered from archaeological contexts can speak to a wide range of research interests, including subsistence and animal management, aesthetic and ritual activities, long distance trade and reconstruction of local environmental characteristics. Yet human-bird interactions are underexplored in archaeology, often due to the difficulties in recovering small and fragmentary remains, as well as the limited accessibility of specialists and avifauna collections for identification. Palaeoproteomics has great promise for improving taxonomic identification of avian eggshell and bone, particularly when applied to fragmentary and morphologically unidentifiable remains. Recent research has demonstrated the utility of palaeoproteomic techniques for identifying avifauna from archaeological sites, including proteins within the mineral matrix of eggshells which can survive into deep time, far longer than proteins can survive within animal bones. We present new research from the ArchaeoBiomics laboratory at the University of Turin, Italy, where we are refining the methodologies to extract proteins from avian eggshell and expanding reference libraries to improve the taxonomic resolution for identification of both bone and eggshell. Drawing on the data from these reference collections and annotated proteins from newly sequenced genomes from the Bird 10K Genomes Project (B10K), we discuss the theoretical possibilities and limitations of palaeoproteomic techniques to identify avian remains. We consider the practical implications of this research within the context of environmental reconstruction during the late pleistocene to holocene transition in northeastern Jordan. We predict that in the coming years, palaeoproteomic approaches to avifauna will invigorate interest in human-bird relationships, and encourage the adoption of avifauna as a proxy to reconstruct local environmental conditions.

ABSTRACT NOV-004

Cleaning the Dead: Decontamination of skeletal elements for palaeoproteomics

Speaker: **Zandra Fagernäs**
University of Copenhagen, Denmark

Co-authors: Gaudry Troché[1], Frido Welker[1]

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Abstract:

Reliable data forms the base of any robust biomolecular study. However, over time, biomolecules in archaeological materials get increasingly overpowered by contaminants, stemming from sources such as the burial environment, excavation, handling, and storage. Contaminants may impact downstream analyses both by masking endogenous biomolecules, due to their sheer amount and more intact state, and by introducing modern sequence variation into the analysed material. In palaeoproteomics, a range of decontamination methods have been used prior to protein extraction, but thus far no studies have compared their efficiencies, or quantified the impact they have on the already fragmented and damaged endogenous proteome. Here, we compare five commonly used methods for decontamination in palaeoproteomics: UV irradiation, bleach, EDTA, HCl, and water. The comparison is conducted on Pleistocene herbivore skeletal elements, which have been artificially contaminated by a modern dog saliva proteome. This approach ensures that endogenous and contaminating proteins can be separated bioinformatically, and the efficiency of each method can thereby be measured. The extracted proteins are analysed through LC-MS/MS, and proteome size and composition, protein coverage, and post-translational modifications are quantified. The results show that there are significant differences between the tested methods in the amount of contaminating proteins that are removed. The tested decontamination methods also cause different amounts of damage to the endogenous proteins. Our study thus clearly indicates the necessity of carefully evaluating each method when aiming for maximising the fraction of endogenous proteins available for analysis. This study is the first of its kind and highlights the importance of carefully assessing laboratory processing of archaeological skeletal material prior to the retrieval of ancient proteins.

ABSTRACT NOV-005

Reconstruction of Middle and Late Paleolithic metagenomes to access natural products

Speaker: **Alexander Hübner**
Max Planck Institute for Evolutionary Anthropology, Germany

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Abstract:

Microbial genomes contain a large repertoire of biosynthesis pathways to produce natural products, but their adaptation to ever changing environments can lead to a change or a loss of the genes comprising these pathways over time. Studying changes in the diversity of biosynthetic pathways by analyzing the genes of a large number of present-day microorganisms is limited because this approach cannot recover gene diversity that has been completely lost. However, archaeological remains, e.g. ancient dental calculus, provide snapshots of past microbial diversity over time. To investigate the diversity of biosynthesis pathways in the past, we de novo assembled deeply sequenced metagenomic data obtained from dental calculus samples of 52 anatomically modern humans (ca. 30 ky ago to present-day) and 12 Neanderthals (ca. 102 ky ago to 40 ky ago) and non-reference binned the resulting contigs. Despite short DNA molecule lengths, we were able to obtain 25 nearly complete high-quality metagenome-assembled genomes (MAGs) and 110 medium-quality MAGs. The majority of these MAGs showed evidence for the presence of ancient DNA damage and most were taxonomically classified as members of the oral microbiome. One well-preserved MAG was taxonomically classified as a close relative of the green-sulfur bacterium Chlorobium, and it formed a monophyletic clade with seven other genomes recovered from Middle and Late Paleolithic samples across western Eurasia and northern Africa. In silico analysis of this MAG led to the identification of a conserved biosynthetic gene cluster across all members of this clade. Synthesis and heterologous expression of the key biosynthetic genes of this ancient cluster in a host chassis resulted in the successful production of a previously undescribed natural product. This recovery of a novel natural product from a reconstructed pathway demonstrates that ancient DNA samples can be successfully used to study the past diversity of microbial biosynthetic pathways.

ABSTRACT ODA-001

Advances in amino acid dating of mammalian tooth enamel: testing for endogeneity, and the effects of taxonomy and taphonomic alteration

Speaker: **Marc Dickinson**
University of York, UK

Co-authors: Laila Patinglag[1], Kirsty Shaw[1], Kirsty Penkman[2]

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Abstract:

Directly dating mammalian remains is difficult beyond the limits of radiocarbon dating (~50 ka). One possible direct dating method is to use the predictable breakdown of proteins and amino acids in biominerals that contain closed-system protein. This has been a powerful tool for Pleistocene age estimation in calcium carbonate biominerals (back to ~2.5 Ma), but the application of this technique to mammalian remains has been challenging. Our novel method targets a proteinaceous fraction in enamel protected within the biomineral crystals (the intra-crystalline fraction), which has alleviated difficulties associated with contamination, leaching and environmental influences. Elephantid enamel has been used to assess the correlation between the extent of intra-crystalline protein degradation (IcPD) against known age material from the British Isles, the East European Plain and the Mediterranean, showing a strong correlation between IcPD and age. These frameworks can now be used to provide direct age estimates for unknown age elephantid material from these regions. We have also begun to expand our amino acid dating frameworks to other species (e.g. equids and bovids), allowing us to test the influence of taxonomy on the rates of amino acid breakdown and to apply the method to more regions (e.g. southern Africa). To better understand the mechanisms of amino acid preservation, we have used a combination of high-resolution imaging techniques and elemental analysis to identify changes to the inorganic structure of enamel. This allows us to identify enamel (or regions of enamel) that has undergone mineralogical changes which might influence the preservation of endogenous organics. We are also developing a new microfluidics technique that will hopefully greatly reduce the masses of samples required from ~30 mg to ~1 mg and to ultimately enable IcPD dating to be undertaken outside specialist labs.

ABSTRACT ODA-002

The collagen, the whole collagen, and nothing but the collagen: testing alternative extraction protocols for dating large numbers of poorly preserved mid-Holocene bones at Vráble, Slovakia

Speaker: **John Meadows**
Centre for Baltic and Scandinavian Archaeology, Germany

Co-authors: Christian Hamann[1], Brendan Culleton[2], Ivan Cheben[3], Martin Furholt[1]

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[2] Penn State University, USA
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Abstract:

Recent fieldwork at Linearbandkeramik settlements at Vráble, Slovakia resulted in >100 plausible 14C ages on filtered bulk collagen from human and animal bones, but collagen yields were often poor, and lower-yielding bones often gave younger ages (Meadows, et al. The Holocene 2019). The discovery in 2022 of a mass grave with dozens of headless skeletons provoked a reassessment of the current site narrative, which relies on animal bone 14C ages to argue that domestic occupation continued for up to a century after a handful of headless burials previously dated to c.5050 BC (Müller-Scheeßel, et al. Antiquity 2021). We wish to find a practical but rigorous approach to dating bones on this site, and to validate or replace the current site narrative. We re-dated a set of bones which gave a wide range of bulk collagen yields and 14C ages in the earlier dating programme, using three different protocols on each bone: 1. ultra-filtration of gelatinised bulk collagen (retains long-chain gelatin molecules) 2. ninhydrin extraction of gelatinised bulk collagen (retains amino-acid carboxyl groups) 3. chromatography through XAD resin of hydrolysed bulk collagen (retains bulk amino acids) All three methods are more readily implemented than hydroxyproline isolation by preparatory HPLC, the best-known compound-specific technique. Method 1 is cheap, widely used and permits EA-IRMS to confirm that collagen is suitable for dating, but produces more failures when collagen is degraded, and may retain contaminants binding degraded collagen into long chains. Method 2 is relatively straightforward, but only selects ~25% of the carbon in collagen, which is extracted as CO2 and is unsuitable for EA-IRMS. Method 3 is more laborious and difficult to apply at scale, but limits the loss of material while allowing EA-IRMS. We compare the results and recommend a strategy for 14C dating at sites like Vráble.

ABSTRACT ODA-003

Towards predicting the geographical origin of ancient samples with metagenomic data

Speaker: **Davide Bozzi**
University of Lausanne, Switzerland

Co-authors: Samuel Neuenschwander[1], Diana Ivette Cruz Dávalos[2], Bárbara Sousa da Mota[2], Hannes Schroeder[3], J. Víctor Moreno-Mayar[3], Morten E. Allentoft[4], Anna-Sapfo Malaspinas[2]

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Abstract:

Reconstructing the history of ancient individuals is a fundamental goal in ancient DNA (aDNA) studies. However, knowing the place of death can be particularly challenging when samples come from museum collections with incomplete or erroneous archives. A large fraction of sequenced molecules in aDNA studies derive from exogenous DNA. This DNA is constituted mostly by microbial DNA from soil-dwelling microorganisms that have colonized the buried remains post-mortem. In this study, we hypothesize that remains of individuals buried in the same or close geographic areas, exposed to similar microbial communities, could harbor more similar metagenomes. We propose to use metagenomic data from ancient samples' shotgun sequencing to locate the place of death of a given individual. We used a k-mer-based approach to compute similarity scores between metagenomic samples from different locations and propose a method based on dimensionality reduction and logistic regression to assign a geographical origin to target samples. We apply our method to several public datasets and observe that samples from closer geographic locations tend to show higher similarities in their metagenomes compared to samples of different origin, allowing good geographical predictions of test samples. Moreover, we observe that the genus Streptomyces commonly infiltrates ancient remains and represents a valuable biomarker to trace the samples' geographic origin. Our results provide a proof of concept and show how metagenomic data can also be used to shed light on the place of origin of ancient samples.

ABSTRACT ODA-004

An Algorithm for Optimally Partitioning Spatiotemporal Archaeological and Genetic Data

Speaker: **Victor Yan Kin Lee**
University of Copenhagen, Denmark

Co-authors: Adrian Timpson[1], Jan Kolar[1], Robert Staniuk[1], Stephen Shennan[1], Mark G. Thomas[1], Fernando Racimo[2]

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Abstract:

Human history is characterized by intertwined cultural, ecological and biological processes. To understand these processes, it is often necessary to discretize space and time in order to compare and contrast them across different periods and/or regions of the world. However, partitioning archaeological and biological data into analytically comparable spatiotemporal groupings is far from straightforward. The general approach in archaeology is to group observations into archaeological cultures based on the similarity of discovery circumstances, such as proximity, material culture and stratigraphy. Depending on the type of discretization used, archaeological cultures could have various definitions which do not lend themselves naturally to a comparative analysis with other types of datasets (e.g. genetic information). Here, we propose a novel spatiotemporal clustering algorithm designed for local time-series analysis that aims to aggregate data points in an automated manner, driven by the distribution of the data itself. The algorithm is characterized by an approach that searches for an optimal division of space-time based on user requirements. In our specific case, we sought to compare and contrast time-series data in different geographical regions. Thus, our current implementation works by seeking to minimize within-group variance in spatial locations, while - at the same time - maximizing the dispersion of data across the temporal dimension. We have applied this algorithm to the newly-created Big Interdisciplinary Archaeological Database (BIAD) with records spanning the European Neolithic and Bronze Age, enabling us to jointly compare and contrast evolutionary and cultural processes in different regions of Western Eurasia. We expect our method to be widely applicable to archaeo-scientists aiming to model different types of ancient datasets in a statistically explicit and reproducible manner, allowing for more rigorous interdisciplinary studies of the past.

ABSTRACT ODA-005

DNA from ancient shipwrecks: where it comes from and why it matters

Speaker: **Lisa Briggs**
Cranfield University, UK

Co-authors: Roselyn Ware[1], Evangelos Dimopoulos[2], Mladen Pesic[3], Cemal Pulak[4], Stella Demesticha[5], Ludovic Orlando[6], Robin Allaby[1], Greger Larson[2]

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Abstract:

Ancient DNA analysis has been proposed as a method to investigate underwater archaeological sites. More specifically, DNA analysis by PCR has been used to assess amphorae contents from ancient shipwrecks (Foley, et al. J. Archaeol. Sci. 2012), characterise genetic signatures of waterlogged botanical remains (Ramos-Madrigal, et al. Nat. Plants 2019), and assess the presence of tuberculosis in skeletal remains from submerged cemeteries (Hershkovitz, et al. PLoS ONE 2008). Despite these efforts, the presumed endogenous source of the identified DNA has not been confirmed, and it remains possible that the DNA may have been derived from exogenous sources including the underwater deposition environment or post-excavation storage environments. Here, we tested potential exogenous sources of DNA by extracting and characterising the isolated DNA from amphorae, cargo items, and environmental samples including seafloor sediment, seawater, and storage unit dust from five ancient shipwrecks dating to the 14th century BCE - 4th century CE and one artefact storage facility. Our results demonstrate that DNA reads present in the libraries constructed from DNA extracts derived from environmental samples of seafloor sediment, seawater, and shelving-unit dust match the genomes of several species of Mediterranean plant species (including olive, grapevine, and pine) that were widely consumed and traded in the ancient world. In addition, these reads do not possess the damage patterns characteristic of ancient DNA thus suggesting they derive from modern exogenous sources. These results suggest that previous studies that claimed to have recovered endogenous genuine ancient DNA from within the ceramic matrix of shipwreck amphorae require additional confirmation. As the investigation of biomolecules from recovered from underwater archaeological sites grows in importance, this study seeks to address the fundamental question of where DNA found on submerged cultural heritage sites comes from, and why it matters.

ABSTRACT PLE-001

Fine-scale genetic history of North-Western European Late Neandertals

Speaker: **Alba Bossoms Mesa**
Max Planck Institute for Evolutionary Anthropology, Germany

Co-authors: Mateja Hajdinjak[1,2], Hélène Rougier[3], Isabelle Crevecoeur[4], Patrick Semal[5], Grégory Abrams[6], Thibaut Deviése[7], Stéphane Pirson[8,9], Kévin Di Modica[6], Divyaratan Popli[1], Cesare de Filippo[1], Arev P. Sümer[1], Stéphane Peyrégne[1], Elena Essel[1], Cosimo Posth[10,11], Matthias Meyer[1], Janet Kelso[1], Benjamin M. Peter[1]

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Abstract:

Palaeogenomic research has made considerable progress in reconstructing the genetic history of Neandertals in recent years. However, the extremely low levels of endogenous DNA preserved in Pleistocene remains have made studies of fine-scale Neandertal population structure difficult. Recent advancements in ancient DNA methods have enabled a shift towards a more regional and temporal focus. For example, in Skov, et al. Nature 2022 we described a Neandertal population from Chagyrskaya Cave (Altai mountains, Russia), and found that they lived in small and isolated communities, resulting in high-levels of homozygosity and low genetic diversity. To explore whether these patterns hold for Neandertals more broadly, we screened 24 skeletal elements of late Neandertals, dating from ~39,000 to ~49,000 years before present, from four archaeological sites in the Mosan Basin (Belgium), an area remarkably rich in Middle to Upper Palaeolithic occupations: Fond-de-Forêt (Première caverne du Bay-Bonnet), Troisième caverne of Goyet, Trou Magrite and Spy cave. Of those, 20 contained enough endogenous DNA to generate genome-wide data at different levels of completeness (autosomal, mitochondrial and Y-chromosomal capture data), in addition to a new high-coverage genome from Goyet Q56-1 (24-fold coverage). Overall, our preliminary results suggest that the Belgian Neandertals had higher genetic diversity than that observed in Neandertals from the region of Denisova and Chagyrskaya Caves, with fewer long tracts of homozygosity – comparable to that of the Vindija 33.19 Neandertal from Croatia who lived around the same time. We also do not find evidence of genetic structure or biological kinship among the late Neandertals in Belgium. Thus, the population genetic structure of late North-Western European Neandertals contrasts with the one found in the Altai mountains, showing that Neandertal community structure differed across their temporal and geographical range.

ABSTRACT PLE-002

Using ancient biomolecules to reveal the social structure and behaviours of the Upper Palaeolithic Magdalenian at Gough’s Cave, UK

Speaker: **William Marsh**
Natural History Museum, UK

Co-authors: Selina Brace[1], Silvia Bello[1], Ian Barnes[1], Oliver Craig[2]

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Abstract:

The human remains excavated from Gough’s Cave represents the largest deposit in Britain associated with the Upper Palaeolithic Magdalenian culture (dated to ~15k calBP). Evidence of anthropic modifications associated with processing of human remains post-mortem and cannibalism is prevalent across the 205 cranial and postcranial remains (MNI=6), with the most remarkable examples including three skull cups manufactured from cranial vaults. Prior biomolecular results have shown one individual to share ancestry with the genetic cluster associated with Magdalenian populations across western Europe, with two separate individuals showing bulk isotope signatures consistent with a terrestrial diet. Here, we expand these biomolecular methods onto a larger set of skeletal remains to further clarify the composition, ancestry, and diet of the group, which when combined with previous archaeological studies develop our understanding of the Magdalenian more generally. Compound specific isotope analyses support an omnivorous diet, with no measurable marine component. Of the six individuals sequenced from the cave, all show an autosomal genetic affinity to the GoyetQ2 cluster associated with the Magdalenian culture. Four show a second degree or higher degree of relatedness, with two separate close family groups identified. Both sexes are represented, which when considered alongside the presence of juvenile remains suggests group composition mirroring that seen in modern hunter gatherer groups. A low effective population size is inferred, along with a lack of close kin breeding, compatible with sexual behaviours that avoided close union despite the inferred high level of group relatedness. The skeletal elements for five sequenced individuals show evidence of cannibalism and post-mortem modification, indicative of endocannibalism and a kin-mediated funerary behaviour. Genetic results conform with the predicted group structure of the Magdalenian where small groups containing related individuals.

ABSTRACT PLE-003

Geographical and Chronological patterns of archaic introgression in ancient Human genomes

Speaker: **Marco Rosario Capodiferro**
Trinity College Dublin, Ireland

Co-authors: Linda Ongaro[1], Lara Cassidy[1], Emilia Huerta-Sanchez[1,2]

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Abstract:

After the encounter between anatomically modern and archaic humans, our history was characterized by migrations, admixtures, and selection events due to changes in the environment. These and other events have shaped the patterns of genetic diversity that we observed in present-day populations. Therefore, archaic variants in anatomically modern humans (AMH) continued to evolve over time and be affected by the demographic history of modern human populations. The archaic regions introgressed may have also played a crucial role in the rapid adaptation of AMH outside Africa, acting as an essential source of genetic variation. In this study, we take advantage of ancient genomes– which provide windows into the past– to study patterns of archaic introgression in human genomes through time. To identify introgressed archaic regions in ancient genomes, we have first imputed publicly available ancient genomes. This allows us to use approaches specifically developed for ancient genomes as well as those suited for present-day genomes. Comparing the results from different approaches, we are able to observe the evolution of the introgressed regions in two dimensions, both geographical and chronological, and eventually, identify archaic genomic regions that have played an important role in adapting to some environmental changes that humans have faced in their past.

ABSTRACT PLE-004

Proteomic and mtDNA species identification of archaeological bone remains in cave Ilsenhöhle Ranis (Germany).

Speaker: **Dorothea Mylopotamitaki**
Collège de France, France; Max Planck Institute for Evolutionary Anthropology, Germany

Co-authors: Marcel Weiss[1,2], Helen Fewlass[2,3], Elena Irene Zavala[2,4,5], Geoff M. Smith[2,6], Karen Ruebens[2,7], Virginie Sinet-Mathiot[2], Florian S. Harking[8], Jesper V. Olsen[8], Harald Meller[9], Holger Dietl[9], Jörg Orschiedt[9], Matthias Meyer[2], Frido Welker[8], Shannon P. McPherron[2], Tim Schüler[10], Jean-Jacques Hublin[2,7]

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[3] Francis Crick Institute, UK
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Abstract:

The unclear association of specific human groups with transitional cultural entities or technocomplexes 50,000-40,000 years ago complicates our understanding of the Middle to Upper Palaeolithic transition in Europe. One such technocomplex is the Lincombian-Ranisian-Jerzmanowician (LRJ), which covers an area in northern Europe from Poland to the UK. To date, no unambiguous human or Neanderthal fossils are directly associated with the LRJ, and as a result, the biological nature of its makers remains debated. Recent methods for high-throughput proteomics of archaeological faunal specimens allow us to identify morphologically non-diagnostic remains that can be abundant in Palaeolithic archaeological sites. We used the development of MALDI-TOF MS-based peptide mass fingerprinting (PMF) of collagen type I, known as ZooMS, and the DIA-based species identification based on limited bone proteome sequence databases, called SPIN, to proteomically identify 2,131 bone fragments from Ilsenhöhle Ranis (Germany), one of the eponym sites of the LRJ. In this series, we identified eight hominin bones derived from renewed and previous excavations. Additionally, proteomic screening allowed us to furthermore characterise the presence of fauna species groups, including Bovidae, Cervidae, Equidae, and a variety of carnivores. Among the animal remains, we observed some conflicting identifications when comparing ZooMS with SPIN, most of them possibly related to the absence of the relevant species in the reference database. Subsequent mitochondrial DNA analysis of the hominin bones resulted in their identification as Homo sapiens. Our results provide the first reliable association of the LRJ with Homo sapiens and further illustrate the potential of high-resolution mass spectrometry approaches to Late Pleistocene faunal remains. Additional radiocarbon and genomic analyses are ongoing on selected specimens for extensive research.

ABSTRACT PLE-005

High coverage genomes of two of the earliest Homo sapiens in central Europe

Speaker: **Arev Pelin Sümer**
Max Planck Institute for Evolutionary Anthropology, Germany

Co-authors: Hélène Rougier[1], Vanessa Villalba-Mouco[2], Helen Fewlass[3], Anja Furtwaengler[2], Elena Essel[2], Yilei Huang[2], Leonardo N. M. Iasi[2], Stéphane Peyrégne[2], Cesare de Filippo[2], Alba Bossoms Mesa[2], Elena I. Zavala[4], Hugo Zeberg[5], Alexander Stoessel[2], Holger Dietl[6], Jörg Orschiedt[6], Janet Kelso[2], Geoff Smith[2], Dorothea Mylopotamitaki[2], Karen Ruebens[7], Virginie Sinet-Mathiot[2], Frido Welker[8], Marcel Weiss[9], Tim Schüler[10], Shannon McPherron[2], Jean-Jacques Hublin[7], Jaroslav Brůžek[11], Petr Velemínský[12], Harald Meller[10], Matthias Meyer[2], Benjamin M. Peter[2], Harald Ringbauer[2], Mateja Hajdinjak[2], Kay Prüfer[2], Johannes Krause[2]

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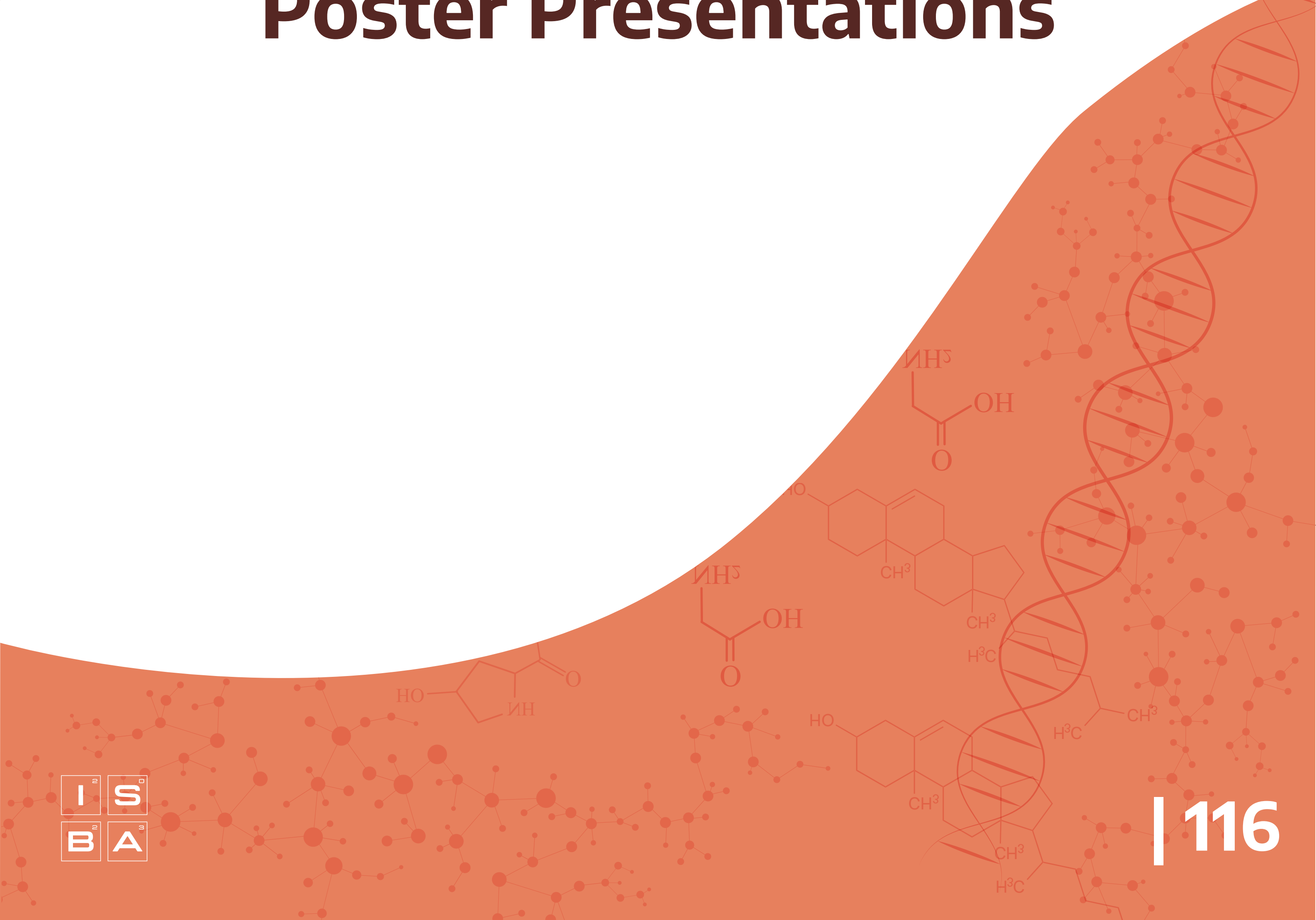
[12] National Museum Prague, Czech Republic

Abstract:

To date there is little genetic data available to characterize Homo sapiens spanning the Middle to Upper Paleolithic transition in Eurasia, and only one genome, that of the ~44,000-year-old Ust'-Ishim individual from Siberia, has been sequenced to high coverage (Fu, et al. Nature 2014). We present two high-coverage genomes from individuals found at two sites in central Europe that are approximately 230 km apart: one from Ilsenhöhle Ranis ('Ranis') in Germany and one from Zlatý kůň in Czechia (Prüfer, et al. Nat. Ecol. Evol. 2021). These individuals are among the oldest Homo sapiens known from Europe, and likely older than Ust'-Ishim, based on radiocarbon and molecular dating. We also sequenced low coverage genomes from four individuals from Ranis, dated to between 46,800 and 42,200 years ago. All Ranis genomes show the highest genetic similarity to the genome of Zlatý kůň rather than to any other individual from ancient or present-day populations. Interestingly, the two high-coverage genomes share long identical-by-descent regions, indicating that these individuals also lived close in time to one another. Despite having genome-wide heterozygosity levels similar to present-day Europeans, we detect long runs of homozygosity in the two high coverage genomes, suggesting that there was a recent reduction in population size and/or recent inbreeding among their ancestors. We also detected long tracts of Neandertal ancestry in both genomes that are best explained by a single pulse of Neandertal introgression - likely the major Neandertal introgression event shared among all non-Africans. We used the length distribution of these fragments to estimate when this introgression occurred.

Abstracts
Poster Presentations



ABSTRACT AFP-001

Understanding Early Pottery Uses and Social Interactions at two Late Archaic Shell Rings in the Southeastern United States through Organic Residue Analysis

Speaker: **Anne-Julie Bilodeau**
Université Laval, Canada

Co-authors: Karine Taché[1]

[1] Université Laval, Canada

Abstract:

The analysis of organic residues left by human activity on inorganic matrices paved the way for challenging many long-standing archaeological hypotheses and offers new perspectives on the study of human activity in the past. The time now seems perfect to conduct these analyses on the oldest pottery in North America. Ceramics uncovered at St. Catherines and McQueen shell rings, located on St. Catherines Island off the coast of Georgia, USA, and dating from approx. 4300 to 3800 BP are studied employing techniques borrowed from analytical chemistry. Specifically, my research aims to define the use(s) of these ceramic containers and identify different culinary practices through the analysis of lipid residues preserved in pottery and clay nodules, the latter thought to have been used as boiling stones in an indirect method of cooking. Preliminary results already provide new empirical data that allow a better understanding of Late Archaic period (5150-3200 cal. BP) foodways in the Southeastern United States. Results thus shed light on coastal occupations associated with a poorly documented period, and on cultural practices newly accessible to archaeologists. Ultimately, this graduate research project will test the hypothesis according to which different communities of practice occupied these two shell rings and gathered there to feast.

ABSTRACT AFP-002

Expanding our knowledge of prehistoric cooking technology through the chemical analysis of heat-altered stones

Speaker: **Margherita Cantelli**
Universitat Autonoma de Barcelona, Spain

Co-authors: Xavier Terradas[1], Didier Binder[2,3], Martine Regert[2,3], Andre Carlo Colonese[4]

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[3] Cultures et Environnements Préhistoire, Antiquité, Moyen Âge, France
[4] Universitat Autònoma de Barcelona, Bellaterra, Spain

Abstract:

Neolithic cooking technologies have been mostly investigated through the analysis of ceramic artefacts, while other potentially used tools such as boiling and cooking stones have only received cursory attention. This gap impinges upon our understanding of prehistoric culinary practices, the evolution of cuisine, and its impact on the overall diet and economies in the past. Here we address this research bias by analysing archaeological stones that were potentially used for the preparation of foodstuffs and other products in Early Neolithic sites in southwestern Europe. Specifically, we combined morphological (3D and photogrammetry), visual inspection (evaluation of fractures, shape and colour) and chemical analysis of extracted lipids (GC, GCMS and GCCIRMS) of stones (sandstones, marl and limestones) recovered from contexts with evidence of culinary activities at the Neolithic sites of La Draga (Spain) and Abri Pendimoun (France). Lipids were extracted from the surface and the underneath stone deposits to check for variations in lipid absorption and molecular characterization. Our results, although preliminary, revealed distinct lipid concentrations (varying between stones and extraction areas), with some samples preserving relatively large amounts of lipids, possibly related to plant products. This multidisciplinary approach may, therefore, shed light on the varied culinary practices, as well on subsistence resources and prehistoric diet in the Western Mediterranean.

ABSTRACT AFP-003

Multi-proxy Analysis of Starchy Plant Consumption: A case study of pottery food crusts from Late Iron Age settlement at Pada, NE Estonia

Speaker: **Shidong Chen**
University of Tartu, Estonia

Co-authors: Kristiina Johanson[1], John Alphonsus Matthews[1], Sandra Sammler[1], Marie Anna Blehner[1], Siim Salmar[1], Ivo Leito[1], Ester Oras[1,2]

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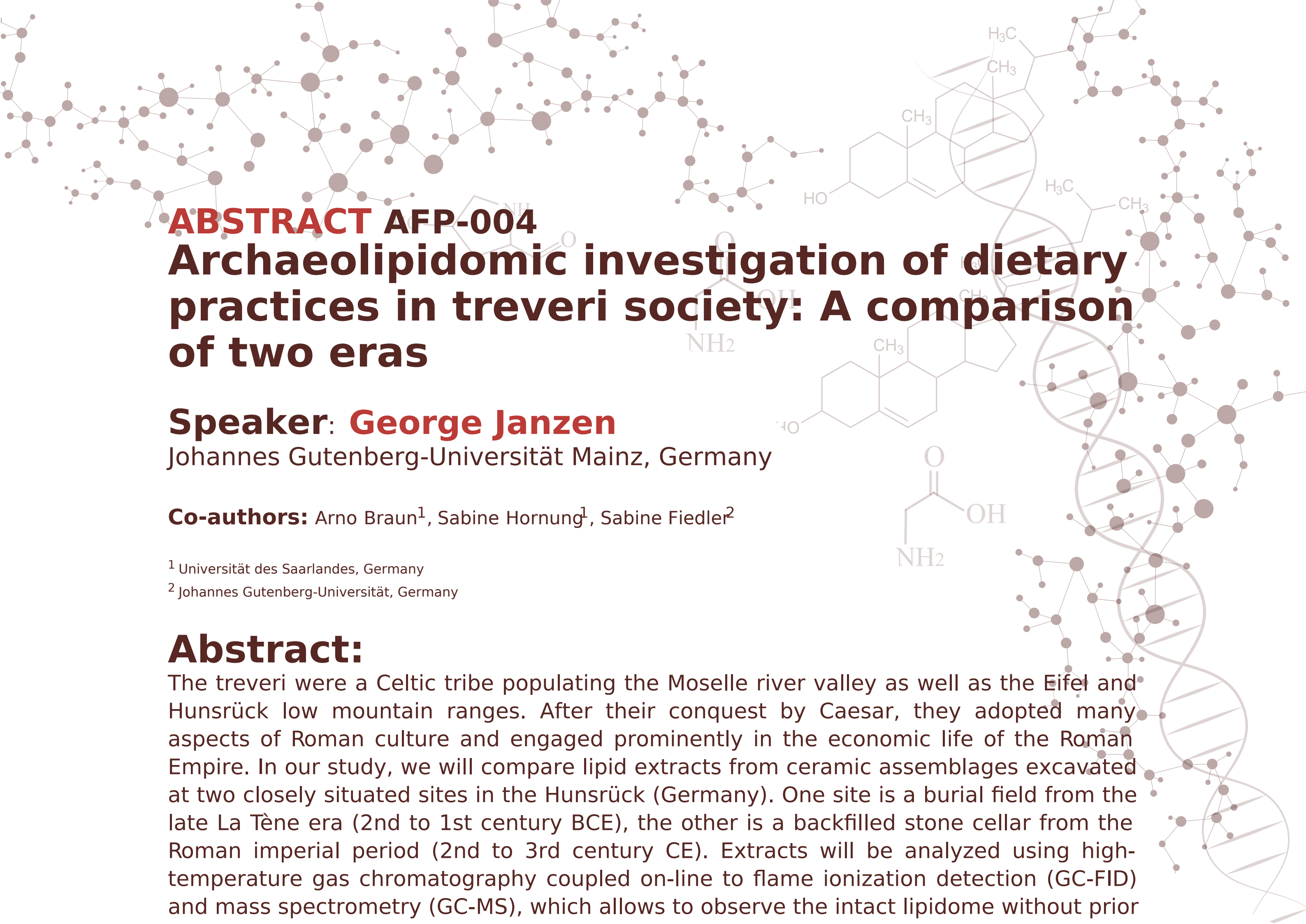
Abstract:

Plant-based food, especially cereals, plays an essential role in prehistoric human dietary practices and economy. The earliest plant cultivation in the eastern Baltic was noted in the 3rd millennium BC, with the Corded Ware culture and their partly agricultural economy. Despite the role of cereal cultivation in ancient subsistence systems, the investigation of cereal consumption in prehistoric periods faces several obstacles: the scarcity of macro-botanical evidence and poor preservation of hydrophilic organic residues. In our study, we proposed a multi-proxy methodology for tracing cereal consumption in ancient societies, focusing on the informative potential of pottery-related food crusts. 24 food crust samples from Pada Middle Iron Age (500-800 AD) settlement site in North Estonia were selected for a multi-approach analysis. We applied conventional microscopic analysis of plant micro-remains (phytoliths and starch grains) and bulk stable isotope analysis using isotope ratio mass spectrometry (EA-IRMS) in combination with lipid-based organic residue analysis (ORA) using gas chromatography-mass spectrometry (GC-MS). The multi-methodological data were further compared and correlated by a statistic method, correspondence analysis (CA). Our multi-proxy method provides new insights into unravelling the composition of food crusts with complex content. Plant microfossil analysis and GC-MS analysis complement the compositional information down to the species and biomolecular level based on the main substances classified by EA-IRMS. CA confirms consistency within our multi-proxy data and distinguishes major “culinary groups” in our samples based on their main compositional elements. Based on the discovered recipe and cooking habits, we can demonstrate the development of C3 cereal cultivation and animal husbandry at the Pada settlement site. Yet, the spread and cultivation of C4 millet may not have emerged in this region.



ABSTRACT AFP-004

Archaeolipidomic investigation of dietary practices in treveri society: A comparison of two eras

Speaker: **George Janzen**
Johannes Gutenberg-Universität Mainz, Germany

Co-authors: Arno Braun[1], Sabine Hornung[1], Sabine Fiedler[2]

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Abstract:

The treveri were a Celtic tribe populating the Moselle river valley as well as the Eifel and Hunsrück low mountain ranges. After their conquest by Caesar, they adopted many aspects of Roman culture and engaged prominently in the economic life of the Roman Empire. In our study, we will compare lipid extracts from ceramic assemblages excavated at two closely situated sites in the Hunsrück (Germany). One site is a burial field from the late La Tène era (2nd to 1st century BCE), the other is a backfilled stone cellar from the Roman imperial period (2nd to 3rd century CE). Extracts will be analyzed using high-temperature gas chromatography coupled on-line to flame ionization detection (GC-FID) and mass spectrometry (GC-MS), which allows to observe the intact lipidome without prior deconvolution by transmethylation, as well as stable isotope ratio analysis (GC-IRMS) to deduct dietary lipid sources from δ13C values. Data mining methods will be employed to process the complex chromatograms obtained from GC-MS.From this we hope to trace dietary practices of the indigenous inhabitants of this area before and during Roman rule, with special regard to developments in grain farming, animal husbandry, and trade. As the burial field covers all strata of the population, it will also be possible to differentiate the pre-Roman data according to social status.

ABSTRACT AFP-005

Northeast North American archaeology, lipid analysis, Late Woodland pottery, Iroquoian foodways

Speaker: **Karine Taché**
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Co-authors: Roland Tremblay[1], Alexandre Lucquin[2], Marjolein Admiraal[2], John P. Hart[3], Oliver E. Craig[2]

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Abstract:

Iroquoian groups inhabiting the St. Lawrence Valley in the 15th and 16th centuries practiced agriculture and supplemented their diet with fish and a variety of wild plants and terrestrial animals. However, important gaps remain in our knowledge of Iroquoian foodways shortly before contact with Europeans, including the relative proportion of cultivated versus wild foods and the importance of fish in the diet. This presentation summarizes the results of lipid residue analyses carried out on some thirty ceramic containers recently discovered at the Dawson site within the actual city of Montreal, Canada. A combination of analytical techniques yielded molecular and isotopic data showing that ceramics from this important Iroquoian village were used to prepare a range of foodstuffs, primarily freshwater fish and maize but possibly also other animals and/or plants. Characterizing mixtures of foods is a significant challenge frequently encountered when interpreting the results of organic residue analysis. Here, an attempt is made at evaluating the contribution of different food sources to the archaeological residues from the Dawson site based on mixing models. Although these efforts led to plausible reconstructions of the relative contribution of maize and aquatic oils to these residues, an equifinality problem limits the level of confidence that can be attached to these interpretations. While reminding us of the need to refine our reference data and mixing models, the organic residue analysis carried out on ceramics from the Dawson site clearly shows the potential of this approach to provide a more realistic portrait of past culinary practices.

ABSTRACT AFP-006

Farmers hunt: multi-proxy analysis reveals complex subsistence systems at the dawn of early farming in the NE Baltic

Speaker: **Ester Oras**
University of Tartu, Estonia

Co-authors: Mari Tõrv[1], Kristiina Johanson[1], Eve Rannamäe[1], Anneli Poska[2], Liivi Varul[3], Alexandre Lucquin[4], Jasmine Lundy[4], Vanda Visocka[5], Dardega Legzdina[5], Gunita Zariņa[5], Lembi Lõugas[3], Samantha Brown[6], Lucy Cramp[7], Volker Heyd[8], Michaela Reay[7], Łukasz Pospieszny[9], Harry K. Robson[4], Kerkko Nordqvist[8], Carl Heron[10], Aivar Kriiska[1], Oliver E. Craig[4]

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[4] University of York, UK
[5] University of Latvia, Latvia
[6] University of Tübingen, Germany
[7] University of Bristol, UK
[8] University of Helsinki, Finland
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Abstract:

The transition from hunter-gathering to farming has been one of the key questions for tackling economic and socio-cultural changes in the past. Here we present how combined biomolecular methods can reveal new intriguing and alternative interpretations for this crucial economic change, challenging the notions of hierarchical economies. The most extensive multi-proxy dietary overview combining zooarchaeological, archaeobotanical, dietary stable isotopes and rich new dataset of pottery lipid residue analysis is presented, to reveal the nature and extent of early farming in the 3rd millennium cal BC in the NE Baltic; a region characterised by stable and affluent forager communities in northern latitudes. Our results show that the initial exploitation of domesticates introduced by the incoming Corded Ware (CWC) populations co-existed in parallel with separate forager economies throughout the 3rd millennium cal BC. At the same time, within these new CWC communities, a certain dietary segregation existed, with some groups having privileged access to domesticates, whereas the others relied on local wild resources. There was no clear-cut and linear transition from hunting, fishing and gathering to farming. Instead, a complex system of parallel worlds and mixed economies combining animal husbandry and forager livelihood persisted for several centuries after the first encounter with the early domesticates.

ABSTRACT CEP-001

Assessing Age-related Post-Mortem Metagenomic Diversity in Historical and Ancient samples

Speaker: **Elsa Peters**
Smithsonian Institution - National Museum of Natural History, USA

Co-authors: Marcela Sandoval-Velasco[1], Anna Penna[1,2], Melissa Hawkins[3], Logan Kistler[1]

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Abstract:

Collections from natural history museums and herbaria have long been recognized as agreat source of information as they can help us understand species that are not accessible in the wild and provide a comprehensive record of nature over the last 200 years (Raxworthy & Smith, Science Direct 2021). During the last decade, robust protocols for studying DNA obtained from these types of samples have been well-established and refined. However, this has less often been the case for the study of the microorganisms and other exogenous DNA that accompany these specimens, which are often neglected by focusing on the endogenous content of target species only. Ancient metagenomics (Sarkissian, et al. Nature Reviews Methods Primers 2021) is an important emerging field providing us with another perspective to understand the species of interest, including parasites, symbionts, and an overall description of the ecosystems our species of interest thrived in. Recently, groundbreaking work has been done by reconstructing ancient oral microbiomes, or postglacial ecosystems based on sedaDNA. However, probing these questions about past organisms and ecosystems requires us to 1) disentangle the ancient from the post-mortem metagenome, 2) understand biases in survival, recovery, and analysis, and 3) have robust strategies for balancing specificity and sensitivity in highly mixed datasets. Here, we use a range of highly variable systems and collection histories including samples for 14 species of Galagidae (small primates) across a variety of museums, Agave samples from herbarium specimens, ancient Agave samples from Prehispanic Mesoamerica from archaeobotanical collections, and publicly available data to explore age-related patterns of metagenomic diversity in collections and shed light into unique post-mortem metagenomic properties related to museum conservation and sample manipulation.

ABSTRACT CEP-002

How the Steppe was Sown: Transcontinental Origins and Local Innovations at Mongolia's Earliest Sites of Indigenous Agriculture (c. 250 BC-150 AD)

Speaker: **Christina M. Carolus**
Yale University, USA

Co-authors: Asa Cameron[1], Joshua Wright[2], Amartuvshin Chunag[3], Paul Szpak[4], William Honeychurch[1]

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Abstract:

The Late Iron Age (c.250 BC-150 AD) marks the genesis of eastern Eurasia’s first agropastoral state as well as Mongolia’s earliest evidence of agriculture. Progenitors of this state, known as the Xiongnu, emerged from Central Mongolia to successfully integrate and maintain one of the largest-scale political configurations in prehistory: at its peak extending territorial control from Manchuria to Kazakhstan, southern Siberia to Inner Mongolia, to the Tarim Basin of Xinjiang. The Xiongnu state’s proto-globalizing networks were foundational to the “Trans-Eurasian Exchange” and what would later be known as the "Silk Road", while its innovative statecraft techniques directly underlaid the synthesis of the later Mongol Empire. The multidimensional transformations associated with the emergence of this state have thus been a focal point of Eurasian steppe archaeological research for decades. Recent research posits a complex and diversified political culture whose success may have been based directly in indigenous development of flexible agropastoralism – particularly the integration of selected foreign crop regimes within well-established pastoral systems. A representative picture of Xiongnu subsistence economy nevertheless remains materially elusive. The nature of the arrival, significance, and diversity of agricultural products – namely foreign cereal products – in Xiongnu foodways has received little dedicated attention despite notable impacts. This paper presents an overview of archaeobotanical, stable isotopic, and archaeogenetic evidence for eastern Eurasian steppe agriculture prior to and during the Xiongnu Period. It then reports results of the first and earliest formal macrobotanical and isotopic analyses (δ13C, δ15N, 87Sr/86Sr) of a multi-sited set of local non-mortuary crop assemblages from Mongolia, including earliest evidence of oats and common millet. Results are drawn together to situate Mongolia within the broader prehistory of the trans-Eurasian crop exchange.

ABSTRACT CEP-003

Herbariomics: genetic diversity of Trochetiopsis (Malvaceae) through anthropogenic pressures

Speaker: **Annabelle de Vries**
University of Warwick, UK; Natural History Museum London, UK

Co-authors: Mark Carine[1], Robin G. Allaby[2]

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Abstract:

Oceanic islands have been, and continue to be, used for in-situ studies of evolution. These islands provide some of the most striking examples of adaptive radiations, while at the same time, rich endemic diversity is globally endangered. This project aims to better understand how human impact has affected island biodiversity patterns and question how robust islands are as model system for studying evolution. For this study, we focussed on the plant genus Trochetiopsis, an endemic of St Helena, to investigate on a genomic level the effect of anthropogenic pressure on an oceanic island endemic. St Helena has historical records of human impact and has a history of botanical collecting spanning the last three centuries. Additionally, it highlights classic examples of evolutionary processes such as adaptive radiation. The genus Trochetiopsis consists of three species of which two extinct (in the wild) and one re-discovered. Its collections spanning 320 years, allows us to look closer at these extinction events. During this project, a de novo genome of Trochetiopsis ebenus was assembled using PacBio long reads obtained from sequencing modern material. This assembled genome will function as a reference genome for the ancient DNA from herbarium collections. The aDNA was analysed using phylogenetics and Genomic Evolutionary Rate Profiling (GERP) to obtain the mutation load and investigate change of the genetic diversity over time.

ABSTRACT CEP-004

Using ancient genomes to investigate responses to climate and anthropogenic impacts in the Atlantic bluefin tuna

Speaker: **Elisabetta Cilli**
University of Bologna, Italy

Co-authors: Adam Jon Andrews[1], Antonio Di Natale[2], Arturo Morales-Muñiz[3], Bastiaan Star[4], Alessia Cariani[1], Fausto Tinti[1]

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Abstract:

Like many commercial marine fish populations, the eastern Atlantic and Mediterranean population of Atlantic bluefin tuna (Thunnus thynnus) has experienced dramatic changes in abundance and complexity during the past 50 years due to overexploitation. Since 2014, this population has shown signs of recovery, yet we have a poor understanding of how it was composed prior to 1970, and thus how those more recent changes reflect long-term population dynamics when exploitation rates were lower and climate conditions were different. Genomic data provides an opportunity to investigate how this species has responded to climate and the Anthropocene in terms of its demography and adaptive traits. This information is much needed to reduce the likelihood of future population declines and predict ecosystem function during dramatic climate events to come. Thus, we present the first analyses on nuclear whole-genome data of this species, which includes sample groups of archaeological and archived ABFT dated to between the 10th century and early 20th century. Furthermore, we present the first data to represent a putative Black Sea population of ABFT, which disappeared rapidly during the 1970's. We successfully sequenced medium-coverage modern and ancient genomes and applied a battery of methods to identify adaptive loci and study allele frequency changes between spatiotemporal sample groups using both hard-called genotypes and genotype likelihoods. These novel data have implications for the management of ABFT since they elucidate the current population structure and allow for the forecasting of responses following what has been observed with this robust dataset during several climatic and cultural events during the last millennia.

ABSTRACT CEP-006

SedaDNA analysis of Durrington Walls: a new class of Neolithic monument

Speaker: **Teri Hansford**
University of Warwick, UK

Co-authors: Vincent Gaffney[1], Robin Allaby[2]

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Abstract:

Durrington Walls superhenge is located on the Stonehenge world heritage site, just 3km North-East of the original monument. Previous archaeological investigations at this site conducted by the Stonehenge Hidden Landscapes Project (SHLP), revealed a series of large geophysical anomalies surrounding the superhenge. Geophysical surveys discovered that the anomalies were huge circular pits with a surface diameter upwards of 20m and a depth of at least 5m. Mechanical coring of a selection of these pits was conducted in order to provide sediment samples to determine their nature. Radiocarbon and OSL dating suggests that these pits are indicative of the Late Neolithic period, and consequently a Neolithic structure of an unprecedented scale in Europe. We have employed sedimentary DNA techniques in order to analyse the metagenomic profiles of core samples taken, with the aim to reconstruct the paleoenvironment of the landscape. SedaDNA analysis to date has revealed variable preservation of signal, but that the area was likely a meadow landscape. Preliminary evidence suggests that the pits have an association with large mammals, suggesting further investigation is required to elucidate this relationship. In order to assess this further, mitochondrial capture has been employed to analyse the animals present in order to determine the exact species and origin.

ABSTRACT CEP-007

Sedimentary Ancient DNA across Australia

Speaker: **Dawn Lewis**
The University of Adelaide, Australia

Co-authors: Dawn A. Lewis[1], Bastien Llamas[1], Bruno David[2], Russell Mullett[3], GunaiKurnai Land and Waters Aboriginal Corporation[3], Joanna Fresløv[3], Zenobia Jacobs[2]

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Abstract:

Dry land sedimentary ancient DNA (sedaDNA) is an emerging field of ancient DNA research which has evolved from environmental benthic studies. Current hypotheses suggest that fragmented sedaDNA adsorbs to charged particles in sediment, which confers a level of protection to the DNA molecules. The geochemical makeup of the sediment may thus act as an additional factor to local environmental conditions in the post-depositional degradation of ancient DNA.In this paper we discuss whether sediments from different geological regions across Australia contain preserved sedaDNA. Comparing the extractive capacity of sediments from the Kimberley (NW Australia) with the Snowy Mountain foothills (SE Australia) provides invaluable insight into the availability and accessibility of sedaDNA. Such work would allow for the expansion of sedaDNA analysis where archaeological remains are scarce and poorly preserved. This may open avenues for research about key periods of human evolution, population movements and landscape engagement. This work is undertaken in partnership with and under the guidance of Traditional Owners whose knowledge of places (in Aboriginal Australia, 'Country') is integral to determining the culturally appropriate direction of research and archaeological interpretations at sites and landscapes. As sedaDNA may contain traces of any and all biological organisms who frequented a place at given moments of the past, engaging with Indigenous peoples through partnership research is paramount to ensure that those places are treated with the cultural respect they are due, and that community research priorities feature appropriately. With respect to sedaDNA, these concerns relate not only to human remains but to the entire spectrum of biota in Country. The importance of culturally appropriate partnership research with Indigenous peoples when utilising non-conventional substrates to extract genetic information of biota, such as sedaDNA, is emphasised herein.

ABSTRACT CEP-008

Reconstructing Microbial Communities Within Roman Turf Ramparts: A Proof-of-Concept Study

Speaker: **Caroline Orr**
Teesside University, UK

Co-authors: Gillian Taylor[1], Ben Russell[2], Tom Gardner[3], Andrew Birley[4], Tanja Romankiewicz[2]

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Abstract:

The Grassroots project used microbial and geochemical methods to study turf blocks taken from preserved turf ramparts at the Roman fort of Vindolanda, UK. The turf blocks used to build these ramparts presented visually intact sequences of prehistoric and Roman vegetation covers as well as topsoil and subsoil layers. Our aim was to develop a proof-of-concept methodology for reconstructing ancient environmental conditions and studying land use. For this study a range of samples were taken: (1) bulk grab samples across two vertical profiles taken at systematic intervals in the field, (2) boxed field samples, sub-sampled in the lab targeting different soil horizons and infill layers as characterised by micromorphology, and (3) samples drilled out from resinated box samples from which thin section slides had been prepared already. This poster presents results of the bacterial and fungal communities identified within the samples specifically focusing on linking the microbial communities to the identified soil horizons within the turf. It is thought that preservation of the environmental conditions within turf at Vindolanda stabilises the microbial community and is indicative of soil conditions at the time. It is hoped that studying these communities further allows a more detailed understanding of microbially mediated processes such as nutrient cycling at the time.

ABSTRACT **CEP-009**

A 14-thousand-year high resolution metagenomic exploration of Lake Constance

Speaker: **Yi Wang**

University of Konstanz, Germany

Co-authors: Sebastian Schaller[1], Anna Chagas[2]

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Abstract:

The perialpine Lake Constance has experienced significant ecological changes since the end of the Last Glacial Period, driven by climatic and anthropogenic forcings. Its large deep Upper Lake is assumed to have been influenced mainly by natural environmental changes through most of its history. Postglacial climatic perturbations and biological successions, for example, are among the processes that affected the ecosystem of the lake and the surrounding area. To study the impact of these changes, we extracted ancient DNA from a 24-meter-long sediment core and built a shotgun data series consisting of 34 samples spanning the last 13,500 years. After taxonomic profiling, the overall DNA damage in a sample is shown to correlate with depth/age for both eukaryotic and bacterial taxa, although in the latter case, taxa with lower DNA damage are present, likely from living microbes in the sediment. Major transitions in plants and bacteria composition are approximately in sync in the data series: starting with a pronounced change at the onset of the Younger-Dryas, taxa composition change slowed down in the Early Holocene. From the Mid Holocene, a new development started along a different trajectory, and was altered again a few centuries ago. This last change was especially fast and evident in the bacterial community, putatively a result from agriculture and industrialisation. Through integrating time series of taxa from all trophic levels, we aim to reconstruct ecological changes to reveal the evolution of a lake ecosystem under the ever-changing environment.

ABSTRACT CEP-010

Millennia-long human-wildlife co-existence recorded in mesocarnivoran isotopic signal

Speaker: **Maciej Krajcarz**
Polish Academy of Sciences, Poland

Co-authors: Chris Baumann[1,2], Magdalena Sudoł-Procyk[3], Jarosław Wilczyński[4], Magdalena Krajcarz[1]

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Abstract:

Since the Neolithization, humans have actively and drastically altered the natural environment. In central Europe, the anthropopressure particularly affected the carnivorans, especially through direct extirpation, competition, or habitat loss. Some species, mostly large carnivores, become extinct. Most small and mid-sized carnivorans survived until now, but not unharmed – with habitats altered, ecological niches shifted, geographical ranges shrank or – in the case of highly adaptative species, such as red fox – the colonization of new artificial environments. Our study focuses on the last 10,000 years of mesocarnivoran ecological history in Polish Jura (south. Poland). This region witnessed many major cultural changes, including the early Neolithization connected with flint mining, then the development of nearby large agricultural centers during the Eneolithic, through Bronze Age–Iron Age Celtic settlement, followed by depopulation during the Migration Period and intense use again in late Middle Ages. These cultural changes created numerous ecological threats and opportunities for mesocarnivorans. Moreover, we have a collection of numerous fossils of four mesocarnivoran genera (Vulpes, Martes, Meles and Felis) from this region, from well preserved and extensively studied Holocene cave sediments, with stratigraphic constraints and a large number of direct radiocarbon dates. In our project, we attempt to track the biomolecular record of diachronic (across millennia) trophic response of the mesocarnivorans to the regional anthropopressure. We use stable isotope analysis of collagen C and N to reconstruct the nutrition-related ecological issues, including both intra-taxon characteristics and inter-taxa relationships. We track the chronology of variable ecological adaptations and changes within the mesocarnivoran guild to identify the ecological shifts caused by human impact. The study was funded by the National Science Center of Poland, grant No. 2017/27/B/NZ8/00728.

ABSTRACT CEP-011

Paleogenomic Analysis of Archaeological Rockfish Diversity in the North Pacific: Insights into Past Human-Fish Interactions and Contemporary Ecological Challenges

Speaker: **Robin Singleton**
University of Oklahoma, USA

Co-authors: Alice Lee[1], Karissa Hughes[1], Emma Elliot Smith[2], Todd Braje[3], Breana Campbell[3], John R. Johnson[4], Milton Love[5], Madonna Moss[6], Catherine West[7], Peter Sudmant[8], Courtney Hofman[1]

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Abstract:

The rockfishes (Sebastes sp.) are an extremely diverse genus of fishes found throughout the northeastern and northwestern Pacific Ocean which live in a variety of distinct environments and are mostly visually distinguishable from one another. However, due to the similarity of the skeletal morphologies among the species, when rockfishes are found in an archaeological context they are difficult to identify. Here we characterize archaeological rockfish diversity in the North Pacific through the genetic analysis of 70 rockfish samples from archaeological sites along the coasts of California and Alaska. Samples were prepared for metagenomic sequencing with the SCR library preparation protocol. Taxonomy was assigned using Kraken2 and a custom reference database of recently published rockfish genomes. Simulation experiments suggest that most species can be confidently assigned to the correct species with this approach. We identified at least 11 species of fish from several habitat types which were extant between approximately 4700 - 210 BP based on previous radiocarbon analyses and nine new direct dates. In doing so we have investigated patterns of rockfish harvest and consumption amongst past Californian and Alaskan human populations. These data contribute to past and present understandings of fishery management and demonstrate the relevance of the biomolecular analysis of archaeological samples to contemporary ecological challenges.

ABSTRACT CEP-012

Insights Into the Ecology and Extinction of the Japanese Sea Lion Using Ancient DNA and Stable Isotope Analysis

Speaker: **Hope Loiselle**
University of Washington, USA

Co-authors: Jodi Yoshimi[1], Logan Kistler[2], Katsunori Takase[3]

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Abstract:

The Japanese sea lion is an extinct pinniped that once inhabited the Japanese and Kuril archipelagoes. Their abundance in archaeological middens suggests that the sea lions played an important role in the subsistence of coastal groups throughout the late Holocene. Although the species did not go extinct until the mid 20th century, little is known about their population and ecological role prior to this. Using ancient DNA, specifically captured mitogenomes, we seek to investigate the past population size and structure of this top marine predator. We also use bone collagen δ13C and δ15N values to identify shifts in primary productivity of the environment and trophic level changes of the sea lions through time. We sampled from 11 archaeological sites around Hokkaido and the Kuril Islands. The ancient DNA and isotope data are integrated with other environmental and archaeological proxies to improve our understanding of the sensitivities of subsistence hunter-gatherers to potentially vulnerable prey. We explore the inherent resilience in a now extinct marine mammal species to climate change, human harvesting, and habitat disruption.

ABSTRACT CEP-013

Diving into palaeogenomic analyses of shipwreck ivory

Speaker: **Patricia Pecnerova**
University of Copenhagen, Denmark

Co-authors: Nuno Filipe Gomes Martins[1], Marianne Dehasque[2], Timmy Gambi[3], Teresa L. Santos[4], Edana Lord[2], Yasuko Ishida[5], Alfred L. Roca[5], Hans R. Siegismund[1], Juan-Luis Arsuaga[6], M. Thomas P. Gilbert[1], Love Dalén[2]

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Abstract:

Elephants have been under anthropogenic pressure for thousands of years as ivory was and still is perceived as a valuable commodity. Elephant ivory shaped historical trade routes and brought local populations to extinction, and today remains one of the main drivers of extinction in living elephants. To gain insights into elephant genetic diversity prior to the potential declines in the Roman times, in the colonial period, and in the last decades, we analyzed waterlogged and shipwreck ivory from two sites in the Mediterranean, which are putatively dated to the Phoenician period. The results indicate that the historical samples represent elephant diversity that is currently extinct. Genomic estimates of elephant diversity from this time period allow us to evaluate the baseline levels of diversity before the intensified anthropogenic pressure and provide the necessary context for understanding the genetics of present-day elephant populations.

ABSTRACT CEP-014

Animal management and sacrificial power: Using ancient genomics to study golden eagle (Aquila chrysaetos) sacrifice in Teotihuacán

Speaker: **Robin Singleton**
University of Oklahoma, USA

Co-authors: Nawa Sugiyama[1], Karissa Hughes[2], Megan Judkins[3], Ron Van Den Bussche[4], Courtney Hofman[2]

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Abstract:

Excavations of the Moon and Sun Pyramids (1998-2004) at Teotihuacán (1-500 AD) in present day México have yielded both human and animal sacrifices interred as part of state rituals. These rituals demonstrated the power of the state, and the species chosen reflected that power, being primarily large predators. Isotopic and zooarchaeological analyses of the sacrificed animals show that some of them were held for extended periods of time before their deaths—they have skeletal lesions associated with restraints and evidence of maize based diets—while others were sacrificed fairly quickly. We conducted genomic analysis on 20 golden eagle (Aquila chrysaetos) remains that were sacrificed and interred in Teotihuacán to determine the relationships among sacrificed individuals and to compare them with extant populations. We also explored different genetic sexing approaches to assess their viability for low coverage data and look for sex-biases in sacrificed eagles. To increase DNA yield in these highly degraded samples (79bp mean fragment length), a variety of different laboratory protocols—including different library preparation techniques, adjusting capture parameters, and increasing indexing inputs were tested. Despite poor preservation, we were able to substantially increase DNA yields in most samples. Preliminary analyses indicate the presence of multiple sibling pairs among the ancient samples, suggesting that eagles were gathered from nests as chicks and raised for sacrifice. These data provide insight into how the eagles were procured and managed before sacrifice as well as into ancient Mesoamerican golden eagle populations. Additionally, this ancient population data can improve understanding of past and present genomic diversity and can be used to assess ongoing conservation efforts of the Mexican golden eagle, an important national emblem featured on the Mexican flag.

ABSTRACT CEP-015

The impacts of human exploitation on marine life: a comparative analysis of extant and extinct sirenians

Speaker: **Lydia Furness**
University of Oslo, Norway

Co-authors: Bastiaan Star[1], Cristina Brito[2], James Barrett[3]

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[2] NOVA University Lisbon, Portugal
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Abstract:

Throughout history, marine resources have been integral to human society. However, knowledge about how, where and when they were used is limited, making it challenging to assess impacts of exploitation. Fitting within a multidisciplinary project, we investigate impacts of human exploitation on Sirenia, a taxon of large, herbivorous marine mammals. Despite their cultural and economic importance, sirenians remain chronically understudied and their extinction is a growing concern. Populations are slowly disappearing. 250 years ago, we saw the extinction of the last Arctic adapted species – Steller's sea cow. And over the last decade we have observed localised extinctions, such as Okinawa and China Sea dugongs. Despite conservation efforts, human activity is clearly having a detrimental impact on sirenians. There is likely significant population substructure and genetic differentiation within species, and differing intrapopulation genetic diversity. The extent of this is un explored; many prior population genetic studies have been limited to specific regions and/or the mitogenome D-loop. We have compiled the largest assemblage of historic sirenians, on a global scale, to date. All extant species and one extinct species are represented in our dataset. This includes significant numbers of African and Amazonian manatees, both of which are largely neglected within published literature. We have successfully sequenced whole mitogenomes from historical specimens of all extant species, and selected those with highest endogenous DNA (>50%) for deeper whole genome sequencing. Our objective is to use these novel genetic data to better understand 1) why Steller's sea cow became extinct, 2) how extant species have been impacted by human activity, and 3) if these impacts differ across space and over time. The findings from this study will be placed in the wider framework of historical ecology and, crucially, contribute to sirenian conservation in the context of on going human activity.

ABSTRACT CEP-016

A comparative study of commercially available minimally invasive sampling protocols on Early Neolithic humeri analysed via palaeoproteomics

Speaker: **Jakob Hansen**

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Co-authors: Joannes Dekker[1], Maria Saña Sequí[2], Frido Welker[3]

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Abstract:

Due to methodological improvements in archaeological sciences, an increasing number of archaeological specimens undergo destructive sampling. However, the preservation of cultural heritage is one of the primary concerns. Therefore, it is crucial to maintain a fair balance between obtaining sufficient material for a meaningful analytical outcome while ensuring the integrity of the remains for potential future analyses. Within palaeoproteomics, a number of minimally invasive sampling approaches exist, all with their respective limitations and benefits. To date, all such comparative studies have considered material from homogenous preservation environments using Zooarchaeology by Mass spectrometry (ZooMS). Here we expand on these earlier studies, extending the comparison to samples from two highly different environments present at the same archaeological site. We compare five sampling approaches on 10 Bos sp. humeri from the Early Neolithic site of La Draga, Spain, analysed using both ZooMS and Liquid-Chromatography Tandem Mass Spectrometry (LC-MS/MS). We further assess their invasiveness using microscopy and 3D imaging. Five humeri originate from Sector A (a dry terrestrial environment), while the remaining humeri originate from Sector B (a mostly phreatic/aquatic environment). We show that there is a significant difference in protein recovery in regard to sampling approaches applied and between local burial environments. Additionally, various surface modifications were observed depending on the specific sampling technique applied. It is essential to assess the protein preservation for each site before performing sampling on precious material, as protein preservation can be highly inter- and intra-site-specific.

ABSTRACT CEP-017

beDNA: A project for systematic collection of archaeological human samples for palaeogenetics purposes

Speaker: **Céline Bon**
Muséum national d'Histoire naturelle, France; Université de Paris, France; Musée de l’Homme, France

Co-authors: Pauline Ehrhardt[1,2,3], Philippe Chambon[1,2,3], Eric Gimel[1,2,3], Evelyne Heyer[1,2,3], Sophie Lafosse[1,2,3], Pascal Sellier[1,2,3], Aline Thomas[1,2,3]

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[3] Musée de l’Homme, France

Abstract:

Palaeogenetics is becoming increasingly important in archaeological studies. However, analyses of ancient DNA can be hampered by the state of preservation of samples due to poor storage conditions, and contamination by modern DNA. Moreover, the dispersion of samples in a multitude of structures makes sample tracking complex and results in the implementation of variable criteria for each invasive study authorisation, making analysis requests more complicated. The beDNA project for a national archaeological genetic data and sample bank (banque d’échantillons et de Données Nationale Archéogénétique), set up by UMR 7206 Éco-Anthropologie (EA) aims to develop the ways to facilitate future palaeogenetic analyses by systematically storing human skeletal samples from all current and future archaeological operations in France. The beDNA bank, placed under the authority and control of the French Ministry of Culture, will provide optimal conservation conditions for ancient DNA and a centralized monitoring of samples. This project includes (1) a systematic sampling protocol for archaeological human remains common to all archaeological operations, (2) a storage space for the samples, dedicated to the project and suited to aDNA preservation at the Musée de l’Homme (MNHN Paris), (3) a database linking sites with the samples stored in the bank, accessible to all researchers carrying out a genetic study project as well as (4) an approval of sample analysis requests by the French authorities, after a pair review. The test phase of the project, which began in September 2020 in the Île-de-France region, enabled us to evaluate and adjust both the sampling protocol in the field and the transfer process to the beDNA bank, with samples taken during various archaeological operations. Since the beginning of the test phase, as of March 2023, the beDNA banks holds a total of 337 samples corresponding to 194 individuals collected from 19 excavation sites.

ABSTRACT CEP-018

Towards more sustainability in palaeoproteomics? A digestion time comparison for cost and electricity reduction in ancient bones analyses

Speaker: **Louise Le Meillour**
University of Copenhagen, Denmark

Co-authors: Virginie Sinet-Mathiot[1], Jakob Hansen[2,3], Dorothea Mylopotamitaki[1,4], Jorsua Herrera Bethencourt[2], Karen Ruebens[4], Gaudry Troché[2], Huan Xia[5], Ragnheiður Diljá Ásmundsdóttir[2], Geoff M. Smith[6], Zandra Fagernäs[2], Frido Welker[2]

[1] Max Planck Institute for Evolutionary Anthropology, Germany
[2] University of Copenhagen, Denmark
[3] Universitat Autònoma de Barcelona, Spain
[4] Collège de France, France
[5] Lanzhou University, China
[6] University of Kent, UK

Abstract:

Climate change is a major crisis society is facing, and the scientific community needs to take part in this massive challenge. One way of transitioning to a more sustainable science is by reducing electricity and plastic consumption in the lab. This can be achieved by re-thinking steps in existing protocols, such as the enzymatic hydrolysis of proteins in (palaeo)proteomics sample preparation prior to mass spectrometry analyses. Palaeoproteomic methods such as ZooMS (Zooarchaeology by Mass Spectrometry) and SPIN (Species by Proteome INvestigation), allow for retrieval of biological information from archaeological material, and classically imply digestion with trypsin overnight (18h), with the samples placed in heating blocks to maintain an optimum temperature of 37°C. Here we explored the effects of reducing digestion time from 18 to 3 hours on herbivore skeletal elements from Baiyisha Karst Cave (China) and La Draga (Spain), covering a chronological range from the Middle Pleistocene to the Early Holocene and representing various preservation stages. Each sample was reduced to powder and split between digestion conditions (3, 6 and 18 hours digestions) and then analytical methods (MALDI-ToF-MS and LC-MS/MS). Our results indicate no statistical changes between 3 and 18 hours digestion, and a reduction of electricity consumption. Reducing digestion time from 18 to 3 hours enables proteome recovery, COL1 sequence coverage, and taxonomic identifications to be retained while optimising protocol time efficiency and sustainability. The SPIN analysis indicates the identification of non-collagenous proteins (NCPs) for two additional samples with 3h digestion time compared to both 6h and 18h, while species identification success was similar for all digestion times. Thus, our analyses show that environmental impact can be reduced without affecting data quality, thereby taking an important step towards more sustainable scientific practices.

ABSTRACT CEP-019

Tracking the role of marine resources to food security and livelihoods in postcolonial southern Brazil through chemical analysis of pottery

Speaker: **Alice Di Muro**
University of York, UK; Universitat Autònoma de Barcelona, Spain

Co-authors: Oliver Craig[1], André Carlo Colonese[2]

[1] University of York, UK
[2] Universitat Autònoma de Barcelona, Spain

Abstract:

The southern Atlantic Forest coast of Brazil is considered a world biodiversity hotspot due to its high levels of biodiversity and endemism. However, the region has experienced significant anthropogenic impacts in recent decades, including overfishing, pollution, and habitat destruction, which have led to declines in marine biodiversity and increased vulnerability of coastal ecosystems and the people who depend on them. As a response, small-scale fisheries are becoming a prime example of sustainable coastal use in mainstream conservation agendas. Despite their importance, these fisheries and their communities have been historically neglected, as is typical of tropical and subtropical regions. Archaeological sources attest and study pre-colonial fishing activities, emphasising the importance of marine resources for coastal native peoples (Fossile, et al. PANGEA 2019; Toso, et al. Cell Press 2021). In the 16th century, when Europeans started to settle in this territory, new agricultural plantations, new techniques for the exploitation of natural resources and new urban centres were developed (Pereira, et al. Science Direct 2017). Nevertheless, little is known about the extent coastal resources were exploited in Brazil before incentive to industrial fisheries, and even less is known about the role of fisheries in early urban centres, the establishment of plantation economies, and the country's economic growth during post-colonial time. In this study we used organic residue analysis of ceramic artefacts to shed light into the subsistence and importance of aquatic resources in late 17th and 18th century coastal villages in southern Brazil. We will present the preliminary results of the molecular (GC, GCMS) and isotopic (GC-c-IRMS) analysis of lipid residues extracted from ceramic vessels, which show considerable variability in fishing processing in ceramic vessels

ABSTRACT CEP-020

Working with AROLD. What is the ARchaeological Organic residues Literature Database?

Speaker: **Léa Drieu**
Université Côte d'Azur, France; Cultures et Environnements Préhistoire, Antiquité, Moyen Âge, France

Co-authors: Camielsa Prévost[1,2], Martine Regert[1,2], Antoine Pasqualini[1,2]

[1] Université Côte d'Azur, France
[2] Cultures et Environnements Préhistoire, Antiquité, Moyen Âge, France

Abstract:

For 50 years, Organic Residue Analysis (ORA) in archaeology has flourished and produced exponentially more data which has resulted in an extensive literature. To obtain an overview of the state of the art on lipids, proteins and short-chain polar acids preserved in archaeological archives, and to make it easier to consult and synthesize the data, we designed a database to gather data from published articles in a collaborative way. Currently, The ARchaeological Organic residues Literature Database (AROLD) references data from 397 papers (i.e. 1214 archaeological sites, 1570 sample lots and 25009 archaeological samples). This tool can be used by ORA and non-ORA scientists, via two different user interfaces for collaborators and non-collaborators. The current compilation does not include any critical reviews of the published work, inviting readers to refer to the articles holding the data. The collection and standardization work to build and fill in the database revealed a high variability of data in the literature and highlighted methodological discrepancies. In order to further complete the database and make the published data more accessible to non-ORA specialists, the database is intended to be open to new collaborations to consolidate its objectives and strengthen data moderation. An article dedicated to the elaboration and functioning of this database has now been published: Prévost, C., Drieu, L., Pasqualini, A., & Regert, M. (2023). The ARchaeological Organic residues Literature Database (AROLD): construction of a tool for reviewing and querying published lipid data in organic residue analysis. Archaeometry. https://doi.org/10.1111/arcm.12869. Presenting a poster at ISBA is an opportunity to share this burgeoning work and to invite the community to get involved in this project and discuss with us how AROLD will be incremented and upgraded with future studies.

ABSTRACT DENP-001

Herbarium DNA confirms 20th-century presence in Europe of Phytophthora lineage that caused Irish Potato Famine

Speaker: **Donikë Sejdiu**
University of Zurich, Switzerland

Co-authors: Jurriaan M. de Vos[1], Reinhardt Berndt[2], Simon Aeschbacher[3], Verena J. Schuenemann[3]

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Abstract:

Plant pathogens may have a strong impact on human societies by infecting crops and causing economic losses and famine. An example of a pathogen with devastating consequences is Phytophthora infestans, an oomycete that induces late blight on potato and tomato. After its introduction to Europe in the mid-19th century, P. infestans caused severe outbreaks, including the Irish Potato Famine. Previous herbarium genomic studies identified HERB-1 as the lineage responsible for these historic outbreaks, but also suggested that HERB-1 was globally replaced by other lineages during the first half of the 20th century. However, HERB-1 genomes have recently been isolated from Mexico and South America in the 1980s and 2000s, and one HERB-1 lineage was sampled in Germany in 1926. If and when HERB-1 went extinct in Europe thus remains uncertain. To address this question, we extracted herbarium DNA from 26 infected potato and tomato specimens collected in Europe in the 19th and 20th century . We sequenced 19 mitochondrial genomes at 6- to 34-fold mean coverage and combined them with 73 published historical and modern mitochondrial genomes. Phylogenomic analyses revealed that HERB-1 still existed in Europe in 1946, confirming that HERB-1 did not go extinct in Europe shortly after the 19th century outbreaks, but rather persisted well into the 20th century. Further, we see the rise of new lineages, for instance US-1, which continues to cause severe outbreaks. Our results demonstrate the value of herbarium genomics in biogeographic analyses of plant-pathosystems.

ABSTRACT DENP-002

Palaeoproteomic and Genomic Analyses of Bronze Age Population from Unětice Culture, Moravia, Czech Republic

Speaker: **Eva Chocholová**
Masaryk University, Czech Republic

Co-authors: Eva Chocholová[1], Anna Šenovská[1], Pavel Roudnický[2,1], Zbyněk Zdráhal[2,1], Kristýna Brzobohatá[1], Dana Fialová[1], Petr Kos[1], Eva Drozdová[1]

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Abstract:

Mitogenome research offers an intriguing insight into the history, origin, contacts, and variability of past populations and has become standard in the study of past populations. Dental calculus is also a well-known and valuable source of information that is used to investigate health, diet, or habits in the context of biomolecular archaeology. The studied individuals were excavated at a Bronze Age site of Brno-Tuřany, Moravia region, Czech Republic. They belonged to the Unětice culture, dated to 2300-1600 BC. For the present study, we decided to combine both approaches: genomic analysis of mitochondrial DNA in 16 individuals and proteomic analysis of dental calculus in 8 individuals. Sampling, decontamination, ancient DNA extraction, library preparation, and the first stages of protein extraction were carried out in the specialised facility for ancient biomolecules in the Laboratory of Biological and Molecular Anthropology. DNA was purified using silica columns and the whole mitogenome libraries were prepared according to Šenovská et al. (Forensic Sci. Int. 2021) with mtDNA capture. The proteins were extracted with the FASP protocol modified for ancient biomolecules. LC-MS/MS analysis was performed on timsTOF Pro combined with nanoElute (Bruker). Based on mtDNA, the population from Brno-Tuřany was very variable and six general haplogroups were found: N (1), W (1), H (4), V (2), K (1), and the most frequent U (7). No shared haplotype occurred between the studied individuals. The identified dietary proteins originated from, e.g. Bos sp., Ovis/Capra sp., Triticum aestivum or Brassica sp. Biomolecular approach in archaeology therefore offers new insights into past populations.

ABSTRACT DENP-003

Exploring Dietary Change in Ireland through Proteomic and Lipid Analysis of Dental Calculus

Speaker: **Meaghan Mackie**
University College Dublin, Ireland; University of Turin, Italy

Co-authors: Susan Flavin[1], Federica Dal Bello[2], Dominique Scalarone[2], Meriel McClatchie[1], Cynthianne Spiteri[2], Beatrice Demarchi[2], Robert C. Power[3]

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Abstract:

In the last decade, many studies have turned to the potential of ancient dental calculus, or the mineralisation of plaque biofilm created by a wide range of microscopic organisms residing in the oral cavity, in order to better understand ancient diets. During the mineralisation process, elements from ingested food, inhaled particles, the oral microbiome, and the human host get trapped and preserved within the mineral matrix. This allows one to investigate direct evidence of consumption on an individual level, and examine patterns of change throughout time and place. Dental calculus analysis is especially useful where preservation of zooarchaeological and archaeobotanical remains is not ideal, such as the fairly acidic soils of Ireland. Therefore, calculus samples from early modern Ireland (c. 1550–1650) were examined here with proteomics and lipid mass spectrometry analysis techniques. These approaches were chosen due to their potential ability to not only identify species, but also the specific tissue or source (such as meat vs milk), which is critical for the study of dietary components. While palaeoproteomics has increasingly been applied to ancient dental calculus, lipid analysis is still not mainstream and this study examines the potential of their combined and complementary use. In addition, this study is important for understanding the highly transitional diet during the early modern period, caused by religious reformation, colonisation and globalisation. New foods arrived in Europe during this time, including many that are now seen as quintessential to European and specifically Irish diets. Combining dental calculus analysis and historical records will help give a better overview of this transition and when certain foods become available in specific contexts. Not only is this important for the understanding of diet and trade in this period, the results will be useful for understanding the potential of calculus, even where no written record survives

ABSTRACT DENP-004

Palaeoproteomic evidence reveals dairying supported prehistoric occupation of the highland Tibetan Plateau

Speaker: **Li Tang**
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Co-authors: Shevan Wilkin[1], Kristine Korzow Richter[2], Ashley Scott[2], Madeleine Bleasdale[3], Ricardo Fernandes[4], Patrick Roberts[4], Robert Spengler[4], Yuanhong He[5], Shuai Li[5], Feng Yang[5], Haibing Yuan[5], Hongliang Lu[5], Michael Petraglia[6], Fallen K.Y. Teoh[7], Yan Tong[8], Tinlei Tsering[8], Yang Tsho[8], Zujun Chen[8], Wei He[8], Shargan Wangdue[8], Lin Xi[9], Nicole Boivin[10,11,12,13]

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[5] Sichuan University, China
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[10] Max Planck Institute for the Science of Human History, Germany
[11] University of Queensland, Australia
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Abstract:

The extreme environments of the Tibetan Plateau offer significant challenges to human survival, demanding novel adaptations. While the role of biological and agricultural adaptations in enabling early human colonization of the plateau has been widely discussed, the contribution of pastoralism is less well understood, especially the dairy pastoralism that has historically been central to Tibetan diets. Here, we analyze ancient proteins from the dental calculus (n=40) of all human individuals with sufficient calculus preservation from the interior plateau. Our palaeoproteomic results demonstrate that dairy pastoralism began on the highland plateau by ~3500 years ago. Patterns of milk protein recovery point to the importance of dairy for individuals who lived in agriculturally-poor regions above 3700 masl. Our study suggests that dairy was a critical cultural adaptation that supported expansion of early pastoralists into the region’s vast, non-arable highlands, opening the Tibetan Plateau up to widespread, permanent human occupation.

ABSTRACT DENP-006

New biomolecular methods for exploring vitamin D status in the past and a case study from Nunalleq, Alaska

Speaker: **Eléa Gutierrez**
University of Aberdeen, UK

Co-authors: Orsolya Czére[1], Baukje De Roos[1], Gary Duncan[1], Kate Britton[1]

[1] University of Aberdeen, UK

Abstract:

Vitamin D deficiency is linked to a wide range of adverse health effects, the risk of which are increased for populations living at latitudinal extremes where limitations are placed on the dermal synthesis of vitamin D3 due to insufficient sunlight, particularly during winter. This represents a significant health challenge for populations living in the circumpolar north, past and present. The consumption of food sources with high vitamin D content, however, can mediate this risk. Indeed, traditional subsistence strategies in high-latitude areas are often focused on food sources rich in vitamin D3, such as salmon and marine mammals. Recent developments in biomedical sciences have offered non-invasive means of quantifying vitamin D status in individuals through the determination of 25(OH)D3 content in hair (Zgaga, et al. Nutrients 2019). Where this tissue is preserved, this technique has the potential to allow an empirical indication of vitamin D status in archaeological individuals and can permit co-analysis with dietary indicators. Here, we will present intra-strand 25(OH)D3 data extracted from archaeological hair samples for the first time. Our case study focuses on hair recovered from non-mortuary contexts from the precontact Yup'ik site of Nunalleq (1450-1650 AD), Alaska. The detection of seasonal variability (δ18O, δ2H) of 25(OH)D3 content in incremental samples of hair, in tandem with the analysis of dietary (δ13C, δ15N) indicators, reveals important new insights into dietary seasonality, and links to vitamin D status at the site. We warmly thank Qanirtuuq Inc, Nunalleq Museum, and the people of Quinhagak for permissions to undertake this research.

ABSTRACT DENP-007

Reconstructing Viking diets in Aarhus, Denmark with compound-specific isotopic analysis of amino acids

Speaker: **Kyungcheol Choy**
Hanyang University, South Korea

Co-authors: Hee Young Yun[1], Benjamin T. Fuller[2], Dain Swenson[2], Jacob Kveiborg[3], Kenneth Ritchie[3], Mogens Høegsberg[3], Jette Linaa[3], Lars Krants Larsen[3], Jesper Olsen[2], Marcello A. Mannino[2,3]

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[2] Aarhus University, Denmark
[3] Moesgaard Museum, Denmark

Abstract:

Compound specific stable isotope analysis of amino acids (CSIA-AA) is a powerful tool for explaining dietary behaviors in complex environments and improving dietary reconstructions based on bulk collagen. In this study, we applied the CSIA-AA method to humans (n= 4) and animals (n=35) from Viking Age contexts in Aarhus (Denmark) to investigate dietary patterns. Results of estimated trophic positions (TP) using d15N AA Glx-Phe show that these Viking individuals from Aarhus relied heavily on terrestrial sources (livestock and poultry), even though some of their bulk nitrogen isotope values are quite high. Principal component analysis of essential amino acid (EAA) d13C values (Val, Leu, Ile, Thr, Phe, Lys) and d15N values (Val, Leu, Ile, Phe) show that Viking humans closely cluster with domestic birds and mammals, suggesting high consumption of terrestrial resources. Quantitative estimation by MixSIAR confirmed that the main EAA sources for the Viking humans were from domestic mammals and birds. The results of this compound specific analyses will be interpreted in the light of contextual archaeological information, as well as zooarchaeological evidence and stable isotope analysis of human bulk collagen samples.

ABSTRACT DENP-008

Island life before violent death - multi-isotopic analysis of plants, animals and humans from Sandby borg, Öland (Sweden)

Speaker: **Gunilla Eriksson**
Stockholm University, Sweden

Co-authors: Kerstin Calleberg[1], Markus Eklund[1], Matti Leino[1], Kerstin Lidén[1]

[1] Stockholm University, Sweden

Abstract:

The Migration Period ringfort of Sandby borg, situated at the coast of the Swedish island of Öland in the Baltic Sea, was violently attacked in the sixth century CE. Excavations of about 10% of the area inside the fortified dwelling, has uncovered more than 30 victims of this massacre, and previous osteoarchaeological analysis of these has demonstrated the brutality of their death. Less is known about their life prior to the assault – their diet, origin, mobility and agricultural practices. To remedy this, human and faunal skeletal remains as well as charred cereals from the site were subjected to multi-isotopic analysis (carbon, nitrogen, sulphur, strontium). The results will be discussed both with regards to various methodological considerations, and in the context of the social unrest of that time, which also includes the 536 CE climatic event.

ABSTRACT DENP-009

Assessing the weaning process of ancient individuals using machine learning and Bayesian modeling on stable isotope data of dentinal collagen

Speaker: **Elissavet Ganiatsou**
Democritus University of Thrace, Greece

Co-authors: Angelos Souleles[1], Angeliki Georgiadou[1], Tania Protopsalti[2], Stavroula Tzevreni[2], Krino Konstantinidou[2], Stella Vasileiadou[2], Christina Papageorgopoulou[1]

[1] Democritus University of Thrace, Greece
[2] Ministry of Culture and Sports, Greece

Abstract:

In this study, we combined multiple computational approaches to reconstruct the weaning practices in ancient Thessaloniki, the capital of Provincia Macedonia and one of the largest metropoles of the Roman Empire. Our sample population comprises of isotopic measurements (δ13C, δ15N) of first permanent molars from 66 individuals (780 samples) mostly dated between 168 BC-323 AD. We developed the first tool that estimates the weaning duration mathematically using serial measurements of stable nitrogen ratios1. We employed the Bayesian model MixSIAR to estimate the relative proportion of breast milk in the weaning diet using for the first time isotopic data from dentinal collagen. Furthermore, we used the k-means algorithm to identify patterns related to physiological stress based on the premise that carbon and nitrogen ratios change oppositely during periods of stress. Overall, the examined individuals were weaned by the age of 2.0 on average, but cases of prolonged (after the age of 3.0) and shortened (less than one year) weaning duration were found underpinning the diversity of life conditions and cultural practices, which influenced the decisions made regarding the timing of weaning. The duration of weaning did not correlate with the proportion of breast milk, indicating that the frequency of breast milk feeds wasn't gradually reduced over time but rather abruptly discontinued. The k-means algorithm identified a cluster of individuals with isotopic evidence of stress during and after the weaning process. Our study introduces new ways of analysing isotopic data and shows how machine learning and Bayesian modelling techniques can be incorporated into bioarchaeological research to answer more complex research questions and gain insights into the feeding strategies of ancient societies. Ganiatsou, et al. Archaeol. Anthropol. 2023

ABSTRACT DENP-010

The Baltic Kindergarten: a multifaceted study of infant health and feeding practices in medieval and early modern Estonia through stable isotope analysis

Speaker: **Alessandra Morrone**
University of Tartu, Estonia

Co-authors:

Abstract:

Studying non-adult diet and stress through stable isotope analysis provides direct insights into the lives of vulnerable groups in the past. The diet of children in medieval and early modern Livonia, as well as the effects of the numerous famines, wars, and epidemics of the time on the non-adult population, are still an unknown topic in Baltic bioarcheology. With this presentation, a new research project aimed at exploring non-adult diet in urban/rural Estonian communities during the 12th-18th centuries AD is introduced, covering aspects such as feeding practices and physiological stress during this period of Estonian history. The impact of socio-economic circumstances on childhood nutrition, affecting the growth and overall survival of young children, represents the focus of this research. In our recent study, cross-sectional analysis was performed on bone collagen from 176 individuals between the fetal and the 7-15 age categories from four urban/rural South-Estonian cemeteries via EA-IRMS for δ13C and δ15N. Results indicated that South-Estonian children had a staple terrestrial C3 diet integrated with animal proteins. Significant differences were observed between urban/rural sites and among rural subgroups. Breastfeeding was likely practiced for 1-2 years, introducing supplementary foods at around 1 year of age. The weaning process was probably concluded around the age of 3. The isotopic values of older children were comparable to those of adults, indicating their diets became similar after weaning, when labor started and they obtained a more mature status. Furthermore, the numerous perinates allowed exploring the impact of maternal physiological stress, malnutrition and metabolic disorders on their isotopic values. Together with this preliminary data, results of the ongoing research on seven additional Estonian sites will be revealed, providing the first bone and dentine incremental data regarding infant feeding practices in medieval and early modern Livonia.

ABSTRACT DENP-012

The function of the early Patagonian hunter-gatherer pottery (Argentina) explored through organic residue analysis

Speaker: **Alejandro Serna**
University of York, UK; Universidad Nacional de La Plata, Argentina

Co-authors: Alexandre Lucquin[1], Marjolein Admiraal[1], Javier A. Montalvo-Cabrera[1], Luciano Prates[2], Daniela Saghessi[2], André C. Colonese[3], Paola Ponce[1], Gustavo Martínez[4], Erika Borges Vaz[4], Florencia Borella[4], Cristina Bellelli[5], Verónica Aldazábal[5], Alberto E. Pérez[6], Julieta Gómez Otero[7,8], Emiliano Mange[2], Lucio González Venanzi[2], Victoria Romano[2], Federico L. Scartascini[9,10], Marcelo Vitores[11], Miguel Á. Zubimendi[2,10], Laura Miotti[2,10], Oliver E. Craig[1]

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[3] Universitat Autònoma de Barcelona, Spain
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[5] Universidad de Buenos Aires, Argentina
[6] Universidad Católica de Temuco, Chile
[7] Centro Nacional Patagónico, Argentina
[8] Universidad Autónoma de Chile, Chile
[9] Universidad Nacional de Rio Negro, Argentina
[10] Consejo Nacional de Investigaciones Científicas y Técnicas, Argentina
[11] Universidad Nacional de Luján, Argentina

Abstract:

Ceramic technology is a key feature for allowing more efficient exploitation of the environment and for fostering different kinds of cultural expressions associated with it. While recent data from the Northern Hemisphere suggest that pottery was a hunter-gatherer innovation aimed at the processing of aquatic resources, the adoption of pottery in other regions remains poorly understood. In Patagonia, the southernmost limit of pottery dispersal in the Americas, pottery was scarcely used by hunter-gatherers over a predominantly arid/semi-arid vast landscape for ca. 2000 years. Here we explore the function of Late Holocene Patagonian hunter-gatherer pottery through organic residue analysis. One-hundred pottery samples from sites across Patagonia were analyzed using gas chromatography-mass spectrometry (GC-MS) and compound-specific isotope analysis of individual lipids by GC-combustion-isotope ratio-MS (GC-c-IRMS) (C16:0, C18:0). Through well-established molecular and isotopic criteria, we discern the types of commodities (e.g., marine, freshwater, ruminant, non-ruminant and plant) that might have been processed using ceramic containers. Our results are used to examine whether the adoption of pottery by Patagonian hunter-gatherers was driven by the need to process aquatic resources, as is suggested for the Northern Hemisphere, or if different processes are at play in this southernmost region of pottery dispersal in the Americas.

ABSTRACT DENP-013

Metabolic adaptations reflect increased dependence on an aquatic diet in the Neolithic transition of Eastern Europe

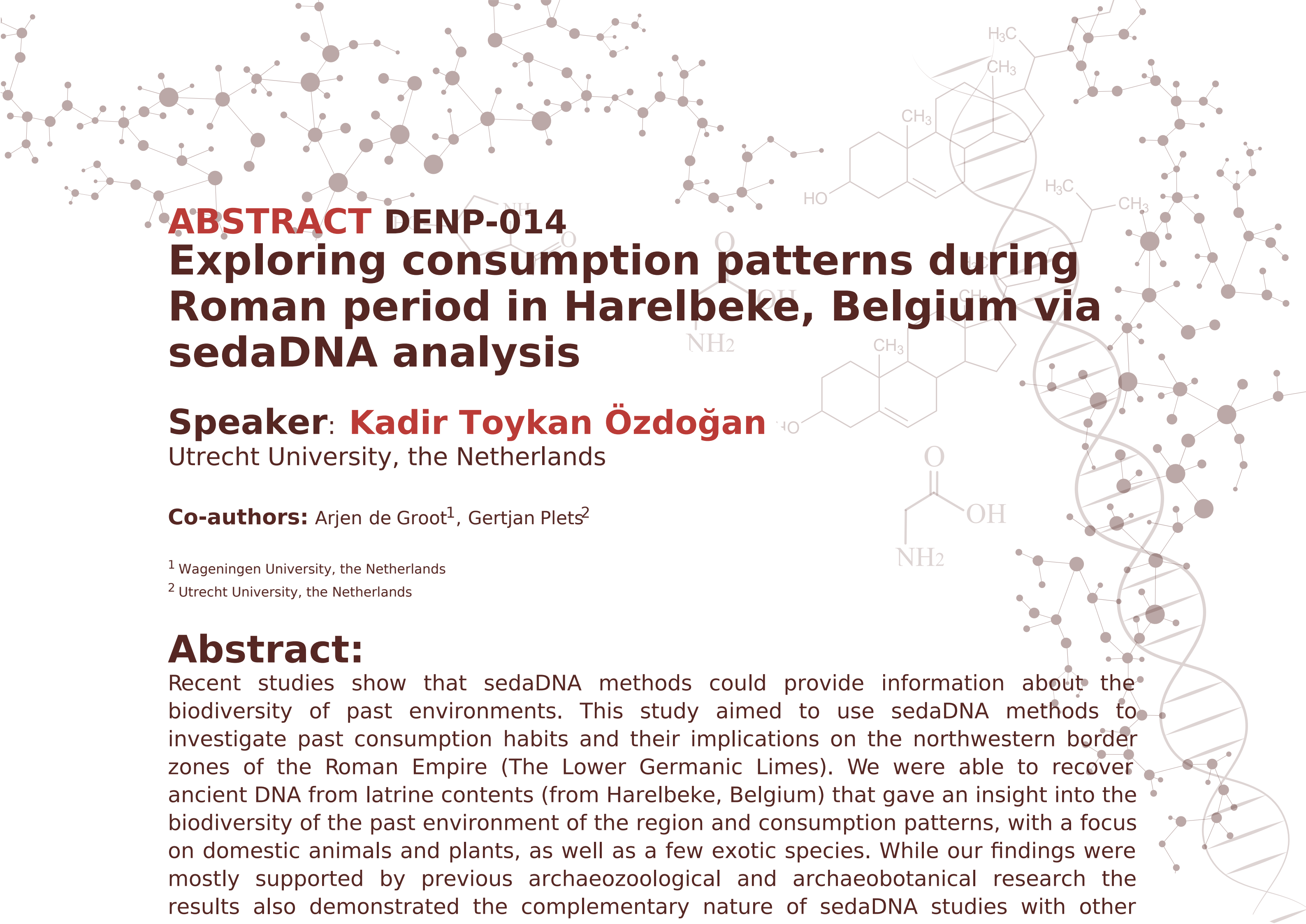
Speaker: **Kaur Kivirüüt**
University of Tartu, Estonia

Co-authors: Anders Eriksson[1]

[1] University of Tartu, Estonia

Abstract:

There were two distinct waves of neolithization across Europe. The first, originating from the Near East, spread quickly westwards across the subcontinent and introduced animal husbandry, agriculture and pottery. In contrast, in Eastern Europe (specifically areas that encompass modern-day Latvia and Ukraine), agriculture was not adopted as a primary subsistence economy until the beginning of the Bronze Age, although some features of the Neolithic package, such as ceramics, appeared earlier, possibly originating instead from East Asia. During the Late Mesolithic and Early Neolithic these differing communities lived side-by-side for well over a millennium. Although there is evidence of interaction between them, the intensity and range of trade and mixing remains unclear. The possible introduction of cattle and grains from western farmers to eastern hunter-gatherers would have likely constituted as a significant change in environment and food sources. Here we test the hypothesis that such lifestyle changes were accompanied by natural selection at genetic loci related to metabolism. In order to compare populations from different environments and across time periods, polygenic scores (PGS) were calculated by combining genetic information from human remains (ancient DNA) with estimates of the effect of genetic variants on blood concentrations of circulating metabolites from a recent genome-wide association study. We tested formally for selection by comparing the observed metabolite PGSs to the distribution of PGS from randomly chosen genetic variants with matching frequencies in the ancestral population. We find a strong decrease in triglyceride levels along with a shift from low- to hight-density cholesterol particle concentrations and demonstrate that these changes in Early Neolithic Eastern individuals are not caused by gene-flow from neighbouring farming communities but more likely arise from an increasing reliance on an aquatic diet rich in omega-3 fatty acids.



ABSTRACT DENP-014

Exploring consumption patterns during Roman period in Harelbeke, Belgium via sedaDNA analysis

Speaker: **Kadir Toykan Özdoğan**
Utrecht University, the Netherlands

Co-authors: Arjen de Groot[1], Gertjan Plets[2]

[1] Wageningen University, the Netherlands
[2] Utrecht University, the Netherlands

Abstract:

Recent studies show that sedaDNA methods could provide information about the biodiversity of past environments. This study aimed to use sedaDNA methods to investigate past consumption habits and their implications on the northwestern border zones of the Roman Empire (The Lower Germanic Limes). We were able to recover ancient DNA from latrine contents (from Harelbeke, Belgium) that gave an insight into the biodiversity of the past environment of the region and consumption patterns, with a focus on domestic animals and plants, as well as a few exotic species. While our findings were mostly supported by previous archaeozoological and archaeobotanical research the results also demonstrated the complementary nature of sedaDNA studies with other archaeological methods for investigating historical periods, especially for the species which are difficult to detect with other methods. Therefore, this study highlights the potential of sedaDNA methods for improving our knowledge of the past and contributes to our understanding of ancient societies and their interactions with the environment. Furthermore, the future sedaDNA research in the Limes area has the potential to provide a more comprehensive understanding of consumption habits in the border zones of the Roman Empire.

ABSTRACT DENP-015

Identification of oral pathogens and dietary components from three chewed pitch pieces from Huseby Klev

Speaker: **Emrah Kırdök**
Mersin University, Turkey

Co-authors: Natalija Kashuba[1], Hege Damlien[2], Mikael A. Manninen[3], Bengt Nordqvist[4], Anna Kjellström[5], Mattias Jakobson[1], A. Michael Lindberg[6], Jan Stora[5], Per Persson[2], Björn Andersson[7], Andrés Aravena[8], Anders Götherström[5,10]

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Abstract:

Ethnographic accounts describe the use of birch bark pitch as an adhesive from many parts of the northern hemisphere. Potentially because of anti-inflammatory properties,the pitch was also chewed, while the chewed pieces contain human DNA sequences and sequences of human oral bacteria. This kind of material has great potential to provide information on oral bacterial composition and diet (Kashuba, et al. Communications Biology 2019; Jensen, et al. Nature Communication 2019). Here we present pathogen- and diet related DNA sequences from three chewed pitch pieces, or “chewing gums”, obtained from the Mesolithic Huseby Klev site, that have produced the earliest human DNA in Scandinavia, dated to 9890-9540 cal BP (Jensen, et al. Nature Communication 2019). To understand the metagenomic content in the chewed pitch material, we first identified bacterial composition and compared it to the human microbiome dataset. The composition in the studied chewed pitch pieces show higher similarities to human oral microbiome samples than other parts of the human microbiome. Next, we authenticated microbiome related ancient DNA reads and the results show a high abundance of commensal and pathogenic microbes that cause periodontal and systemic diseases. Several of these pathogens (e.g. Treponema denticola) are confirmed to be found in periodontitis specific conditions. Moreover, we identified DNA sequences from eukaryotic species such as red fox, red deer, hazelnut, and apple. Huseby Klev is located in a transitional ecotone between terrestrial and marine ecosystems, and the analysis of the archaeozoological remains and plant macrofossils from the site also identified the same species (Boethius, et al. Quaternary Science Reviews 2022). Therefore, the animal and plant DNA in the pitch material is supported by the archaeological data. In conclusion, our results show a Mesolithic hunter-gatherer site with members who had periodontitis specific oral bacteria and utilized both terrestrial and marine resources.

ABSTRACT DOMP-001

Tracking ancient livestock pathogens across the domestication process.

Speaker: **Louis L'Hote**
Trinity College Dublin, Ireland

Co-authors: Pernille Bangsgaard[1], Lisa Yeomans[1], Marjan Mashkour[2], Melinda Zeder[3], Kevin Daly[4]

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Abstract:

The Neolithic era in Southwest Asia was marked by the domestication of livestock, which facilitated increased human-animal interactions and amplified the risk of zoonotic disease transmission both within and between animal herds and humans. Despite the successful recovery of numerous ancient human pathogen genomes through high-throughput sequencing techniques, the number of livestock pathogen genomes retrieved remains limited. Our research is directed towards acquiring pathogen and animal metagenomic aDNA from various livestock species and timelines. Specifically, we are interested in obtaining aDNA from 10,000-year-old sheep and goat material from the Zagros Mountains in Iran, a region with some of the earliest evidence of goat herding and the zoonotic brucellosis in humans. The objective of this project is to recover livestock pathogens from the earliest phases of domestication, to understand its impact on the evolution and spread of zoonoses within livestock populations and across species barriers. Additionally, we are exploring the genetic health of ancient ovicaprids by examining patterns of inbreeding and genetic diversity at the immune gene and genome levels.

ABSTRACT DOMP-003

Genomic analysis of ancient emmer wheat sheds light into the evolution of the first domestics

Speaker: **Laura Botigué**
Centre for Research in Agricultural Genomics, Spain

Co-authors: Ferran Antolín[1], Alice Iob[2], Nathan Wales[3]

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[2] Centre for Research in Agricultural Genomics, Spain
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Abstract:

Domestic wheat emerged in the Fertile Crescent around 11,000 years ago and dispersed towards Africa, Asia and Europe together with agricultural practices, adapting to new climates and ecological niches. Previous work done in our group has found evidence supporting either a dual domestication of emmer or a long differentiation process prior to its dispersal out of the Fertile Crescent. Briefly, modern emmer landraces from the northwest (Euope and Iran) are closest to wild emmer from northern Levant, while modern emmer landraces from the southeast (Africa, Arabian Peninsula and India) form a differentiated cluster with influence from wild emmer from southern Levant. Incidentally, a 3,000-year-old emmer specimen from Egypt clusters with the southeast group, confirming that the genetic architecture of the southeast group is ancient and representative of the initial germplasm that dispersed out of the Fertile Crescent. We have recently obtained eight more wheat specimens from two archaeological sites in Egypt (Deir el-Bahari and Abusir). Initial screening of the genomic libraries showed that samples from Deir el-Bahari showed excellent preservation (>20% endogenous content), while samples from Abusir, even if more degraded (0.4% endogenous content) were suitable for exome sequencing. Genetic variability from these samples will be analysed together with the previously published ancient sample in order to better understand how the ancient Egyptian emmer clusters with the modern southeast germplasm, and will be used to assess the influence of wild emmer from southern Levant. Results will shed light into the dispersal of early domestics out of the Fertile Crescent and the contributions of the different wild germplasms into the domestic pool.

ABSTRACT DOMP-004

Molecular clocks and archaeogenomics of a Late Period Egyptian date palm leaf reveal introgression from wild relatives and highlight the role of Economic Botany Collections

Speaker: **Natalia Przelomska**
Royal Botanic Gardens Kew, UK

Co-authors: Oscar A. Pérez-Escobar[1], Sidonie Bellot[1], Jonathan M. Flowers[2], Mark Nesbitt[1], Philippa Ryan[1], Rafal M. Gutaker[1], Muriel Gros-Balthazard[3], Tom Wells[4], Benedikt G. Kuhnhäuser[1], Rowan Schley[1], Diego Bogarín[5], Steven Dodsworth[6], Rudy Diaz[1], Manuela Lehmann[7], Peter Petoe[8], Wolf L. Eiserhardt[8], Michaela Preick[9], Michael Hofreiter[9], Irka Hajdas[10], Michael Purugganan[2], Alexandre Antonelli[1], Barbara Gravendeel[11], Ilia J. Leitch[1], Maria Fernanda Torres Jimenez[12], Alexander S. T. Papadopulos[13], Guillaume Chomicki[14], Susanne S. Renner[15], William J. Baker[1]

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Abstract:

The date palm, Phoenix dactylifera, has been a cornerstone of Middle Eastern and North African agriculture for millennia. The earliest evidence for its domestication traces to the Persian Gulf, and its evolution appears to have been influenced by gene flow from two wild relatives: P. theophrasti, currently restricted to Crete and Turkey, and P. sylvestris, widespread from Bangladesh to the West Himalayas. Genomic data from ancient date palm seeds show that gene flow from P. theophrasti to P. dactylifera may have occurred by ~2,200 years ago. Here, we generate DNA sequence data from a ~2,100-year-old P. dactylifera leaf from Saqqara (Egypt), an object currently held at the Royal Botanic Gardens, Kew. Integrating archaeogenomic analysis, molecular-clock dating, coalescence approaches and population genomics, we investigate hybridization between the date palm and its two closest relatives and provide timestamps for its reticulated evolution. The Saqqara date palm shows a close genetic affinity with North African date palm populations, and we find genomic admixture from both P. theophrasti, and P. sylvestris, indicating that both had contributed to the date palm genome by 2,100 years ago. Molecular clocks placed the divergence of P. theophrasti from P. dactylifera/P. sylvestris and that of P. dactylifera from P. sylvestris in the Upper Miocene, but strongly supported, conflicting topologies point to older gene flow between P. theophrasti and P. dactylifera, and between P. sylvestris and P. dactylifera. Our research, the findings of which which could have implications for modern date palm breeding, was only possible thanks to support from RBG Kew's Economic Botany Collections. We highlight recent work concerning these collections, involving Kew's Interdisciplinary Research group.

ABSTRACT DOMP-005

Archaeogenomics of maize evolution in the South American Andes

Speaker: **Shuya Zhang**
The University of Warwick, UK

Co-authors: Hsiao-lei Liu[1], Logan Kistler[1], Christine A. Hastorf[2], Robin G. Allaby[3]

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Abstract:

Maize used as a staple crop evolved from a wild plant called teosinte due to human activities in Mexico approximately 9000 years ago. It then migrated through Central America by approximately 7500 years ago and spread into South America around 6500 years ago. While it is widely known when maize spread to various regions, there is still debate regarding whether maize had undergone complete domestication prior to its arrival in South America. In this project, the evolution and spread of maize through the Andes were examined directly over several millennia with the application of next-generation sequencing and analysis technologies using archaeological maize specimens. Screening for the best-preserved representative samples across the collection of Andean maize specimens established 9 samples to take forward for genome analysis. Structure analysis placed the ancient genomes of the Andes, all pre-Inca, into a single group to the exclusion of modern Andean landraces. Genetic distances between ancient genomes established links between maize samples from distinct cultural groups and the occurrence of network hubs. Analysis of selection signatures showed two possible episodes of selection involved in the adaptation to altitude, the first in pre-Inca times and the second more recently. The relationships revealed between ancient genomes provide evidence for cultural interaction through maize in the Andes spreading from a hub in the Southeast, and later spreading across the continent to Brazil. The evidence also suggests the hypothesis of a second wave of maize into the Andes, possibly as late as the Inca period, which may have brought secondary adaptations to altitude. This project will form the foundation of a larger project to sample many more of the archaeological Andean genomes and bring a greater resolution to this period of maize history.

ABSTRACT DOMP-006

Diving into the genomic make-up of turkey (Meleagris gallopavo) domestication

Speaker: **Aurélie Manin**

University of Bordeaux, France; National Museum of Natural History of Paris, France

Co-authors: Benoît Clavel[1], Simon Davis[2], Quentin Goffette[3], Günther Karl Kunst[4], Karl Laumbach[5], Giedre Piličiauskienė[6], Camilla Speller[7]

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Abstract:

The genomics of bird domestication have been only scarcely studied despite their importance in our economy today. The turkey (Meleagris gallopavo) has been domesticated ca. 2000 years ago in at least two regions of North America: the United States Southwest and Central Mexico. When they reached Central America, the Europeans were impressed by the domestic turkeys that they described as “large and tasty chickens” and brought back some individuals as breeding stock. The turkey quickly spread through the backyards of Europe and was subjected to selective breeding over the following centuries. Previous mitochondrial DNA analyses have shown that the modern commercial turkey breeds were the descendents of the turkeys domesticated in Central Mexico. With this study, we push the analysis further to explore the genomic make-up of domestic turkeys through the nuclear DNA. We analyse early introduced birds from Portugal, France, Belgium, Austria and Lithuania to cover for the extent of their rapid spread into Europe. We compared them to a pre-contact domesticated turkey from the United States Southwest as well as published genomes of modern commercial breeds and wild turkeys. This population genomics approach allows us to clarify the process of early turkey selection in Europe as well as to better understand the independent domestication events happening in Mesoamerica and the United States Southwest.

ABSTRACT DOMP-007

The genetic history of sheep in the Iberian Peninsula over the last thousand years

Speaker: **Laura Viñas Caron**
University of Copenhagen, Denmark

Co-authors: Jazmín Ramos Madrigal[1], Matthew Teasdale[2], Christian Carøe[1], Matthew Collins[1,2]

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Abstract:

Sheep were a central component of medieval and early modern economies. In this period, there is evidence of an increase in the wool trade and the growing dominance of the Merino breed as a principal source of wool production worldwide. This breed originated in the Iberian Peninsula during the Middle Ages and today is the most important wool breed in the world. However, its origins and genetic history remain uncertain. The Muslim conquest and later population movements had a tremendous effect on this region's economy and were accompanied by the introduction of new plants and farming techniques. It has been argued that the development of the Merino sheep could have been facilitated by the introduction of new varieties of sheep during the Islamic period, possibly from northern Africa or the Middle East, and/or local improvements in wool quality. Here, we present preliminary genetic data from Spain over the past 1,000 years to explore sheep genetic variability and animal exchanges within the Mediterranean and North Africa. In addition, a significant difficulty in previous studies has been recovering ancient DNA from warm environments such as the Iberian Peninsula. We explore a novel approach to circumvent this challenge, integrating parchment manuscripts and archaeological remains from various geographic contexts. We found that endogenous DNA levels recovered from parchment were typically higher than those of skeletal elements and presented low deamination. Thus, we show the potential that parchment holds to uncover the recent history of livestock species.

ABSTRACT DOMP-008

Reconstructing reindeer grazing and mobility patterns in northern Fennoscandia – multi-isotope analyses of reindeer bones from the Piteå and Skellefteå River valleys in northern Sweden

Speaker: **Markus Fjellström**

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Silvermuseet/INSARC, Sweden

Co-authors: Aikaterini Glyokou[1], Kerstin Lidén[1], Anna-Kaisa Salmi[2]

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Abstract:

Reindeer has always been an important asset to people living in northern Fennoscandia. No matter whether they were wild or domesticated, hunted or herded. The aim of this study is to explore the development of reindeer domestication in a Sámi context from the Late Iron Age to the 20th century from the mountains to the Bothnian Sea along the Piteå and Skellefteå River valleys in northern Sweden. The archaeological material consists of unburnt reindeer skeletal remains from archaeological sites, such as Stállo foundations, hearths, a market place, and a Forest Saami timbered hut. Interdisciplinary methods were deemed necessary since the material is rather scarce in order to retrieve the most information about past landscape use in relation to reindeer grazing and mobility. To address the research objectives, we applied multiple stable isotope analysis (δ13C, δ15N, δ34S, δ18Op) and 87Sr/86Sr combined with radiocarbon dating. By studying reindeer grazing patterns, local geology, and climatic variation we show that there was variation in diet and mobility through time at different archaeological sites. Further, our study indicates a difference in diet and mobility that highly likely reflects both a nomadic and/or semi-nomadic way of life and that reindeer has been hunted or/and herded at all sites in the study.

ABSTRACT DOMP-009

Evidence for differences in amino acid carbon isotope values of domestic and wild fauna, but how do we explain them?

Speaker: **Colin Smith**
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Co-authors: Maddison Crombie[1,2], Eneko Iriarte[3], Cristina Valdiosera[2,3], Marian Galindo[4], Ignacio de Gaspar-Simón[5], Juan Luis Arsuaga[5,6], José-Miguel Carretero[3]

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Abstract:

Compound specific stable isotope analysis of amino acids is a technically challenging endeavour, requiring advanced equipment and skills and determined approaches to data processing. Analysis of amino acid nitrogen has been a recent focus as it facilitates detailed interpretation of trophic position in ecosystems. Nevertheless, carbon isotope analysis of amino acids still has a lot to offer, considering the potential questions that can be explored relevant to carbon routing, especially in faunal studies, e.g., animal husbandry practices: especially foddering, manuring or niche partitioning (human mediated or otherwise). While contextualising some data from the Spanish Holocene site of the El Portalon del Cueva Mayor from the Sierra de Atapuerca, we noticed some unusual patterns in δ13C values of some amino acids. Following this data driven approach, we propose some amino acid indicators that could potentially be used to differentiate wild and domestic fauna in some in stances. We will also speculate on some explanations for the observed phenomena.

ABSTRACT DOMP-010

Home is where the herd is: Detection and analysis of domesticated mammals in houses from Bronze Age Slovakia through sedaDNA

Speaker: **Stephanie Dolenz**
Max Planck Institute for Evolutionary Anthropology, Germany

Co-authors: Knut Rassmann[1], Jozef Bátora[2], Norbert Benecke[1], Matthias Meyer[3], Benjamin Vernot[3]

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Abstract:

Recent advances have allowed the recovery of ancient faunal mitochondrial DNA (mtDNA) from Pleistocene caves (Zavala, et al. Nature 2021), and even mastodon mtDNA from 2 million year old permafrost samples (Kjaer, et al. Nature 2022). Caves and permafrost may provide a uniquely protective environment for the preservation of such DNA, but most of life does not take place in caves. Humans and associated domestic species tend to settle in open-air environments, and in principle they may leave their DNA behind. Here we demonstrate the first recovery of faunal DNA from open air settlements, specifically from individual houses and alleys in Vráble and Rybnik, two Early Bronze Age settlements in Slovakia. Vráble was inhabited for nearly 500 years, with a maximum size of 800 individuals, and has been the subject of extensive scholarship (Bátora et al., 2012). Rybnik, at the foot of the Carpathians, was much smaller and housed groups of hunters and miners. From both sites, we identify mitochondrial DNA from domestic dogs, goats, sheep, cows and pigs; in some cases we are able to obtain haplogroup-level resolution. Although our methods targeted a broad swath of mammalian taxa, we do not identify any non-domestic species. This dominance of domestic fauna lies in stark contrast to archaeozoological data from Vráble and Rybnik, where between 10 and 30% of all mammalian faunal remains originate from wild deer. The disconnect between archaeozoological and DNA data suggest that different activities result in deposition of skeletal remains and DNA, and point to an area of future analysis. This study demonstrates that it may be possible to study the interactions of humans and their associated domestic species at unprecedented spatial resolution, determining which animals were present in specific parts of Holocene settlements.

ABSTRACT DOMP-012

Tracing the early spread of domestic cat in Central Europe: Human-mediated dispersal or natural introgression?

Speaker: **Danijela Popović**
University of Warsaw, Poland

Co-authors: Magdalena Krajcarz[1,2], Maciej T. Krajcarz[3], Zora Bielichová[4], Jelena Bulatović[5,6], Péter Csippán[7], Vesna Dimitrijević[6], Michał Golubiński[8], Daniel Makowiecki[1], Adrian Marciszak[9], Nemanja Marković[6], Ivana Živaljević[10], Jarosław Wilczyński[3], Mateusz Baca[8]

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Abstract:

Despite significant progress in paleogenomics and the increasing amount of new data on animal domestication, we still know little about the history of cats. Until now, it was known that only one subspecies, the Near Eastern wildcat (Felis silvestris lybica), was domesticated. The domestication area was assumed to be the Near East during the Neolithic period, with a prominent role in ancient Egypt. From this region, the cats spread through the Mediterranean and beyond. It has been accepted that the primary role in the expansion of cats through northern Europe was that of the Roman legions. However, we found that cats that carried mitochondrial DNA (mtDNA) haplotypes of wildcats from the Near East were present in Central Europe already in the Neolithic, much before Roman times. This indicates that the cats' route from the domestication centers to Central Europe might have been more complex than previously thought and could have been related to the Neolithic expansion. Our new results reveal the presence of the mtDNA haplotypes of the Near Eastern wildcats in Poland even in the pre-Neolithic period. This may suggest that the Near Eastern wildcats could spread across Europe independently of the expansion of farming, and, in consequence, the natural range of the Near Eastern wildcat could have been much broader than previously assumed. To understand how and when domestic cats appeared in Central Europe, we perform a target enrichment of ca. 57,000 genomic SNPs. We believe that it will allow us to finally determine whether the appearance of the Near Eastern wildcat mtDNA in Central Europe was a natural admixture between two subspecies or was human-mediated dispersal of tamed/domesticated cats. The study is supported by the National Science Centre, Poland, grant no. 2019/35/B/HS3/02923.

ABSTRACT DOMP-013

Genetic analysis of ancient and contemporary sheep in Estonia

Speaker: **Eve Rannamäe**
University of Tartu, Estonia

Co-authors: Matthew Teasdale[1], Urmas Saarma[2], Anneli Ärmpalu-Idvand[3], Johannes Lenstra[4], Elena Ciani[5], Salvatore Mastrangelo[6], Camilla Speller[7]

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Abstract:

The presentation gives an overview of the results of genetic research that was conducted on Estonian sheep (Ovis aries) populations in the last decade. The study material were ancient sheep remains from the Late Bronze Age to Modern Period (around 800 BCE to 1900 CE) and blood samples from a local breed called the Kihnu native sheep. Methods included the analysis of mitochondrial DNA, retroviral insertions, nuclear DNA, and 50K SNP-chip data. The research results showed: 1) there is continuity in the maternal lineages from the Late Bronze Age sheep to present-day Kihnu individuals (Rannamäe, et al. PLoS ONE 2016); 2) both ancient individuals and Kihnu sheep share so-called ‘primitive’, ‘Nordic’, and other ‘ancient’ retrotypes that confirms their shared ancestry and their place among the Northern Short-tailed sheep (Rannamäe, et al. Sci. Rep. 2020); and 3) sheep populations in Estonia from different eras are related and share affinities also to other northern breeds on a nuclear genome level (Rannamäe & Teasdale et al. in prep.). Overall, the important outcome of this research is that the Kihnu native sheep is truly one of the preserved northern European ‘primitive’ breeds and deserves conserving as a native endangered breed. Another important outcome has been to demonstrate how study on ancient material can contribute to the study on extant native populations.

ABSTRACT DOMP-014

Paleogenetic analysis of cat mummies from ancient Egypt

Speaker: **Valentina Rovelli**
University of Rome Tor Vergata, Italy

Co-authors: Bea De Cupere[1], Wim Van Neer[1], Marica Baldoni[2], Marco de Martino[2], Claudio Ottoni[2]

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Abstract:

Situated at the crossroads of Africa, Asia, and Europe, Egypt is considered one of the two potential cradles of cat domestication (Felis catus). Here, cats most likely developed their relationship with humans with a dual role. In fact, on the one hand Egyptian iconography depicts cats as skilled hunters, and on the other hand as companion animals, quietly sitting under the chairs of noble people and as guardians of the deceased (Yoyotte & Vernus 2005). Egyptian cats were objects of a cult dedicated to the goddess Bastet, and from the 1st millennium BC until the 4th century AD were mummified as votive offerings. Previous ancient DNA (aDNA) investigation (Ottoni, et al. Nat. Ecol. Evol. 2017) showed that cats in ancient Egypt possessed two maternal lineages commonly found in modern domestic cats. Haplotype-C, which spread all over the Old World since Classical Antiquity from Northern Africa, and haplotype-A, which was associated with an earlier cat dispersal from the Levant during the Neolithic. DNA from cat mummies represents a key tool to unravel the role of Egypt as a possible independent center of domestication, despite the fact that the retrieval of aDNA from mummified tissues has greatly been challenged by DNA preservation. Here, we show the preliminary results of aDNA analyses conducted on more than 50 Egyptian cat mummies from Beni Hassan and Gourna (Luxor), dated to the Greco-Roman period. By comparing different methods (e.g. single and double-stranded genomic library construction), we provide an extensive case for screening DNA preservation in arid regions, and within different tissues, such as hair, claws, and petrous bones. We also explore the potential to gain novel insights into the dispersal of domestic cats from Egypt in Classical Antiquity through mitochondrial and genome-wide data.

ABSTRACT DOMP-015

Pig colonisation in the Pacific: A population genomic study

Speaker: **Aurélie Manin**
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Co-authors: David W.G. Stanton[1,2], Anna Linderholm[3], Allowen Evin[4], Linus G. Flink[5], Thomas Cucchi[6], Keith Dobney[5,7,8,9], Greger Larson[10], Laurent Frantz[1,11]

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Abstract:

The origins and ancient dispersal routes of the Austronesian peoples and associated Lapita culture have been a subject of debate for several decades. The majority of genetic evidence has pointed towards an origin in Taiwan, expanding directly from there into Island South East Asia and remote Oceania. However, specific dispersal routes, and the extent to which this expansion was associated with agricultural practices and language remains highly controversial. For example, there appear to be multiple expansion waves that replaced most of the human ancestry in Vanuatu, but not the native languages. Ancient mitochondrial DNA studies focussed on the expansion of pigs into the region indicate that while East Asian pigs did expand a short distance out of Taiwan, the expansion that led to the colonisation of the entire region is characterised by a unique mitochondrial clade that appears to have originated in peninsular South East Asia. We compare pig mitochondrial and nuclear genomes in Island Southeast Asia and Oceania to those around the world, to revisit this question of pig dispersal. We identify that hybridization has played an important role in shaping the diversity of the region, and argue that long-term evolutionary processes must be considered if these questions are to be resolved. We discuss this dispersal within the framework of suid diversity and evolution across their distribution, and the implications of this for our understanding of the spread of people and culture in Island South East Asia.

ABSTRACT DOMP-016

The Impact of Human Actions and Wild Introgression in the History of Domestic Cattle on the Iberian Peninsula

Speaker: **Cristina Valdiosera**
Universidad de Burgos, Spain; La Trobe University, Australia

Co-authors: Torsten Günther[1], Jacob Chisausky[1], Marian Galindo[2], Eneko Iriarte[3], Oscar Cortes Gardyn[2], Paulina Eusebi[2], Irene Ureña[4], Marta Moreno[5], Alfonso Alday[6], Manuel Rojo[7], Juan Luis Arsuaga[2], José-Miguel Carretero[3], Anders Götherström[4], Colin Smith[3,8]

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Abstract:

Cattle has been a valuable food resource since prehistory; indeed, this species accounts for the highest biomass on the planet today. Since the initial expansion of domestic cattle into Europe during the Neolithic period, taurine cattle (Bos taurus) and their wild ancestor, the aurochs (Bos primigenius), had overlapping ranges leading to ample opportunities for intentional and unintentional hybridization. We screened 50 Bos remains from Northern Iberia from the Mesolithic to the Roman period. This large archaeogenomic dataset allows us to investigate the extent of domestic-wild hybridization over time providing insight into the species' behavior and human management by aligning changes with cultural and genomic transitions in the archaeological record. Our results show frequent hybridization during the Neolithic and Chalcolithic, likely reflecting a mix of hunting and herding or relatively unmanaged domestic herds, with mostly male aurochs and female domestic cattle involved in hybridization. Aurochs ancestry remains relatively constant from about 4000 years ago, probably due to extensive herd management and selection against hybrids. While the arrival of steppe ancestry in humans and domestic horses to the peninsula take place during a similar time frame, the earliest observation of human genetic variants associated with lactase persistence in Iberia post-dates this transition. Here, we take a genomic glance on the impact of human actions and wild introgression in the establishment of cattle as one of the most important domestic species today.

ABSTRACT DOMP-017

Genetic analysis of Late Copper Age to Bronze Age horses from the Carpathian Basin

Speaker: **Noémi Borbély**
Eötvös Loránd University, Hungary

Co-authors: Zoltán Dicső[1], Géza Szabó[2], Róbert Bozi[3], Botond Heltai[1], Viktória Kiss[1], Gabriella Kulcsár[1], Anna Szécsényi-Nagy[1], Dániel Gerber[1]

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Abstract:

In this study we present new genetic data on horse populations from the Late Copper Age to Middle Bronze Age Carpathian Basin. We report a new shotgun genome and six mitochondrial genomes dating from ~3600-1600 BCE, which were used to investigate the population structure of horses in the Carpathian Basin. The results indicate that the local horse population remained largely unchanged throughout the investigated period. In agreement with previous observations, Early and Middle Bronze Age horses formed a natural genetic cline from Anatolia to Northern Europe, with the Carpathian Basin samples situated in an intermediate position. The mitochondrial haplogroup distribution revealed two major local clusters (haplogroups A’D and Q), that are also intermediate between North and South. We provide a newly sequenced shotgun genome of a near complete horse skull from Tompa archaeological site dated to 1870-1620 cal BCE, that showed traces for a special nose bit wearing. Genomic make up of this specimen showed affinity to other two published Hungarian Bronze Age horses, but with slight increase of steppe ancestry. We performed several population genomic tests to infer the origin of this component. The results imply that the DOM2-like ancestry was most probably due to geographic cline rather than actual recent admixture, despite the presence of DOM2 horses among Bronze Age settlements from Central Europe a couple of hundred years earlier. We also show reduced population size for local stocks. Our results point to delayed replacement of the local horses with DOM2 breeds in the Carpathian Basin, revealing further bits of archaeologically documented horse keeping practices in the region.

ABSTRACT DOMP-020

Ancient cattle genomics: domestication and the impact of Bronze Age migrations

Speaker: **Deborah Diquelou**
Trinity College Dublin, Ireland

Co-authors: Daniel Bradley[1], Victoria Mullin[1], Valeria Mattiangeli[1], Conor Rossi[1], Kevin Daly[1]

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Abstract:

The domestication of plants and animals was a major watershed in human history. Studying the genomes of domesticated animals can inform us of not only past animal populations but also past human populations and society. Themes that can be explored using ancient genomes include the timings of when domesticates appeared and the genetic impacts of subsequent human-mediated migrations. This research focuses on ancient Bos taurus cattle and aims to generate and study a spatiotemporal dataset of ancient genomes. Research aims include analysing early populations of domesticated cattle in Southwest Asia with a specific interest in Georgia and assessing introgressions of wild aurochs and Asian Indicine cattle. In particular this research aims to understand the genetic impact of the Bronze Age human Steppe migration on the cattle populations of Eastern Europe; testing whether the story of domestic livestock is one that resonates or is discordant with that of humans.

ABSTRACT DOMP-021

Multi-proxy research shines light on the transition to animal husbandry in the Dutch wetlands

Speaker: **Jolijn Erven**
University of Griningen, the Netherlands

Co-authors: N.Ø. Brusgaard[1], M. Dreshaj[1], V.E. Mullin[2], L.M. Kootker[3], V. Mattiangeli[2], M. Dee[1], O. Madsen[4], D.G. Bradley[2], C. Çakırlar[1], D.C.M. Raemaekers[1]

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Abstract:

To date the question of the transition to animal husbandry in North-west Europe remains unresolved, largely due to the shortage of detailed multi-proxy research. Previously, zooarchaeological and morphometrics evidence was not comprehensive enough to resolve this transition to animal husbandry. Consequently, A multi-proxy research project centred on pigs (Sus sp.) and cattle (Bos sp.) was constructed to provide clarity on this complex process in the Dutch wetlands. This study combines zooarchaeological, Sr-O-C-N isotope analyses, paleogenomic, and precise Bayesian radiocarbon modelling on two archaeological sites from Swifterbant (4300-4000 BC), the Netherlands. The data obtained on cattle, which are morphologically domestic, indicate two distinct dietary clusters, and extensive mobility, indicating potential different management strategies or origins. This is in line with paleogenomic data, where both dietary clusters have domestic maternal haplogroups but fall in separate clusters. The pigs are more complex due to heavy interbreeding with local European wild boars. Paleogenomic, isotopic, and zooarchaeological evidence in the Dutch wetlands points towards the presence of at least some morphologically domestic, managed pigs. These results provide new evidence for animal husbandry, potential management strategies, and possible exchange between communities, as early as 4250 BC in the Dutch wetlands. This project conveys the importance of multi-proxy research for tackling these complex transitions and reminds that broad trends do not necessarily dictate how regional and local approaches to this transition should be viewed.

ABSTRACT DOMP-022

Investigating the impact of human Steppe migrations on Neolithic and Bronze Age sheep populations

Speaker: **Áine Halpin**
Trinity College Dublin, Ireland

Co-authors:

Abstract:

Genomic analysis of ancient domestic animals can reveal important information about prehistoric societies, culture and even human behaviour. Possible research themes to be explored include the timing of domestication events, human driven migrations of livestock, selection of traits, and the subsequent development of breeds. This research focuses on the extending of a spatiotemporal dataset of ancient sheep genomes, aiming to assess the impact of human migrations and selection pressures on the sheep genome. In particular this research focuses on Neolithic and Bronze Age sheep populations in eastern Europe and Southwest Asia, exploring whether the prehistoric migrations of humans, especially the third millennium BC human migrations from the Steppe to northern and central Europe, mirror those of domestic sheep.Many researchers have contributed to this work and will be fully acknowledged.

ABSTRACT FAUP-001

Identification and characterization of Erysipelothrix rhusiopathiae in ancient cats remains

Speaker: **Marica Baldoni**
University of Rome “Tor Vergata”, Italy

Co-authors: Valentina Rovelli[1], Marco De Martino[1], Bea De Cupere[2], Francesca Alhaique[3], Eugenio Cerilli[4], Emanuela Ceccaroni[5], Sonja Vuković[6], Cleia Detry[7], Idoia Grau[8], Lluís Lloveras[9], Jacopo De Grossi Mazzorin[10], Claudia Minniti[10], Marta Moreno[11], Jordi Nadal[9], Vedat Onar[12], Vera Pereira[13], Nicolai Spassov[14], Barbara Wilkens[4], Joris Peters[15], Wim Van Neer[2], Claudio Ottoni[1]

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Abstract:

Zoonoses represent a significant threat for human health. While recent efforts in microbial archaeology and palaeopathogenomics contributed to shed light on disease etiologic agents and epidemics during human history (Spyrou, et al. Nat. Rev. Genet. 2019), the role of animal hosts in zoonotic diseases still remains marginally explored. Due to their role as pest control agents and their long-standing relationship with humans, cats may have played a key part in the transmission of zoonotic pathogens. This research focuses on the analysis of pathogenic microorganisms in ancient cats dated to different periods, from prehistory to recent times, originating from Europe, Southwest Asia, and North Africa. The metagenomic screening performed through the use of multiple classifiers led to the identification of a few zoonotic candidates including Erysipelothrix rhusiopathiae, the bacillus responsible of the swine erysipelas (Brooke, Riley J. Med. Microbiol. 1999; Kobayashi, et al. IDCases 2019). This bacterium primarily infects swine and farmed animals but it may also be transmitted to humans (Brooke, Riley J. Med. Microbiol. 1999; Kobayashi, et al. IDCases 2019). Although the majority of human infections are due to work-related exposure and mainly derive from the contact with infected livestock animals, the transmission through cat bites was also documented (Brooke, Riley J. Med. Microbiol. 1999; Kobayashi, et al. IDCases 2019). Here we show the preliminary results of the ancient genomic analyses conducted to identify and characterize E. rhusiopathiae in ancient cats. This may represent a valuable source of information for investigating the evolution of the pathogen and the pattern of inter-species transmissibility.

ABSTRACT FAUP-002

Investigating prehistoric zoonotic disease reservoirs

Speaker: **Anne Kathrine Runge**
Max Planck Institute for Infection Biology, Germany

Co-authors: Kamilla Pawłowska[1], Rosalind E. Gillis[2], Ian Light[3], Regina Uhl[2], Sabine Reinhold[2], Jana Eger[4], Michal Ernée[5], René Kyselý[5], Philipp Stockhammer[6,7], Ken Massy[7], Norbert Benecke[2], Kai Kaniuth[7], Svend Hansen[2], Felix M. Key[3]

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Abstract:

The recovery of ancient pathogens from organic archaeological remains has provided new insight into the spread and evolution of infectious diseases through time. To date, these studies have focused primarily on human hosts, while animal populations have remained largely unexplored. As is clear by now, infectious diseases often have zoonotic origins, and many ancient pathogens likely circulated in animal populations before they spilled over into humans. With the introduction of animal domestication and the changes it brought about in both human and animal lifeways, multiple factors converged to increase the chance of zoonotic events within early pastoralist settlements. Through a combination of palaeopathology and ancient DNA, this study focuses on understanding health and diseases in Bronze Age animal populations in particular. More specifically, the identification of pathological lesions on animal bones is utilised to provide sampling targets for ancient DNA analyses. The generated genomic data is then screened for preserved pathogen DNA with the aims of identifying potential disease reservoirs in animal populations that could have contributed to prehistoric zoonotic spillovers, of comparing ancient animal disease diversity to modern exemplars of diseases, and of exploring the underlying genetic mechanisms behind the potential spillover.

ABSTRACT FAUP-003

Enamel proteome of Pleistocene Cave Bears from Sierra de Atapuerca Sites

Speaker: Amanda Gutiérrez Carbajal

National Research Center on Human Evolution, Spain; Universitat Pompeu Fabra, Spain

Co-authors: Elena Santos Ureta[1,2,3], Esther Lizano[4,5], Tomàs Marquès i Bonet[4,5], Juan Luis Arsuaga[2,6], José María Bermúdez de Castro[1,7], María Martinón Torres[1,7]

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Abstract:

This study presents the proteomic characterization of the cave bear lineage based on the dental proteome of several species, each of them representative of a different period of the Pleistocene in Sierra de Atapuerca archaeological sites (Burgos, Spain). A total of n=20 dental enamel samples from fossils assigned to the species U. dolinensis and U. deningeri have been analyzed. The fossil remains studied were recovered from Gran Dolina (ca. 910ka) and Sima de los Huesos (ca. 430ka) sites, where human presence was documented during the mid-Middle and Early Pleistocene (Bermúdez de Castro, et al. Science 1997; Arsuaga, et al. Science 2014). It is from the TD6 level (ca. 860 ka) of the Gran Dolina site, where proteins have recently been extracted from Homo antecessor dental remains (Welker, et al. Nature 2020). Due to the optimal state of conservation, it has been possible to successfully extract peptides from all the cave bear samples, which has allowed us to identify and sequence for the first time the dental proteome of these species. The results obtained reveal that species from Middle and Late Pleistocene cave bear lineage differ at a proteomic level from the brown bear lineage, to which some of the extant bear species belong. Consistent variations at amino acid level in protein sequences suggest such differences. The comparison with an enlarged sample including more cave bear remains from other European sites with similar chronologies will allow us to explore the taxonomy and phylogeny of the cave bear lineage.

ABSTRACT FAUP-004

De novo LC-MS/MS proteomics enables Elephantidae speciation using sequence variants in ivory proteins

Speaker: **Florian Harking**
University of Copenhagen, Denmark

Co-authors: Florian S. Harking[1], Patrick L. Ruther[1], Ashley Coutou[2], Alberto J. Taurozzi[1], Ioannis Patramanis[1], Fernando Racimo[1], Jesper V. Olsen[1]

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Abstract:

Ancient and modern genomics have successfully resolved the Elephantidae phylogeny and protein-coding sequence variants are already known for Loxodonta and Elephas genuses. Yet, these reference genomes have not yet been translated into verifiable protein-level sequence variants that can be monitored in ivory to enable the discrimination between the different extant and extinct Elephantidae genuses on the protein level. In this work, we use an unbiased de novo peptide sequencing approach employing high-resolution mass spectrometry (HRMS) to create consensus proteomes of ivory reference samples from Indian and African elephants and Mammoth. In a second step, these consensus proteomes are used to identify putative sequence variants between their genuses. From an overall set of 13 reference samples, 1713 putatively genus-defining Single amino acid polymorphisms (SAPs) could be identified in total – and after thorough filtering, 216 SAPs remained. To verify these variants experimentally, a set of 100 ivory fragment samples of cultural origin, were investigated using a modified version of the recently published Species-by Proteomics (SPIN) workflow. To streamline and increase the throughput of ivory sampling, the Covaris CP02 Automated Pulverizer was used to powderize ivory fragments, which were subsequently processed by protein aggregation capture using magnetic beads followed by on-bead trypsin digestion using further automation. Using ultra-fast LC gradients and High-Resolution data-independent acquisition (DIA) Mass Spectrometry, a 100 samples can be processed from samples to results to LC-MS/MS results in just 4.5 working days is possible. The generated MS data then was searched against the consensus proteomes. From the predicted sites, 27 could be confidently identified of which 9 were used to discriminate between the different genuses. In the furture, these results could be translated into a simplified targeted proteomics assay for academic or commercial interest.

ABSTRACT FAUP-005

Ancient proteins from Iberian equids in the light of ancient DNA

Speaker: **Johanna Krueger**
Parc de Recerca Biomèdica de Barcelona, Spain

Co-authors: Ricardo Fong[1], Xènia Aymerich[2], Ryan Paterson[3], Enrico Cappellini[3], Ludovic Orlando[4], David Alba[2], Tomas Marques[1], Esther Lizano[1,2]

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Abstract:

The evolution of equids over the past millennia has been studied extensively using ancient DNA1. However, there is a fair amount of debate about equid phylogenetics, in particular about evolutionary processes outside the temporal scope of aDNA2. The application of palaeoproteomics could provide some answers since it extends the maximal age of samples that deliver genetic information to millions of years. Also, because of the numerous aDNA studies on equids, we have the opportunity to analyze our palaeoproteomic data in the context of aDNA data. We predicted protein sequences of the enamel proteome from ancient and modern whole genome sequences from several hundred horse individuals across Eurasia. In both, modern and ancient individuals, we identified novel sequence variants in their enamel proteome. These predicted protein sequences were compared to experimental palaeoproteomic data. For this, we extracted ancient peptides from tooth enamel of equids including Equus spp., Plesiohipparion rocinantis, ?Plesiohipparion fissurae, and Hippotherium catalaunicum from sites across the Iberian peninsula. The fossils span an age range from approximately 10 ka to 10 Ma. Some of them were found in close proximity to remains of the hominoid Hispanopithecus, and thus represent an important proxy for potential peptide conservation in these fossils. We sequenced the ancient peptides using nanoLC-MS/MS3. The palaeoproteomic data revealed an isoform of Amelogenin X that has not been reported for horses to date. Currently, we are exploring the palaeoproteomic data for phylogenetically informative peptide sequence variants that could shed some light on equid evolution.

ABSTRACT FAUP-006

An Early Miocene enamel proteome of an early-diverging rhinocerotid from Canada’s High Arctic and a biomolecular phylogeny of Rhinocerotidae

Speaker: **Ryan Paterson**
University of Copenhagen, Denmark

Co-authors: Meaghan Mackie[1], Alessio Capobianco[2], Danielle Fraser[3], Ioannis Patramanis[4], Nicola S. Heckeberg[2], Marisa Gilbert[3], Jazmín Ramos Madrigal[4], Shanlin Liu[5], Abigail Ramsøe[4], Fazeelah Munir[6], Kirsty Penkman[6], Fernando Racimo[4], Natalia Rybczynski[3], Sebastian Höhna[2], Ross MacPhee[7], Enrico Cappellini[4]

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Abstract:

While ancient proteins have emerged as a valuable tool for evolutionary inference in deep-time, the oldest ancient proteins so far used for phylogenetic inference derive only from the Pliocene (3.8 Ma) (Buckley, et al. Journal of Proteomics 2019). Here, we push back the recovery of phylogenetically-informative ancient biomolecules into the Early Miocene by retrieving, and sequencing enamel protein sequences from an early-diverging rhinocerotid from a 21.8 Ma site in Canada’s High Arctic. The Haughton Formation, within the Haughton Crater (75°N, Nunavut) comprises the remnants of a post-impact lacustrine deposit of Early Miocene Age (Hickey, et al. Meteoritics 1988) Vertebrate fossils, found in the active layer atop the permafrost, have been spared from the harshest diagenetic effects, thus serving as an appropriate test for deep-time biomolecular preservation. We applied recently-developed digestion-free extraction protocols (Cappellini, et al. Nature 2019) to enamel fragments of a rhinocerotid from this formation. We successfully recovered an enamel proteome, including 327 unique peptides, covering 1101 spectra, spanning 316 amino acids, and representing seven different proteins commonly found in enamel. The degree of protein preservation is comparable to that of Early Pleistocene enamel from tropical climates. We further analysed the proteome alongside enamel proteomes from the Holocene-Pleistocene, to explore chronological patterns in protein degradation, allowing for the identification of a suite of damage markers associated with advanced degradation. Phylogenetic analysis, performed across a dataset of 3446 total amino acids for 16 extant and extinct perissodactyl taxa, identified the High Arctic rhinocerotid as the earliest diverging rhinocerotid in our analysis.

ABSTRACT FAUP-007

Horse mitochondrial genomes from the Middle Pleistocene open-air site of Schöningen

Speaker: **Arianna Weingarten**
University of Tübingen, Germany

Co-authors: Arianna Weingarten[1], Ella Reiter[1], Ivo Verheijen[1,2], Jordi Serangeli[1], Nicholas J. Conard[1], Cosimo Posth[1,3]

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Abstract:

The genus Equus represents one of the best-known examples of macroevolution, spanning about 55 million years in the fossil record. While the evolutionary history of equids has been classically reconstructed through morphological studies, advancements in ancient DNA have recently provided insights into their divergence, speciation, selection, and demographic history. Yet, excluding a Middle Pleistocene specimen from North American permafrost dating to 780-560 thousand years ago (kya) and a number of Late Pleistocene specimens, most efforts in ancient horse genomics have been focused on tracing the origins of domestication and subsequent periods. However, long before their domestication, horses played a pivotal role in hominin subsistence. One of our earliest insights into this relationship comes from the Middle Pleistocene open-air site of Schöningen (Lower Saxony, Germany). The site is well known for its exceptional preservation, and in particular for the discovery of wooden spears found among butchered horse remains dated to ~300 kya. Here, we present the analyses of largely complete mitochondrial genomes (mtDNA) of two horses (Equus mosbachensis) excavated at Schöningen. Phylogenetic analyses place these Middle Pleistocene horses on a deeply divergent mtDNA lineage, which is an outgroup to most ancient Eurasian horses sequenced to date. In addition, the newly reconstructed mtDNA sequences are basal to all mtDNA diversity observed in extant horses. This ancestral lineage thus provides an important time anchor to better calibrate the horse mtDNA molecular clock, which allows for a more accurate dating of major divergence events within the equid evolutionary history. By pushing back the age limit for mtDNA retrieval from Middle Pleistocene open-air sites, our molecular results fill a temporal and geographic gap while extending our understanding of the origins of modern-day horses.

ABSTRACT FAUP-008

Advances in single amino acid nitrogen isotopic analysis of carnivore trophic position

Speaker: **Magdalena Krajcarz**
University of Tübingen, Germany

Co-authors: Maciej T. Krajcarz[1], Hervé Bocherens[2,3]

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Abstract:

Stable isotope analysis of animal tissues is a powerful tool for investigating the ecology and paleoecology of animal and human populations. Estimating the trophic position is one of the most common applications of stable nitrogen isotopes in paleoecology. Though a powerful method, the bulk δ15N analysis has several important limitations in interpreting trophic relationships. This is because different primary producer taxa and/or ecological groups bear variable δ15N values. This limitation led to seek for more advanced analysis. The development of isolation techniques and mass spectrometry in the last decade allows for measuring the isotopic analysis of individual amino acids (AAs) isolated from fossil collagen. The principal ecological application comes from different fractionation rates of particular AAs along the trophic chain. Some amino acids exhibit no or limited fractionation from diet to consumer tissues ('source AA'); the others undergo distinct fractionation along the trophic chain ('trophic AA'). Ecological and paleoecological studies usually exploit the trophic discrimination factor (TDF) between one source AA (phenylalanine, Phe) and one trophic AA (glutamic acid, Glu). However, the TDF value for terrestrial carnivorous mammals has never been directly measured. There is also a significant lack of knowledge on tissue-specific amino acid fractionation. Better approximation of the TDF is the main objective of the new 'IsoTroph' project, implemented at the University of Tübingen. Our goal is to analyse δ15N values in Phe and Glu of a predator population and that of its prey. The project will involve a study of four different collections of bones of predators (lynx, wolf, red fox, and cave hyena) and their prey. These collections provide insight into mammalian carnivores representing variable ecology (hypercarnivores and omnivores) and chronologies (recent and Pleistocene). The project is funded by the EU Horizon 2020 MSCA grant agreement No 101023317.

ABSTRACT FAUP-009

Ancient stickleback environmental genomes track adaptation across ecological transitions

Speaker: **Jan Laine**
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Co-authors: Sarah S. T. Mak[1], Nuno F. G. Martins[1], Xihan Chen[1], M. Thomas P. Gilbert[1], Felicity C. Jones[2], Mikkel Winther Pedersen[1], Anders Romundset[3], Andrew D. Foote[4]

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Abstract:

Ancient DNA has revolutionised our understanding of the evolutionary histories of past and present-day populations. The sampling of bones, coprolites, seeds, skin and teeth of ancient animals and plants have provided key insights into adaptation, demographic history and extinction. However, individual samples typically provide a snapshot in time. In contrast, time series of ancient DNA that span demographic, ecological and evolutionary change can provide novel insights into the chronology and tempo of evolutionary processes. The advent of sedDNA as a tractable source of genome-scale data offers a potential source of time-series of genomic change. To date, time series in ecosystem biodiversity have been reconstructed from sedDNA, typically using DNA metabarcodes or shotgun sequence data generated from less than 1 gram of sediment. Here we increase sequence coverage by processing two orders of magnitude more sediment per sample than previous studies, which provided genotype resolution results. Reconstructing a time-series of environmental genomes from Late Pleistocene sedDNA we track adaptive genotypes of threespine stickleback (Gasterosteus aculeatus) during the ecological change from marine to freshwater. We find rapid adaptation at known loci of large effect, e.g. EDA. Our findings open up new avenues to explore the temporal context of past evolutionary processes.

ABSTRACT FAUP-010

Reconstructing collared lemming phylogenetic history using ancient and modern genomes

Speaker: **Edana Lord**
Centre for Palaeogenetics, Sweden

Co-authors: Mateusz Baca[1], Danijela Popović[1], Anna V. Goropashnaya[2], John R. Stewart[3], Pierre Noiret[4], Mietje Germonpré[5], Elodie-Laure Jimenez[5], Natalia I. Abramson[6], Sergey Vartanyan[6], Stefan Prost[7], Vadim Fedorov[2], Love Dalén[8]

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Abstract:

Collared lemmings (Dicrostonyx spp.) are key Arctic species present today in the tundra of Siberia and North America. Currently there are three recognised species in North America (D. groenlandicus, D. hudsonius, and D. richardsoni) and one in Siberia (D. torquatus). Previous research on mitochondrial genomes of these species suggests that the North American and Eurasian collared lemmings diverged around 200 thousand years ago. The extent of post-speciation gene flow that may have occurred between collared lemmings is currently unknown. However, a recent study identified conflicting mitochondrial and nuclear phylogenies within the North American collared lemming species. Here, we generated ten modern and eleven ancient genomes from the Eurasian collared lemming, along with eight modern genomes from the three North American Dicrostonyx species. We additionally sequenced the genome of a circa 300 thousand year old mummified Siberian Dicrostonyx. We aimed to evaluate the phylogenetic relationships between the collared lemming species, and furthermore to examine whether post-speciation gene flow occurred during the Late Pleistocene. Preliminary results suggest gene flow from D. richardsoni to D. hudsonius, which may have led to mitochondrial genome replacement.

ABSTRACT FAUP-012

Systematic ancient DNA-based species identification of archaeological remains of large bovines (Bos primigenius and Bison bonasus)

Speaker: **Erika Rosengren**
Lund University, Sweden

Co-authors: Conor Rossi[1], Matti Heino[2], Mikkel Sinding[3]

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[2] University of Helsinki, Finland
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Abstract:

Previous paleontological and zooarchaeological studies have shown that two bovines, aurochs and European bison, coexisted in southern Scandinavia during the late Pleistocene and early Holocene. As few faunal remains of European bison have been reported from the region, the species is generally assumed to have been rare and to have gone extinct during the early Holocene. Conversely, aurochs are thought to have persisted until the early Atlantic period as bovine remains from several Mesolithic archaeological sites have been identified as having belonged to the species. Due to overlap in osteological morphology and the absence of good diagnostic skeletal identification criteria distinguishing aurochs and early Holocene European bison in the faunal record is challenging. This is problematic when studying the past occurrence of the taxa and the roles they played in the subsistence of prehistoric people. By combining shallow whole-genome shotgun sequencing of samples from a large number of bone specimens of bovines with mtDNA hybridisation capture, we validate osteological identifications of bovine specimens. In addition to an assessment of the applicability of this approach to the systematic identification of bovine remains from archaeological sites in general, the results are discussed in relation to the extensive changes in climate and vegetation, as well as human cultural development that occurred in Scandinavia within the time frame spanned by the material.

ABSTRACT FAUP-014

First insights into the population genomics of the extinct Darwin's ground sloth (Mylodon darwinii) from Cueva del Milodón, Chile.

Speaker: **Maria Zicos**
Queen Mary University of London, UK; Natural History Museum London, UK

Co-authors: Selina Brace[1], Laurent Frantz[2,3], Samuel Turvey[4]

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Abstract:

Sloths (Xenarthra, Folivora) were one of the dominant mammalian groups in Southern and Central America until the early Holocene. Folivora used to have a large range of body sizes, locomotion and ecology, while extant sloths are morphologically and ecologically similar. Research into the molecular evolution and biology of sloths, previously limited to extant species, has started to leverage information contained in the large recent fossil record of this group through ancient DNA methods.Cueva del Milodón (Ultima Esperanza, Chile) is renowned for its exceptionally preserved faunal record. Remains of Darwin's ground sloth (Mylodon darwinii) are found there from the end of the last Ice Age to their extinction in the early Holocene. Here we present novel findings from NGS generated genomic data from multiple M. darwinii individuals, exploring genetic diversity in this site. Using ancient DNA methods, nineteen new mitochondrial genomes and three nuclear genomes were recovered from bone, skin and coprolites from Cueva del Milodón in British and Swiss museum collections. The mitochondrial diversity was low, yet higher than that found in another single-locality megaherbivore population, sampled near its extinction: Holocene woolly mammoths (Mammuthus primigenius) from Wrangel Island. This diversity did not appear to fluctuate through time, Raising the question of whether this low diversity stemmed from philopatry or a founder event in the maternal lines represented at the locality. Nuclear diversity in the three individuals sequenced to higher coverage will reveal whether low diversity is also found in the nuclear genome. These findings, combined with direct radiocarbon dates, will be used to reconstruct the demographic history of the species, and to test models for their extinction, hoping to better understand why these sloths became extinct, while extant sloths persisted.

ABSTRACT FAUP-015

Ancient DNA clarifies the evolution of the field vole species complex

Speaker: **Mateusz Baca**
University of Warsaw, Poland

Co-authors: Danijela Popović[1], Michał Golubiński[1], Barbara Bujalska[1], Paulo C. Alves[2], Edouard Bard[3], Claudio Berto[1], Helen Fewlass[4], Jeremy Herman[5], Ivan Horáček[6], Magdalena Krajcarz[7], Anna Lemanik[8], Juan Lopez Garcia[9], Elisa Luzi[10], Xabier Murelaga[11], Joana Pauperio[2], Svetlana Pavlova[12], Piroska Pazonyi[13], Jeremy B. Searle[14], Joanna Stojak[8], Tatiana Strukova[12], Jan M Wójcik[8], Adam Nadachowski[8]

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Abstract:

The field vole is a complex of three cryptic species. The short-tailed field vole (Microtus agrestis) is present over much of Eurasia, the Mediterranean field vole (Microtus lavernedii) is found in southern Europe, and the Portuguese field vole (Microtus rozianus) is limited to western Spain and Portugal. Previous studies showed discordance of mitochondrial and nuclear gene trees and suggested that the Portuguese field voles diverged from Mediterranean and short-tailed field voles ca. 70 thousand years (ka) ago, while the two latter separated about 25 ka ago during the Last Glacial Maximum (LGM). It was suggested that isolation in the different refugial areas was the main factor causing the genetic differentiation of these populations. To elucidate evolutionary history of the field vole species complex, we generated mitochondrial genomes from 75 ancient and 46 modern specimens and nuclear genomes from 10 ancient voles, dated up to ca. 70 ka, and several modern specimens. The calibrated mitochondrial phylogeny shows that the northern lineage diverged from the Portuguese and Mediterranean lineages ca. 200 ka ago, while the latter diverged about 100 ka ago. Preliminary analyses of nuclear genomes also suggest that Mediterranean and short-tailed field voles diverged much earlier than previously estimated, probably before the Last Glaciation (115–11.7 ka ago), but they shared a similar evolutionary history with severe bottlenecks during the LGM. Further analyses will search for the primary factors that contribute to the divergence of the field vole species complex.

ABSTRACT FAUP-016

Palaeogenomes of a lost world: Ancient bovids of the submerged Palaeo-Agulhas Plain of southern Africa

Speaker: **Deon de Jager**
University of Copenhagen, Denmark

Co-authors: Wendy Black[1], Wilhelmina Seconna[1], J. Tyler Faith[2,3], Kaedan O’Brien[2], Eline Lorenzen[4]

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Abstract:

The Palaeo-Agulhas Plain (PAP) refers to the continental shelf off the southern coast of Africa that intermittently provided up to ~85,000 km2 of terrestrial habitat for large mammals and human foragers when cyclically exposed and submerged due to changing sea levels through the Pleistocene [1]. The current coastline and Cape Fold Mountains, that bordered the PAP to the north, provide a rich fossil record from numerous archaeological and palaeontological sites that have provided insights to the behaviour of both ancient humans and animals that roamed the PAP [2]. However, fewpalaeogenetic studies have been attempted from this fossil record to understand the genetic history of either ancient humans or animals. One reason for this lack of research attention may be the expectation that climatic conditions in the region were not favourable for DNA preservation, as is often the case elsewhere in Africa. Here, we present an evaluation of DNA preservation in fossils from five PAP sites through time using teeth and bones of six bovid species (n = 58). A third of the specimens had >1% endogenous DNA, with most of the samples younger than 10 thousand years (ka; median age 4.85 ka). Two older specimens (10.5 ka and 71-130 ka) harboured a low proportion (<1%) of endogenous DNA but were still genetically identifiable to species level. Endogenous DNA content had a significant negative correlation with estimated age (Spearman’s rho = -0.46, p-value = 2.2e-04), while site, species, and material (bone/tooth) did not appear to have an effect. The results from this study were used to successfully motivate for further sampling to allow us to investigate whether genetic diversity of bovids changed along with climate and habitat availability on the PAP. Furthermore, the results should allow the prioritisation of the precious few human fossils from PAP sites that are most likely to yield ancient DNA, which would provide valuable insights into human evolution.

ABSTRACT FAUP-017

Tracking temporal changes in mitochondrial diversity in Scandinavian brown bears

Speaker: Isabelle Feinauer

Centre for Palaeogenetics, Sweden; Swedish Museum of Natural History, Sweden; Stockholm University, Sweden

Co-authors: Johanna von Seth[1,2,3], Erik Ersmark[1], Georgios Xenikoudakis[4], Love Dalén[1,2,3], Ioana Meleg[1,2,5]

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Abstract:

Earlier research combining ancient and historical with modern DNA proved to be a powerful tool in investigating species genetic variation and population history over time in the context of past climatic changes and human impact. One species, whose genetic history has likely been shaped by a postglacial recolonisation event after the retreat of the Fennoscandian ice sheet, around 10,000 years ago, and a recent strong population decline due to intense human persecution approximately 100 years ago, is the Scandinavian brown bear (Ursus arctos). Previous studies on mitochondrial diversity loss in Scandinavian brown bears focused solely on mitochondrial markers and microsatellites. Here, we present 42 complete mitogenomes to examine temporal changes in the Scandinavian brown bears' mitochondrial genetic diversity. The dataset comprises newly generated and re-sequenced Early Holocene, historical and modern mitochondrial genomes, originating from Sweden and Norway, and is analysed together with previously published data. This allows us to investigate how the postglacial recolonisation event and the historical demographic bottleneck have influenced the brown bears genetic structure and diversity over time in Scandinavia. Ultimately, we assess how these events have shaped the modern-day population that recovered after the human persecution leading to ca. 130 surviving brown bears in Sweden and even less in Norway, to ca. 3,000 and 150 individuals in Sweden and Norway respectively, today.

ABSTRACT FAUP-018

Impact of Late and Middle Pleistocene climate change on the evolutionary genomics of megafauna at Denisova Cave

Speaker: **Alexandre Gilardet**
Centre for Palaeogenetics, Sweden

Co-authors: Katerina Douka[1], Edana Lord[2], Peter D. Heintzman[2], Love Dalén[2]

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Abstract:

The impact of past environmental and climatic transitions on evolutionary histories has been widely investigated. So far, most ancient genomics studies have concentrated on samples dated to the Holocene and Late Pleistocene. Recent retrieval and analysis of million-year-old mammoth DNA dated to the Early to Middle Pleistocene showed that evolutionary histories can be reconstructed further back in time. This study will make use of thousands of zoological remains excavated at Denisova Cave, Siberia going back to the Middle Pleistocene (ca up to 400 thousand years ago). Ancient DNA is being extracted from these samples previously identified at the genus level by ZooMS (Zooarchaeology by Mass Spectrometry) in order to resolve taxonomy to the species level. Early screening will allow detection of taxonomic turnovers across interglacial/glacial cycles. We indeed aim to compare the similarity between glacial or interglacial periods, by comparing ecological community composition du ring multiple periods of each. We also hypothesize that cooling and warming climate transitions have induced contrasting selective pressures in cold- and warm-adapted taxa. For example, we hypothesize a diversification of cervids during warming transitions that were linked to the expansion of forest biotopes, while a cooling transition will conversely expose a loss in species diversity for this group in the region. Generation of mitogenomes will also allow to assess previously unsampled and lost diversity across climatic transitions. The aim of this talk will be to present the results of these early analyses.

ABSTRACT HDP-001

A Metagenomic Overview of The Lazzaretto Vecchio, Plague Hospital of Venice

Speaker: **Emily Gaul**
University of Tübingen, Germany

Co-authors: Kim-Louise Krettek[1], Antonino Vazzana[2], Carla Figus[2], Stefano Benazzi[2], Cosimo Posth[1], Maria Spyrou[1]

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Abstract:

Plague, caused by the bacterium Yersinia pestis, has been one of the most destructive infectious diseases in human history. The reconstruction of ancient Y. pestis genomes has provided insights into the global patterns underlying the emergence and evolution of the disease during the First, Second, and Third Pandemics. However, the factors which facilitated its successful persistence or re-introduction in certain regions, and their relation to the pathogen's genetic diversity, remain poorly understood. Particularly affected by the Second Plague Pandemic was the Italian Peninsula. Implicated as one of the points of entry of the Black Death into Europe (1346-1353 AD), it was thereafter subject to recurrent outbreaks until the end of the 17th century. Namely, the port of Venice, an important intersection of people and goods from across Eurasia, is known to have played a major role in the dissemination of infectious diseases throughout the medieval and post-medieval periods. Here, we present the first Y. pestis genomes recovered from individuals at the Lazzaretto Vecchio, Venice's first permanent plague hospital on the small island of Santa Maria di Nazareth. Used as a site of quarantine for the suspected infected from 1423 - 1630-31 AD, it offers a 300-year transect of microbial diversity which we examine through a metagenomic screening of non-targeted sequencing data. By combining archaeological, historical and genomic data we seek to employ a high-resolution, interdisciplinary approach for reconstructing the dynamics and diversity of past infectious diseases within this area, and investigate reported resurgences of plague in 1575-77 AD and 1630-31 AD, through a large cohort of its victims.

ABSTRACT HDP-002

Oral metagenomes from ancestral Native American individuals highlight impact of European colonialism on bacterial strain diversity

Speaker: **Sarah Johnson**
University of Oklahoma, USA

Co-authors: Cara R. Monroe[1], Jacob J. Haffner[1], Tanvi P. Honap[1], Alan Leventhal[2,3], Monica V. Arellano[3], Cecil M. Lewis[1]

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Abstract:

We know little about the impact of colonialism and globalization on the oral microbiome, despite the microbiome driving one the most pronounced global health disparities among marginalized groups, oral health. Here, we studied the oral microbiomes of Native American Ancestors (n=76) from coastal California, U.S.A., in partnership with and permission from the Muwekma Ohlone Tribe of the San Francisco Bay Area, the California Native American Heritage Commission's Most Likely Descendant Tribe. Of these Ancestors, two were dated to the Early Period (~4950-2450 YBP), the majority (n=70) were dated to the Middle Period (~2450-240 YBP), and four were from a Mission site dated to the late 18th century. Primarily hunter-gatherers, these Ancestors had a diet heavy in starch from acorn and seed consumption. DNA was extracted from dental calculus and partially treated with uracil deglycosylase. Double-stranded DNA libraries were prepared and shotgun-sequenced using Illumina technology. Samples from 71 Ancestors displayed an oral signature and were authenticated to be of ancient origin. To the best of our knowledge, this represents the largest ancient metagenome dataset from the Americas. Oral commensals such as Anaerolineaceae bacterium oral taxon 439 and Methanobrevibacter oralis and opportunistic pathogens such as Tannerella forsythia and Pseudoramibacter alactolyticus were present at sufficient abundance in some Ancestors to allow for genome reconstruction. Our phylogenetic analyses showed that T. forsythia strains from pre-contact Americans form a distinct lineage with evidence for strain replacement in post-colonial contexts, whereas Anaerolineaceae bacterium oral taxon 439 strains from pre-contact Americans form a lineage with pre-historic hunter-gatherers from Japan. Ongoing assessment of functional profiles will provide an additional layer to the investigation of how such major events have impacted the oral microbiome, and consequently, oral health.

ABSTRACT HDP-003

Response of the ancient oral microbiome to urbanization in the Black Sea region

Speaker: **Sterling Wright**
Penn State University, USA

Co-authors: Laura Weyrich[1], Marina Chkadua[2]

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Abstract:

Urbanization remains one of the most important cultural developments in human history. While many bioarchaeological studies investigate the effects of urbanization on human health, quantifying its consequences or understanding the biological mechanisms that underpin its associated changes continue to be a significant challenge. As current approaches comparing the skeletal markers between urban and rural cohorts are limited, new tools that assess what health transitions are linked to urbanization need to be developed. Studying the DNA in dental calculus of past populations may bridge this gap because ample evidence on present-day populations suggests that urbanization impacts their oral microbiomes. Here, we analyze the ancient DNA in the dental calculus of populations in the Black Sea region, specifically Georgia and Romania, to examine if urbanization impacted their oral microbiomes and if these observations could be linked to disease. We collected dental calculus samples from individuals dating to the Bronze/Iron Ages (1,500 BCE-500 BCE), Roman antiquity (200 CE-599 CE), and Middle Ages (1,300 CE-1599 CE). Rich archaeological assemblages and paleopathological work indicate that urbanization intensified throughout these cultural periods. We characterized the oral microbiome of these populations using a shotgun metagenomic sequencing approach with MALTn, and authenticated the DNA using MapDamage2, SourceTracker, and decOM. Microbial diversity was evaluated with D-MANOVA, while differentially abundant species were evaluated with MaAslin2. Lastly, paleopathological analyses incorporated into our models assess whether individuals with oral diseases have distinct oral microbiomes from their non-diseased counterparts. Our study is one of the first to compare the ancient oral microbiomes in the Black Sea region and provides a novel way of integrating ancient DNA data alongside traditional bioarchaeological analyses to answer questions related to urbanization.

ABSTRACT HDP-004

Reconstruction of the oral environment of ancient Okhotsk people using palaeoproteomic analysis of dental calculus.

Speaker: **Yoko Uchida-Fukuhara**
Okayama University, Japan

Co-authors: Shigeru Shimamura[1], Rikai Sawafuji[2], Minoru Yoneda[3], Hajime Ishida[4], Hirofumi Matsumura[5], Takumi Tsutaya[2]

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Abstract:

The Okhotsk Culture people were hunter-gatherers who inhabited the region from the Sakhalin and Sea of Okhotsk coasts to north-eastern Hokkaido and the Kuril Islands from the 5th to 13th centuries. Based on stable isotope analysis, marine mammals and marine organisms are thought to have been their main food source. Characteristic oral findings of this population include significant dental calculi deposits and many individuals with periodontal disease, while no individuals with dental caries have been found. However, the molecular biology of why they suffered from such unbalanced oral diseases has never been elucidated. Thus, in the present study, we analyzed dental calculi using palaeoproteomics to investigate both the host response to periodontal disease and its etiology in Okhotsk cultured individuals. We collected dental calculi from HM2-HA-3, which was excavated from the Hamanaka 2 site on the Rebun Island. Compared to other individuals, HM2-HA-3 exhibited more severe periodontal disease and an extremely large amount of abnormal dental calculus deposition. The stable isotope analysis results, on the other hand, showed that the diet was similar to that of the other individuals and consisted mostly of marine products. Palaeoproteomics of dental calculus of the mandibular right first premolar identified proteins of host and oral bacterial origin. Based on the identified proteins, we will discuss our analysis of i) whether the pathogens associated with periodontal disease in this individual differ from those associated with modern periodontal disease, and ii) how extreme the physiological stress of the pathological oral condition was on the host.

ABSTRACT HDP-005

Metagenomics analysis of ancient dental calculus provide an insight into oral microbial ecology in an Anglo-Saxon population

Speaker: **Biancamaria Bonucci**
University of Tartu, Estonia

Co-authors: Toni de-Dios[1], Sarah A. Inskip[2], John E. Robb[2], Christiana L. Scheib[1,2]

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Abstract:

Recent studies show that there is a delicate balance between diet, commensal microbes and overall health status of an individual. Ancient dental calculus has proved to be a valuable resource of ancient microbial, host and dietary biomolecules. Here, we examined 100 human skeletons buried in the same early Anglo-Saxon cemetery in Cambridgeshire, England. From those, we selected the 74 individuals presenting ancient dental calculus, from which we generated shotgun metagenomic libraries. After performing metagenomic profiling, we could not observe differences in the oral microbiome based on social status, age, health or genetic sex. Furthermore, we validated the presence of all the bacterial oral complexes, with an increased abundance of the orange and red complexes. We were then able to reconstruct the phylogenies of several periodontitis associated species (Tannerella forsythia, Porphyromonas gingivalis, Treponema denticola, Campylobacter rectus and Desulfomicrobium orale). We aim to shed light on the relationship between oral health, diseases and ancestry based on the combined analysis of ancient dental calculus with host genome and archaeological data. This study could give a better understanding of oral microbial ecology of Early Medieval populations in England.

ABSTRACT HDP-006

Characterising the oral microbial make-up of Pre-Colonial human populations of the Southern Cone of the Americas

Speaker: Maria Lopopolo

Institut Pasteur, France

Co-authors: Arve Lee Willingham Grijalba[1,2], Gabriel Yaxal Ponce-Soto[1], Julien Fumey[1,2], Elizabeth A. Nelson[1], Miren Iraeta-Orbegozo[3], Pierre Luisi[1], Gaetan Tressieres[1,4], Federico Scartascini[5], Florencia Borella[6], Mónica Berón[7], Eliana Lucero[7], Gustavo Neme[8], Adolfo F. Gil[8], Eva A. Peralta[8], Cinthia Abbona[8], Mariano Del Papa[9], Rafael Goñi[10], Augusto Tessone[7], Solana Garcia Guraeib[11], Sebastian Pastor[12], Luis E. Tissera[13], Ramiro Barberena[14], Paula Novellino[15], Andrea Recalde[16], Iván Díaz[7], Diego Rivero[16], Ludovic Orlando[4], Hannes Schroeder[3], Christiana L. Scheib[17,18], Nicolás Rascovan[1]

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Abstract:

Ancient DNA (aDNA) approaches have revolutionised the field of evolutionary biology by giving novel insights into the origins of modern humans, past human demography, and health. Dental calculus has proven to be a rich source of aDNA permitting genomic-level evaluation of the diversity, evolution, and ecology of the oral microbiome in ancient human populations. Through the contextualization of these data, they can ultimately be used to study the human past, and host-microbial relationships. The Southern Cone of South America offers a unique opportunity to perform complex analyses of the evolution of the oral microbiome. Despite this region possessing a rich and rigorously studied archaeological context, providing a broad time and cultural transect, it remains understudied with paleogenomic approaches. In this study, we collected and sequenced ancient DNA from the dental calculus of 183 individuals dated between the Middle and Late Holocene from the Southern Cone, providing a comprehensive snapshot of the pre-Colonial oral microbial make-up. We combined different techniques to reduce environmental and modern contamination of data, and tested multiple bioinformatic pipelines to perform comparative analyses between the microbiomes of different individuals. Overall, we identified conserved species across temporal and spatial scales, and we are generating a first characterization of the ancient microbial diversity of pre-Colonial South American populations.

ABSTRACT HDP-007

Microbiomes and pathogens in Neolithic Scandinavia

Speaker: **Nora Bergfeldt**
Centre for Palaeogenetics, Sweden; Stockholm University, Sweden

Co-authors: Emrah Kırdök[1], Nikolay Oskolkov[2], Claudio Mirabello[3], Per Unneberg[4], Helena Malmström[4], Magdalena Fraser[4], Federico Sanchez-Quinto[4], Roger Jorgensen[5], Birgitte Skar[6], Kerstin Lidén[7], Mattias Jakobsson[4], Jan Storå[7], Anders Götherström[7]

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Abstract:

With the Neolithic transition, human lifestyle shifted from hunting and gathering to farming. This change altered subsistence patterns, cultural expression, and population structures as shown by the archaeological/zooarchaeological record, as well as by stable isotope and ancient DNA (aDNA) data. Here, we used metagenomic data to analyse if similar transitions in the microbiome composition could be found in 25 Mesolithic and sub-Neolithic hunter-gatherers and 13 Neolithic farmers from several Stone Age Scandinavian cultural contexts. Two pathogenic species of the genus Neisseria were identified in individuals from both Mesolithic and Neolithic hunter-gatherers and represent the earliest findings of these species. Salmonella enterica, a bacterium that may have been the cause of death for the infected individuals, were only found in Neolithic samples from Battle Axe culture contexts Several species of the bacterial genus Yersinia were found in Neolithic individuals from Funnel Beaker culture contexts as well as from later Neolithic context. Transmission of e.g. Y. enterocolitica may have been facilitated by the denser populations in agricultural contexts.

ABSTRACT HDP-009

A detailed analysis of Hepatitis B virus strains and implications for their transmission in early Medieval Eastern Central Europe

Speaker: **Alina N. Hiss**
Max Planck Institute for Evolutionary Anthropology, Germany

Co-authors: Guido Gnecchi Ruscone[1], Luca Traverso[1], Ke Wang[1], Tivadar Vida[2,3], Walter Pohl[4,5], Patrick J. Geary[6], Zuzana Hofmanová[1,7], Johannes Krause[1], Alexander Herbig[1]

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[7] Masaryk University, Czech Republic

Abstract:

The Hepatitis B virus is responsible for severe liver diseases, such as cirrhosis, chronic hepatitis, and liver cancer. Even though it is much less prevalent today due to vaccination efforts, it is still causing nearly 1 million deaths worldwide every year. The virus does, however, not inevitably lead to the death of an infected individual as the infection can either be cleared by the immune system, or remain present in a chronic state over a long period of time. It can be transmitted either horizontally as a sexually transmitted disease, or vertically from mother to child during birth. Ancient DNA of the virus has been detected in individuals dating to the last 10,000 years, providing a detailed overview of genotypes and lineages through time and space (Kocher, et al. Science 2021). Here, we take a look at the virus on a different scale, focussing on the Carpathian basin during the Migration Period (4th-9th c. CE). In the interdisciplinary project “HistoGenes”, whole cemeteries are being sampled to understand more about the genetic ancestry, social structure and relatedness between individuals, and to study pathogens associated with people during this period. We detect the Hepatitis B virus in many individuals across more than 30 sites and will present the genetic diversity of the virus for this time and region, hereby more than doubling the number of published ancient genomes. Given that the virus has often been detected in closely related individuals within larger families, we discuss possible transmission patterns as well as the impact this virus might have had on communities during this time.

ABSTRACT HDP-010

Avian influenza viruses in formalin-fixed, ethanol-preserved historic North American bird specimens

Speaker: **Hsiao-Lei Liu**
Smithsonian Institution - National Museum of Natural History, USA

Co-authors: Audrey T. Lin[1], Sarah C. Hill[2], Ariane Düx[3], Livia Patrono[3], Chris M. Milensky[1], Sébastien Calvignac-Spencer [3], Sabrina B. Sholts[1], Logan Kistler[1]

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Abstract:

The 1918 H1N1 influenza pandemic was the most devastating pandemic in recent history, causing an estimated 50-100 million deaths worldwide. The virus responsible for the pandemic was a highly virulent strain of influenza A virus (IAV) that likely spilled over to humans from North American waterfowl shortly before its global spread. Although conventional PCR-based genetic studies reported fragments of avian influenza virus in some of the specimens 20 years ago, these findings were the result of contamination, highlighting fundamental limits to ancient biomolecular research at the time. To better understand the origin of the 1918 IAV and the evolutionary history of avian IAVs, we re-examined wet specimens of North American shorebird and duck populations collected by the Smithsonian's National Museum of Natural History from late 19th to early 20th century. Sample selection was performed to maximize IAV detection probability, based on contemporary distribution and prevalence of IAVs in their avian hosts. Applying robust high throughput sequencing approaches, we aim to test the following hypotheses: 1) our experimental approach can allow us to detect and analyze ancient IAVs; 2) Historic North American avian influenza A virus sequences belong to Western hemispheric avian influenza A virus clades, within which they likely appear as early offshoots; 3) If detected, H1 segments from historic North American avian influenza viruses are likely most closely related to the 1918 human pandemic influenza virus H1 segments; 4) Internal gene segments from North American avian influenza viruses originate in the middle to late 19th century.

ABSTRACT HDP-011

Molecular evolution of Y. pestis using ancient and modern genomes

Speaker: **Ian Light**
Max Plank Institute for Infection Biology, Germany

Co-authors: Felix Key[1]

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Abstract:

While much work has been carried out on the evolutionary relationships between ancient samples of Yersinia pestis and the modern-day diversity of this disease-causing bacteria, the use of ancient genomes to investigate its molecular evolution over time has been limited. This study aims to address this and focuses on the Late Neolithic Bronza Age (LNBA) lineage of Y. pestis, which is first observed around 5,000 years before present and shows repeated within-lineage genotypic replacement. We hypothesized that the ladder-like shape of the LNBA phylogeny could stem from repeated sweeps of positively selected genotypes replacing existing genetic diversity. We searched for evidence of parallel evolution, i.e. multiple mutations in a single gene, and identified 116 genes, which, however, show a signature of purifying selection in a canonical measure of selection (dN/dS). We extended our analysis to investigate homoplasies, where independent mutations occur at the same site, and many such positions across the entire Y. pestis diversity, including the LNBA. Interestingly, these positions occur at high rates upstream of genic regions, suggesting their role in gene regulation within Y. pestis. Moreover, previous alignment-based analyses of ancient Y. pestis relied on a single reference genome (CO92), providing only a one-sided view about the gene content in the ancient past. Here we investigated the genetic repertoire using a Y. pseudotuberculosis reference, the phylogenetically basal ancestor of Y. pestis. We identify Y. pseudotuberculosis virulence genes uniquely present among LNBA genomes, quantify divergence of Y. pestis clades from its ancestor and show that reliance on an in-group reference genome limits what we can learn about the genetic make-up of ancient genomes. Taken together, these points highlight the benefits for data sharing efforts and illustrate the power to infer the molecular evolution of infectious diseases using ancient and modern pathogen genomes

ABSTRACT HDP-013

Infectious diseases in the Late Viking Age town of Sigtuna

Speaker: **Zoé Pochon**
Stockholm University, Sweden

Co-authors: Emrah Kırdök[1], Nikolay Oskolkov[2], Maja Krzewińska[3,4], Anders Götherström[3,4]

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Abstract:

Infectious diseases are not easy to detect in paleopathology. Long-lasting diseases such as tuberculosis, leprosy, syphilis and brucellosis can leave visible traces on the bones, but this is not the case for most infectious diseases. With the development of next-generation sequencing techniques, it is now possible to recover the genomes of ancient humans but also of the pathogens they were hosting at the time of death such as Yersinia pestis, the agent of plague. Here, we focus on the impact of urbanization on infectious disease with the Late Viking Age town of Sigtuna as a case study. Over 60 individuals were subjected to shotgun sequencing and screening for potential pathogens using a new ancient metagenomics workflow developed in collaboration with the National Bioinformatics Infrastructure Sweden (NBIS), called aMeta and available on GitHub. Preliminary results are promising with the detection of Yersinia enterocolitica, Hepatitis B virus and other pathogens responsible for past epidemics. Today, Yersinia enterocolitica causes primarily a foodborne zoonosis, but transmission through close contact with cattle cannot be excluded in the context of an early urban town. We are generating phylogenetic trees comparing the pathogenic strains found with other ancient and modern strains to better understand the way of transmission of these diseases through time and space. We hope that our study will provide greater insight into the infectious diseases that could have been common in a Late Viking Age early urban site.

ABSTRACT HDP-014

Characterizing the cariogenic bacterium Streptococcus mutans in ancient Chile

Speaker: **Shreya Ramachandran**
University of Chicago, USA

Co-authors: Ricardo A. Verdugo[1], Paola Gonzalez[2], Mauricio Moraga[3], Sergio González Providell[4], Josefa Nuñez Belmar[4], Jaime Andrés Rivas-Pardo[4], Constanza de la Fuente[5], Maanasa Raghavan[5]

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Abstract:

Ancient metagenomics is a rapidly growing field that uses sequencing data from ancient samples to understand the evolution of microbes across time and space. As one example, data from ancient human teeth can be used to trace the evolution of the oral microbiome. Here, I present preliminary data from tooth samples from eight individuals from an archaeological site in the Near North region in Chile. These samples date between 1200 and 1400 BCE. The individuals, representing different times and a variety of archaeological contexts, all show genomic evidence of ancient Streptococcus mutans, a bacterium responsible for causing cavities. I will present phylogenetic analyses that use these ancient time-stamped samples to refine estimates of the evolutionary trajectory of S. mutans and its relationship to human agricultural transitions. I will also discuss the adaptation of S. mutans to its local environment, by analyzing the presence and absence of virulence factors in an archaeological context compared with contemporary S. mutans strains. I will then share my future plans for this project, which involve analyzing other members of the oral microbiome in these individuals to gain a greater idea of their oral health status. In collaboration with archaeologists and anthropologists, I will study the samples in the context of the diet and lifestyle of these individuals. From these analyses, we can gain a greater understanding of determinants of oral health in ancient South America, a region that has been historically understudied from an ancient metagenomic perspective. At the same time, by studying the evolutionary history of pathogens that continue to affect us today, we can gain insight into potential targets for improving human health.

ABSTRACT HDP-016

Prehistoric Borrelia genomes provide insights into the evolutionary history of louse-borne relapsing fever

Speaker: **Pooja Swali**
The Francis Crick Institute, UK

Co-authors: Thomas Booth[1], Kyriaki Anastasiadou[1], Chris Barrington[2], Matteo Borrini[2], Jo Buckberry[3], Rea Carlin[4], Alexandre Gilardet[1], Isabelle Glocke[1], Joel Irish[2], Monica Kelly[1], Megan King[2], Fiona Petchey[5], Frankie Tait[1], Satu Valoriani[2], Mia Williams[1], Kevin Cootes[2], Ian Armit[6], Pontus Skoglund[1]

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Abstract:

Relapsing fever, caused by multiple species belonging to the Borrelia genus, can be transmitted either via tick (TBRF) or via lice (LBRF) vectors. Borrelia recurrentis, the only known louse-borne Borrelia species that can infect humans, is often found in overcrowded populations with poor personal hygiene. Previously, ancient genomics has been able to identify Borrelia recurrentis in a 15th-century individual from Scandinavia (Guellil, et al. PNAS 2018), which gives us insight into the recent past of the pathogen. Here we identify Borrelia recurrentis genomes from Britain dating to 2500-800 years ago to gain a deeper understanding of the evolutionary history of the pathogen.

ABSTRACT HDP-017

Complex analyses of ancient soil samples from burial context

Speaker: **Kateřina Novotná**
Masaryk University, Czech Republic

Co-authors: Eva Drozdová[1], Eva Chocholová[1]

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Abstract:

In the past, soil was typically regarded as a contaminant in paleogenetic research on ancient human populations and was often discarded. However, recent developments in metagenomic analysis of dental calculus and other non-human ancient DNA have shown that soil samples can offer valuable insights into the environmental context of ancestral populations. With our research, we aim to demonstrate the usefulness of soil in enhancing our understanding of ancient human populations and their ways of life on samples from burial site in Czech Republic dated to Great Moravian Empire (9-10th century AD). Our research focuses on identifying the optimal method for extracting ancient DNA from soil samples, which we then subjected to metagenomic sequencing using the Illumina platform to analyze the variable regions V1 and V6 of the 16S rRNA gene. With metagenomic approach, we are potentialy able to reconstruct the gut microbiome of ancient individuals. In an addition, we have collected soil samples from the abdomen of buried individuals for paleoparasitological analysis, which was supplemented with genetical identification of parasites. We believe that soil samples hold great potential for biomolecular analyses and can provide valuable insights into the diet and health of ancient human populations.

ABSTRACT HDP-018

Current allele distribution of the human longevity gene APOE in Europe can mainly be explained by ancient admixture

Speaker: **Daniel Kolbe**
Kiel University, Germany

Co-authors: Nicolas A. da Silva[1], Janina Dose[1], Guillermo G. Torres[1], Amke Caliebe[2], Ben Krause-Kyora[1], Almut Nebel[1]

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Abstract:

Variation in apolipoprotein E (APOE) has been shown to have the strongest genetic effect on human longevity. The three main APOE alleles, ε2, ε3 and ε4, are each associated with a different likelihood of becoming long-lived, which is primarily attributed to the risk of developing cardiovascular or late-onset Alzheimer's disease. In this respect, ε4 is detrimental, whereas ε3 is considered neutral and ε2 protective. The aim of this study was to unravel the evolutionary history of the APOE alleles in Europe. For this purpose, we assembled and analysed 358 diploid APOE genotypes from 3,521 publicly available aDNA datasets going back as far as 12,000 years. We detected significant allele frequency shifts between populations and over time. Our analyses indicated that selection led to large frequency differences between the earliest European populations (i.e., hunter-gatherers vs. first farmers), possibly due to changes in diet, lifestyle and/or inflammatory load. In contrast, the allele distributions in populations from ~4,000 BCE onwards can mainly be explained by admixture, suggesting that it also played an important role in shaping current APOE variation. The resulting allele frequencies strongly influence the predisposition for longevity today, likely as a consequence of demographic processes and adaptations to selective pressures that were independent of longevity.

ABSTRACT HGP-002

Community formation in the early medieval Netherlands; an integrated bioarchaeological case study in Nijmegen

Speaker: **Eveline Altena**
Leiden University Medical Center, the Netherlands

Co-authors: Lisette M Kootker[1], Iñigo Olalde[2,3,4], Constance van der Linde[5], Joep Hendriks[6], Frans Theuws[7], David Emil Reich[3,8,9,10]

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Abstract:

We present a study on a 6th century Merovingian population from a cemetery close to Nijmegen, the Netherlands. The Late Roman Netherlands was characterized by economic, political and social instability. The transition period from the Roman era to the Early Middle Ages, also known as the Migration period, was therefore marked by substantial depopulation of large parts of the country and later repopulation. To understand how new communities were formed in the Netherlands in the early stages of the newly emerging early medieval society, we applied an integrated bioarchaeological approach (osteology, isotopes and genetics) on 57 inhumed individuals, with the aim to reconstruct the demography, kinship ties, genetic ancestry and mobility patterns of this population, and ultimately the social structure of the community that used this cemetery. Our preliminary results indicate a community of diverse genetic and geographic origin, although nearly all of the 18 children (max 8 years old) seem to have been born locally. Half of the investigated population was part of a close kinship, mostly only comprising 1 or 2 generations, but we also have signs of more distant kinships, linking some of the core families. Remarkably we found a parent for only one of the 18 investigated children and no adult siblings. We only see kinships among the main cluster of individuals that are genetically closer to each other. Furthermore, we see distant kinships with contemporary individuals from neighboring countries and even further away, providing insights into the long-distance networks that were present in Europa at this time. The high diversity in both mitochondrial and Y-chromosomal haplogroups indicates a lack of a strong matri- or patrilocal settlement pattern. Altogether our results point towards a community that was formed of people from different origins that started new families here, but used this cemetery only for several generations.

ABSTRACT HGP-003

Genomic analyses of Seleucid and Parthian period population in North Iran

Speaker: **Motahareh Amjadi**
Eötvös Loránd University, Hungary

Co-authors: Maryam Ramezani[1], Kristóf Jakab[2], Balázs G. Mende[2], Abdol Motalleb Shariff[4], Ata Hasanpour[4], Vali Jahani[4], Arezoo Bibak[1], Mahmood Tavallaie[3], Anna Szécsényi-Nagy[2]

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Abstract:

The Seleucids ruled the area of ancient Iran from 312 BC and were subsequently displaced by the expansion of the Parthians, who led a significant political and cultural empire in ancient Iran between 247 BC and 224 AD. The Parthians maintained an imperial state, which stretched from the northern flow of the Euphrates, in what is now central-eastern Turkey to the area of present-day eastern Iran. The Northern Iranian Khorasan's primary trade route, the Silk Road connected the Roman Empire (the Mediterranean Sea) with the Han Empire in China and made the Parthian territories a hub of commerce. Various burial customs prevailed in this long-lasting empire, due to its vast extent and exceptional cultural diversity. Here we report on eleven ancient genomes from the Selucid-Parthian periods, gained via genome-wide SNP capture and shotgun sequencing methods. Sites as Vestemin (North of Iran, Mazandaran province), Liar-Sang-Bon (Amlash-Gilan-North of Iran) and Mersinchal (Mehdishahr-Semnan) are considered in this paper from the Caspian Sea area of North Iran. Ancient DNA is especially scarce from the region and area, with the geographically closest reference data from the Iron Age layer of Hajji Firuz, Tepe Hasanlu and Dinkha Tepe from Northwestern Iran, and the Bronze Age Gonur Tepe in Turkmenistan. The new historical period genomes attest for rather limited connection to the Scythia and the steppe area north of Iran, and the dominance of the Iranian genetic ancestry, traced back to the Neolithic/Mesolithic population of the area. The additional 20-40% Anatolian Neolithic ancestry in their genomes well corresponds to the previously described South Eurasian Early Holocene genetic cline (Narasimhan et al. Science 2019), suggesting continuity in the basic population structure south of the Caspian Sea up to the historic times.

ABSTRACT HGP-004

Ancient DNA shed light on the funerary practices of a Late Neolithic collective burial in Southern France

Speaker: **Ana Arzelier**
University of Bordeaux, France

Co-authors: Harmony De Belvalet[1], Marie-Hélène Pemonge[1], Pauline Garberi[2], Didier Binder[2], Wolfgang Haak[3], Henri Duday[1], Marie-France Deguilloux[1], Mélanie Pruvost[1]

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Abstract:

The Aven de la Boucle (Corconne, Gard, Southern France) is a karst shaft that was used as a collective burial between 3,700 and 2,800 cal BCE. The site encompasses the skeletal remains of approximately 75 individuals, represented by scattered and commingled remains, with only a few remains in anatomical context. The anthropological analysis demonstrated that the primary deposition of the dead followed a selection of a large majority of adult individuals. Further, ceramics differentiated a first horizon corresponding to the early stage of Late Neolithic and a second horizon belonging to a later phase attributed to the "Ferrières" culture (3,300-2,800 BCE). The assemblage characterizing this site thus represents a unique opportunity to address the cultural and biological (dis)continuities of human groups during the Late Neolithic by applying an integrative/multidisciplinary approach to the interpretation of social structure and funerary rites. We combine evidence from archaeology, anthropology, Bayesian modeling of radiocarbon dates, and genomic data from 37 individuals to shed light on genetic profiles, relationships and funerary practices of this community. Genomic results identified 26 Neolithic males and 8 females, suggesting a marked sex-biased selection. Although a full picture of biological kinship networks cannot be drawn, available data stressed the importance of biological relatedness and a male-mediated transmission of social status, as the affiliation to specific male lineages appears to be a preponderant selection factor at the Aven de la Boucle. This study enabled us to track the site use of this sepulchral cavity more precisely. The genomic results argue in favor of "continuous" deposits between 3,700 and 2,800 BCE, carried out by the same community, despite cultural changes reflected by the material culture. Thus, our study further illustrates the complex relationship between biological and cultural affinities of ancient communities.

ABSTRACT HGP-005

Genetic history and health in Medieval Europe with the Belgian town of Sint Truiden as a model

Speaker: **Owyn Beneker**
KU Leuven, Belgium

Co-authors: Stefania Sasso[1], Natasja de Winter[2], April Pijpelink[3], Maxim Hoebreckx[2], Christiana Lyn Scheib[1], Maarten Larmuseau[4], Toomas Kivisild[4]

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Abstract:

Analysis of ancient genomes offers a unique opportunity to study directly population history, health, and social organisation of past populations. While previous ancient DNA research has mainly focussed on prehistoric populations, there are gaps in our knowledge as how fine-scale population structure and differentiation evolved in North Western Europe during the Middle Ages and what impact wars, famines and disease pandemics had on the health of growing medieval town populations. Archaeological work in the city of Sint-Truiden in Belgium has uncovered a medieval parish cemetery of thousands of burials from which teeth of 403 individuals from a transect of time of nine centuries (800AD-1700) were sampled for whole genome sequencing. Majority of the samples showed good preservation and 84% of the individual genomes were shotgun sequenced to a coverage of 0.1 or higher. We find that all individuals had predominantly Northern-European autosomal ancestry, including two samples with mtDNA haplogroups that are atypical to Europe. Individuals from medieval Sint-Truiden were on average more related to early Medieval Germanic populations than to the modern populations of France and the UK. Using a combination of allelic mismatch and IBD based methods we study genetic kinship finding that the proportion of individual pairs with close (1-3rd) degree of relatedness in this large urban parish cemetery is significantly lower than previously reported results on contemporary but smaller urban and rural parish cemeteries elsewhere.

ABSTRACT HGP-006

The genomics of an Iron Age site in Fermo, Marche.

Speaker: **Emily M Breslin**
Trinity College Dublin, Ireland

Co-authors: Carmen Esposito[1], Valeria Mattiangeli[2], Pasquale Miranda[3], Maarten Blaauw[4], Paula Reimer[4], Daniel G Bradley[2]

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Abstract:

The Villanovan, or proto-Etruscan, culture of early Iron Age Italy is key in the study of the processes of urbanisation and mobility in Italy. Genetic studies on Villanovan and Etruscan groups have so far focussed on sites within Etruria, and on individuals from more “typical” archaeological contexts. These ancient genomes revealed that the Villanovans and early Etruscans carry a genetic signature typical of Iron Age European populations, and that the origin of these groups appears to be autochthonous. In this study we present 19 new shotgun sequenced genomes from the Villanovan enclave of Fermo, Marche. Using ancient DNA and isotopic analysis we examine the connections between the population at Fermo and the contemporaneous populations of Etruria, and reveal a pattern of both group and individual mobility. We also examine the trajectory of these Iron Age populations to the present day, and how migration and changes in mobility have shaped the Italian peninsula since the Iron Age. Within Fermo itself we find evidence of extensive kinship networks, illuminating the underlying social structure of the settlement.

ABSTRACT HGP-007

Investigating the occupation history and social structure at an early colonial site in Taiwan through archaeology, archaeothanatology, and archaeogenetics

Speaker: **Selina Carlhoff**
Max Planck Institute for Evolutionary Anthropology, Germany

Co-authors: Kathrin Nägele[1], Elena Serrano Herrero[2], Frédérique Valentin[3], Ellen Hsieh[4], Cosimo Posth[5], Cheng-hwa Tsang[6,7], María Cruz Berrocal[8], Johannes Krause[1]

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Abstract:

Driven by the desire to counterbalance increasing Dutch influence in the region, re-establish trading with China, and accelerate evangelization, the Spanish governor of Manila commissioned the founding of San Salvador de Quelang on Heping Dao, an island situated off the coast of present-day Keelung in northern Taiwan, in 1626. While a large number of historical documents about this and other colonial occupations in the Asia-Pacific region have been analysed, archaeological excavations of colonial sites, which allow the direct study of initial contact, development of the site, and impact on the local communities and environment, are rare. Excavations conducted between 2011 and 2019 at Heping Dao have revealed archaeological evidence of a colonial settlement successively occupied by Taiwanese in prehistory, and Spanish, Dutch, Chinese, Japanese, and the Kuomintang from the early historical period to this day. Nineteen burials were located inside and outside the foundations of a 17th-century church and displayed various body treatments and orientations. We used archaeological, archaeothanatological, and archaeogenetic methods to study this distinctive spatial pattern and to investigate colonial community structure. Our results showed that the distribution of burials likely reflected cemetery use during the Spanish and Dutch occupation and the social structure of the colony, which in turn was connected to genetic ancestry. As the only early colonial-period cemetery exhaustively excavated and analysed so far in the Asia-Pacific, the combination of different scientific approaches allowed for the rendition of a more detailed picture of early colonial settlements in the region.

ABSTRACT HGP-008

Disparate demographic impacts of the Roman and Visigothic presence in the Iberian Peninsula

Speaker: Pablo Carrion

Institut Biologia Evolutiva, Spain

Co-authors: Iñigo Olalde[1,2,3], Pablo García-Borja[4], Miguel-Angel Cuadrado[5], María-Luisa Cerdeño[6], Juan-Antonio Quirós[1], Virginia García Entero[4], Jordi Morera[7], Josep-F. Roig-Pérez[8], Moisés Díaz García[8], Neus Coromina[9], Josep Burch[9], David Vivó[9], Jordi Vivo[9], Jordi Sagrera[9], Juan-Ignacio Morales[10], Josep María Vergès[10], Nadin Rohland[11], Swapan Mallick[11,12], Juan-Manuel Jiménez-Arenas[13], Macarena Bustamante-Álvarez[13], Celia Chaves[13], Maite-Iris Garcia-Collado[1,14], Javier Heras[15], Sergio Vidal[16], Beatriz Campdera[17], Carles Lalueza-Fox[18], David Reich[3,11,12,19]

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Abstract:

The Roman Empire, the fall of its Western part, and the so-called Great Migration period, shaped the modern political landscape of West Eurasia. How they impacted the demography of different regions of the Empire, like the Iberian Peninsula, remains imperfectly understood. We generated genome-wide data from 210 newly reported ancient individuals from Iberia from the Roman period to the Great Migration period. Roman presence in the peninsula started as early as the 3rd century BCE, and its territory was fully annexed by the 1st century BCE and deeply interconnected with other Mediterranean regions via the Roman road system and sea routes until its collapse during the 5th century. Here we show that populations of Roman period Iberia were as demographically cosmopolitan as other parts of the central and western Mediterranean such as central Italy (Antonio, et al. Science 2019), and the Danubian frontier (Olalde, et al. bioRxiv 2021). During the 5th century several groups are historically attested as impacting Iberia, both Germanic (Buri, Suevi, Vandals & Visigoths) and Sarmatian (Alans). Some, like the Suevi, established kingdoms, while the politically most important Germanic kingdom was established by the Visigoths during the late 5th century, lasting until the Umayyad conquest in the 8th century. Although individuals with Germanic ancestry are identified at key sites, overall, we observe a high degree of population continuity with Roman-period Iberian populations, without major demographic changes during this period. These Germanic groups were closely interconnected across vast distances, as reflected close relatives found at distant archaeological sites.

ABSTRACT HGP-009

An archaeogenetic and paleopathological approach to reconstructing life in Early Medieval Iberia at La Olmeda (Spain, 6th – 11th c. CE)

Speaker: **Lorenza Coppola Bove**
Max Planck Institute for Evolutionary Anthropology, Germany; University of Granada, Spain

Co-authors: Vanessa Viilalba-Mouco[1], Casey L. Kirkpatrick[1,2], Adam B. Rohrlach[1,3], Thiseas C. Lamnidis[1], Alfonso Vigil-Escalera Guirado[4], Miguel C. Botella López[5], Johannes Krause[1], Kirsten I. Bos[1]

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Abstract:

The Early Middle Ages in Iberia witnessed the growth of urban centers, and the arrival of distinct groups from neighboring regions that were intertwined with local genetic changes and thespread of infectious disease. However, the scarcity of informative sources from these time periods in Iberia, makes historical reconstruction of these phenomena extremely challenging. Through the analysis of human remains from the Roman Villa of La Olmeda (Palencia, 6th – 11th c. CE), we investigate both disease burden and genetic continuity in this early medieval community. Genomic human data was obtained from 51 individuals spanning 500 years to assess local changes in the genetic composition of these individuals over time. This analysis was then complemented with morphological and molecular analyses of pathological bone to identify any infectious diseases. Through this analysis we reveal a heterogeneous distribution for both uniparentally-inherited markers, as well as genetic variation that spans from individuals showing Iberian Iron Age-like ancestry to admixed individuals displaying a North African ancestry. Furthermore some of the infections we identify support a continuity of diseases that were already common in the Roman world, but were not properly described in early medieval written sources.

ABSTRACT HGP-010

Exploring changes in immuno- and population-genetics in West Germany's Neolithic communities

Speaker: **Nicolas Antonio da Silva**
Kiel University, Germany

Co-authors: Ben Krause-Kyora[1], Almut Nebel[1], Magdalena Haller[1]

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Abstract:

The central European farmers during the Early Neolithic have been associated with the Linear Pottery culture (LBK). After the decline of the LBK in Europe, the middle and late Neolithic periods saw the emergence of diverse, small-scale farmer societies, such as the Wartberg culture (WBC) in western Germany. To examine changes in the population structure and immunogenetic profile that occurred during the 2000-year transition from the Early to the Late Neolithic, we generated whole genome shotgun and capture data targeting the leukocyte antigen complex (HLA) on individuals from six archaeological sites. The population genetic analyses revealed that while the LBK group exhibited only a small amount of hunter-gatherer (HG) ancestry, the WBC group displayed a much greater degree of HG admixture, surpassing that of other contemporaneous Late Neolithic communities in the region. Moreover, an increase in runs of homozygosity due to admixture with HG was observed in the WBC. These findings indicate a shift from a more insular society in LBK (genetically homogeneous) to a more inclusive one in WBC (more willing to integrate local HG). Regarding immunogenetics, we observed significant shifts in HLA allele frequencies between LBK and WBC as well as between both Neolithic groups and modern populations, mostly affecting HLA II loci DQB1 and DRB1. Our study shows that admixture likely played a significant role in driving the major changes in the HLA pool observed between LBK and WBC, while also expanding the dataset available for future population genetic research.

ABSTRACT HGP-012

An admixture of people conquered the Carpathian basin in the 10th century

Speaker: **Ábel Fóthi**
Research Centre for the Humanities, Hungary

Co-authors: Virág Krizsik[1], Alexandra Kovács[1], Dóra Szegő[1], Róbert Kaló[1], Horolma Pamjav[2], Ariana Gugora[3], Balazs Könnyű[4], Bence Gálik[5], Péter Urbán[5], Attila Gyenesei[5], Erzsébet Fóthi[1]

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Abstract:

In the early medieval ages, Ancient Hungarians migrated to Central Europe and conquered the Carpathian Basin. Y-chromosomal and autosomal genetic studies already showed that they were an admixed population. However, the sources of these people are still debated.We studied almost 200 hundred genomes from people of the 10th-century Carpathian basin. Only a smaller portion of these people can be identified as Hungarian Conquerors based on their archeological attributes. Still, their genetic profiles can serve as reference points for identifying the clusters of the Conquerors. We developed a new computational pipeline called Population Genetics Analyzer (PGA) to study the inner structure of our dataset and to make multiple comparisons with publicly available population genetics data. First, we clustered the Conquerors into core groups, labeled them based on their ancestries, and then the archeologically ambiguous samples were classified into these groups. We found that Hungarian Conquerors were a heterogenous population from different sources such as the Ural region, the Caucasus, and the Pontic steppe. The core group of Hungarians came from the Urals, but distinct Eastern European groups were also identified. Their genetic relations with modern-day Uralic and Caucasian people, Scythians, Slavs, and Vikings were also examined. Differentiation of the Eastern European group of the Conquerors from the local, autochthon samples turned out to be rather challenging. Our results suggest a continuous admixture between Hungarians and people getting into contact with them through their migration.

ABSTRACT HGP-014

Y-chromosome analysis of Bronze Age populations from the territory of present-day Poland

Speaker: **Michał Golubiński**
University of Warsaw, Poland

Co-authors: Mateusz Baca[1], Barbara Bujalska[1], Michalina Hoffmann[2], Anna Hyrchała[3], Elżbieta Jarzęcka[4], Tomasz Koczorski[5], Andrzej Kokowski[6], Leszek Kucharski[7], Maciej Kosiński[8], Piotr Miernik[2], Anna Mucha[3], Piotr Pachulski[9], Danijela Popović[1], Wojciech Rajpold[10], Bartłomiej Rzepkowski[2], Iwona Sobkowiak-Tabaka[11], Łukasz Maurycy Stanaszek[12], Magdalena Wieczorek-Szmal[8], Piotr Węgleński[1], Arkadiusz Wiktor[2], Marcin Woźniak[4], Daniel Żychliński[9], Martyna Molak[1]

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Abstract:

The Bronze Age in the area of what in the present-day makes Poland lasted for more than a dozen centuries (2300-700 BC). At that time, this territory was inhabited by various groups of different origins, as well as of different levels of economic and social development. Finally, around 1350 BC, the Lusatian culture emerged amidst this heterogeneous cultural background. Some researchers in the past associate the people of the Lusatian culture with the Proto-Slavs.The aim of this study was to determine the origin and genetic structure of male lineages from the Mierzanowice culture (2300-1600 BC), the Trzciniec culture (1900-1000 BC) and the Lusatian culture (1350-400 BC), which occupied the territory of the present-day Poland using the Y-chromosome-wide SNPs. The analysis of the Y chromosome variation made it possible to test for the continuity of settlement in the mentioned area throughout the Bronze Age and for a possibility of a connection between the Lusatian culture and the younger Iron Age populations. The analysed material consisted of skeletal fragments collected from 46 Bronze Age individuals. The samples with more than 1% of endogenous DNA, after sex determination, were subjected to targeted enrichment with a custom in-house-designed panel of 10k Y-chromosome SNPs and/or with myBaits Expert Human Affinities Prime Plus. The Y-chromosome haplogroup was determined for 25 individuals. Most of the Bronze Age individuals belonged to R1a haplogroup subclades. There were also individuals belonging to haplogroup I2a and O2a-L465. The lack of these Y-chromosome lines identified in the younger Iron Age samples suggests at least some level of discontinuity with the Bronze Age populations. The research is part of the project „Genetic history of Poles" (2018/31/B/HS3/01464) financed by the National Science Centre, Poland.

ABSTRACT HGP-016

A comprehensive picture of the genetic history of Iran

Speaker: **Mogge Hajiesmaeil**
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Co-authors: Francesco Ravasini[1], Flavia Risi[1], Hamid Galehdari[2], Eugenia D'Atanasio[3], Beniamino Trombetta[1], Fulvio Cruciani[1]

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Abstract:

Ancient genome studies revealed that Iran has played a central role in the history of Eurasia being one of the major centers of agriculture invention and cattle domestication. While an "Iranian Neolithic component" is currently recognized in most of Eurasia, the genetic diversity of contemporary Iranians, especially at the Whole Genome Sequencing (WGS) level, has been poorly studied. To paint a more comprehensive picture of the genetic diversity and history of Iranian populations, we conducted novel whole genome sequencing of 87 males spanning 8 different ethnic groups and 3 language families (Indo-European, Afro-Asiatic, Turkic Altaic). After merging our WGS data with relevant available modern and ancient genomes, we found that all the Iranians, regardless of ethnicity, have a predominant pre-Neolithic autochthonous ancestry and significant ancestries from the Neolithic Anatolian farmers and Bronze Age Steppe pastoralists. Nonetheless, striking differences between ethnic groups were found due to varying gene flow from Africa (mainly in Arabs and Southern Iranians), Central Asia (Iranian Turkic-speakers and North-Eastern Persian), and South Asia (Indo-European speakers of Southern Iran). Overall, the genomic history of Iran is a multifaceted story that reflects region's position as a melting pot of diverse cultures, languages, and populations.

ABSTRACT HGP-017

Ancient birch tar as new source material for studying the human past in the Baltics

Speaker: **Kadri Irdt**
University of Tartu, Estonia

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Abstract:

For thousands of years during the Stone Age, birch tar was used as an adhesive for tool making by ancient people. Today, it can be used to shed light on the prehistory of our species. Being an alternative DNA source for those periods in which human bone material is scarce, ancient “chewing gums” can be used to determine e. g. the sex, phenotypic data or microbiome of the users of the birch tar, but also the relationships between the Stone Age communities. Besides that, these “chewing gums” provide a direct link between the people and their culture. As part of a larger project, which investigates Stone Age people from the Baltic region, we conducted a pilot study of 7 samples from South Estonia, from Kääpa and Tamula archaeological sites that are about 4000-6000 years old. For DNA extraction we used previously developed protocols of Kashuba, et al. Commun. Biol. 2019 and Jensen, et al. Nat. Comm. 2019 and shotgun sequenced on Illumina platform. Out of 7 birch tar samples, 2 had enough (~13%) of human DNA for further analysis. One of the “chewing gums” was used by a man and the other by a woman. In addition, metagenomic screening showed that microbial DNA obtained from the “chewing gums” was similar to a regular human oral microbiome. The results of the pilot study allow us to be optimistic about using birch tar samples as an alternative DNA source providing information about the origin, diet and cultural aspects of the Stone Age people of the Baltic region.

ABSTRACT HGP-018

Human mobility patterns during the Holocene

Speaker: **Dilek Koptekin**
Middle East Technical University, Turkey; University of Lausanne, Switzerland

Co-authors: Anna-Sapfo Malaspinas[1,2], Mehmet Somel[3]

[1] University of Lausanne, Switzerland
[2] Swiss Institute of Bioinformatics, Switzerland
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Abstract:

Analysing population dynamics in Southwest Asia over a span of 15,000 years using 440 ancient and present-day genomes, we recently made the following observations: First, the genetic diversity within subregions of Southwest Asia, such as Anatolia and the Levant, consistently increased during the Holocene starting from the Neolithic period, likely due to interregional gene flow. Second, the sources of gene flow shifted over time; in the first half of the Holocene, gene flow occurred mainly within Southwest Asia, while later, gene flow originated from more distant populations. Third, as mobility expanded over time, there was a noticeable trend of increasing male bias in admixture events. These findings have sparked interest in exploring whether similar shifts in mobility patterns, reflected in genetic diversity, can be observed in other regions that have undergone Neolithic Transitions. Here we present results from a similar analysis of published genomes from East Asia.

ABSTRACT HGP-019

Genetic Insights into the Demographic History of Colombia

Speaker: **Kim-Louise Krettek**
Senckenberg Centre for Human Evolution and Palaeoenvironment, Germany; University of Tübingen, Germany

Co-authors: Lilian Andrea Casas Vargas[1], Ella Reiter[2], William Usaquen[1], Jose-Vicente Rodriguez Cuenca[1], Cosimo Posth[2,3]

[1] Universidad Nacional de Colombia, Colombia
[2] University of Tübingen, Germany
[3] Max Planck Institute for Evolutionary Anthropology, Germany.

Abstract:

After human populations entered into the Americas they spread rapidly, reaching the southern tip of South America by at least 14,500 years ago. While recent archeogenomic studies have started describing the genetic history of the Andes, the Atlantic coast and the Southern Cone, a limited number of ancient genomes has been generated from northern South America, the entry point into the subcontinent. To shed light on the initial settlement of this key geographic region and on the genetic transformations of the local populations, we generated genome-wide data of 21 ancient individuals from present-day Colombia spanning the last 6,000 years. With our genomic temporal transect in a spatially confined area, we reveal marked shifts in genetic ancestry through time. The complex population history of Colombia is characterized by early connections with central American populations, as well as by differential affinities to ancient Ceramic-related groups from Venezuela and the Caribbean. Genetic comparisons between ancient and present-day indigenous Colombian populations further highlight major turnovers in Native American ancestry. A detailed investigation of the genetic sources responsible for these demographic events has the potential to uncover recent population movements across northern South America that are omitted from the historical record.

ABSTRACT HGP-020

Tracing ancestral shifts and migration patterns during the trasition from late antiquity to early middle ages - an archaeogenetic study on the Rhineland-

Speaker: **Laura Lacher**
Max Planck Institute for Evolutionary Anthropology, Germany

Co-authors: Elke Nieveler[1], Bernd Päffgen[2], Michael Schmauder[1], Joscha Gretzinger[3], Johannes Krause[3], Stephan Schiffels[3]

[1] Rheinisches Landesmuseum Bonn
[2] Ludwig Maximilians University of München, Germany
[3] Max-Planck-Institute for Evolutionary Anthropology, Germany

Abstract:

The transition from late antiquity to the early medieval period in central Europe has long been a research focus in historical and archaeological sciences. Particularly, whether the observed political and cultural changes are accompanied by demographic changes, remains elusive. Here, we study ancient DNA from multiple cemeteries in the Rhineland spanning the period from 300 to 800 AD, including the transition point at 450 AD. We analyse burials from late Roman military contexts, Bonn and Jülich, and those from local population cemeteries, especially Alt-Inden. We benefit from precise archaeological dating to correlate our genetic results and view them as a high-resolution time-series in the time span before and after 450 AD. First, we find evidence of different ancestry backgrounds between the legionary camps, suggesting that the camps were comprised of people from a similar region, but this origin was different between the two sites. Second we observe signals of ancestry shifts through time in both the legionary burials as well as the local cemeteries, which we interpret as the result of migration into the region. Last, we find haplotype sharing indicative of close familial relationships between Jülich and Alt-Inden, whereas the individuals from Bonn show no relatedness to any other site that we studied. In conclusion, our study provides a new high resolution temporal and spatial insight into the demographic patterns of the transition time between late antiquity and early middle ages in the Rhinish region.

ABSTRACT HGP-021

The crossroad of Europe. Ancient genomes from Poland tell the story of where the West meets the East

Speaker: **Martyna Molak**
University of Warsaw, Poland

Co-authors: Michał Golubiński[1], Mateusz Baca[1], Barbara Bujalska[1], Danijela Popović[1], Piotr Węgleński[1]

[1] University of Warsaw, Poland

Abstract:

Central Europe has long been a European a sort of a cauldron of human populations. The Great European Plain conferred little resistance to movements of larger groups, be it for trade, settlement or warfare, hence providing ground for intense genetic exchange. However, due to hitherto limited paleogenomic research in this region, the timing, direction and intensity of gene flow that has shaped the population of the Vistula and Oder River basins remains largely unexplored and has mostly been inferred from the modern genetic variation. Moreover, the custom of cremating the dead, spread among many cultures from this region between the Bronze Age and the Early Medieval, along with the prevalence of sandy soils accelerating bone decomposition, resulted in significant temporal and geographical patchiness of the skeletal record available for genetic analyses. Our project aims at retrieving genetic data for possibly comprehensive representation of the population of the region throughout space and time to assess the level of genetic continuity as well as the timing and direction of gene flow into and within. By the time of this abstract submission, we had collected remains of over 500 individuals dating to between the Neolithic and Modernity, including several from the subregions and periods in which non-cremated burials are a rarity. We genotyped over 120 of the individuals, and our dataset is being continuously expanded. We performed population genomic analyses based on i.a. F-statistics and IBD sharing, which allowed us to test several hypotheses based on the available archaeological context and historical sources. The data we obtained not only inform the “big picture” of the genetic history of “Poles” but also provide information to several interesting case studies such as familial relationships within the archaeocommunities, or genetic affinities of some distinctive burials. Funding: National Science Centre, Poland grant 2018/31/B/HS3/01464 „Genetic history of Poles”.

ABSTRACT HGP-022

Genetic discontinuity in a Medieval Sicilian community

Speaker: **Aurore Monnereau**
University of York, UK; University of Copenhagen; Denmark

Co-authors: Alice Ughi[1], Paola Orecchoni[2], Richard Hagan[1], Efthymia Nikita[3], Derek Hamilton[4], Alessandra Molinari[2], Martin Carver[1], Oliver Craig[1], Camilla Speller[5], Michelle Alexander[1], Nathan Wales[1]

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[4] Scottish Universities Environmental Research Centre, UK
[5] University of British Columbia, Canada

Abstract:

The medieval period was one of the pivotal moments in the demographic formation of Europe. During this time period, Sicily as a crossroad in the Mediterranean and by its geographical position as an island was coveted by different political regimes, Byzantines (Greek Christian), Muslims (Aghlabids, Fatimids), and later, Latin Christians (Normans and Swabians). These political changes might have led to cultural, social changes, and potentially population movements. Although historical resources about the activities of rulers/elites exist, the impact of regime changes on the biological heritage of the Sicilian population as well as on social and biological interactions between different communities under these circumstances remains unclear. Segesta, an archaeological site presenting two concomitant cemeteries (Christian and Muslim) serves as an ideal study case to investigate population interactions. Ancient DNA analysis was performed on 22 human remains from Segesta dating from the Norman/Swabian Period (12th- 13th CE). DNA was extracted from petrous bones, long bones, and teeth, and double-stranded libraries were sequenced using a whole-genome approach. We assessed patterns of authenticity based on DNA fragment length and deamination pattern as well as contamination estimates from Schmutzi and ANGSD. Only samples showing characteristic ancient DNA patterns, no contamination, no first-degree relationships, and at least 10,000 SNPs underwent further analyses. We applied SmartPCA, ADMIXTURE, and outgroup f3-statistics to identify genetic affinity to ancient and modern populations. The results show that the burial rites at Segesta correspond with distinct populations, with no evidence of admixture between the Muslim and Christian groups. The case study of Segesta shed light on the interaction between religious communities and demonstrates that medieval regime changes had major impacts beyond the political class, leading to significant demographic changes.

ABSTRACT HGP-023

Genetic study of ancient Egyptian human remains dating from the Predynastic Period to the early Islamic Period (ca. 4000 cal. BCE - 800 cal. CE)

Speaker: **Alexandra Mussauer**
Eurac Research - Institute for Mummy Studies, Italy; Ludwig Maximilian University Munich, Germany

Co-authors: Christina Wurst[1,2], Alice Paladin[1], Valentina Coia[1], Frank Maixner[1], Albert Zink[1]

[1] Eurac Research - Institute for Mummy Studies, Italy
[2] Johannes Gutenberg University Mainz, Germany

Abstract:

Due to high-throughput sequencing and targeted enrichment methods, ancient DNA (aDNA) analysis is emerging as a valuable tool for the investigation of ancient Egypt's demographic history. However, the recovery of aDNA from Egyptian human remains is challenging due to poor DNA preservation and a high contamination risk. Thus, so far, less than five ancient Egyptian genome-wide datasets have been published. In addition, mitochondrial genomes are almost exclusively limited to a timespan ranging from the New Kingdom to the Roman Period (1550 BCE - 395 CE) as well as to a single archaeological site (Abusir el-Meleq). To extend the pool of ancient Egyptian genome datasets, both mitochondrial and genome-wide, we report the results of a genetic study of 100 ancient Egyptian human remains. Overall, these individuals exhibit an endogenous human DNA content between 0.01% and 40.84%. Using an enrichment capture targeting the mitochondrial DNA (mtDNA), we were able to reconstruct complete mitogenomes for 25 individuals dating from the Predynastic Period to the Coptic Period (ca. 3500 cal. BCE - 650 cal. CE) and encompassing the archaeological sites of Asyut, Akhmim, Deir el-Bahari, Deir el-Medina, Thebes, the Valley of the Queens, and Gebelein. These genomes exhibit a mtDNA haplogroup diversity similar to ancient Egyptian haplogroup profiles published by Schuenemann, et al. Nat. Comm. 2017. This provides further evidence for shared maternal ancestries between western Eurasian or northern African populations and ancient Egyptians during and after the New Kingdom. In addition, we also found western Eurasian mtDNA haplogroups in individuals dated to periods prior to the New Kingdom. Furthermore, we performed a whole-genome enrichment capture on seven individuals to test these findings also on a genome-wide scale. Overall, this study provides further insights into the demographic history of ancient Egyptians considering a broader geographical context and the older periods of Egypt's past.

ABSTRACT HGP-024

Investigating population structure and patterns of natural selection in Neolithic Europeans

Speaker: **Linda Ongaro**
Trinity College Dublin, Ireland

Co-authors: Lara M. Cassidy[1], Emilia Huerta-Sanchez[1,2]

[1] Trinity College Dublin, Ireland
[2] Brown University, USA

Abstract:

The Neolithic transition was a very dynamic period in Europe, characterized by migrations of the early farmers from South West Asia into the European continent, which was predominantly inhabited by hunter-gatherers. Although this migration had a strong impact on the demography of the continent, forager groups were not completely replaced as they admixed with the newcomer groups, and their descendants harbored varying proportions of genetic ancestry. Even though the broad pattern of genetic differentiation and adaptation in large geo-chronological groups has been uncovered, the fragmentary nature of ancient DNA data has prevented the geographic fine-scale characterization of genomic structure and adaptation in single time periods. In this study, we harnessed imputation algorithms for low-coverage data to reconstruct the genomic profile of almost five hundred West Eurasian individuals from a period of time ranging from the Paleolithic to the Iron Age. To investigate the genetic structure and the patterns of natural selection of Neolithic Europeans, we combined haplotype and frequency-based methods to enable the study of fine-scale genomic characterization of Europeans in the Neolithic through time. Moreover, we characterize the impact of these migration and admixture events and focus on identifying signatures of positive natural selection in specific populations from Neolithic Europe from the British Isles. All co-authors will be acknowledged in the poster.

ABSTRACT HGP-025

The Noaidi of Giggajávri (Fi. Kitka) - Life history of a Sámi shaman found in Kuusamo, Finland

Speaker: **Sanni Peltola**
University of Helsinki, Finland

Co-authors: Ulla Moilanen[1], Miikka Voutilainen[2], Elina Salmela[1], Kerttu Majander[3], Johannes Krause[4], Laura Arppe[2], Markku Oinonen[2], Mika Sarkkinen[1], Antti Sajantila[2], Jussi-Pekka Taavitsainen[1], Päivi Onkamo[1]

[1] University of Turku, Finland
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Abstract:

In 1970, a shallow burial containing the remains of a middle-aged man was discovered in Kuusamo, North-East Finland. The burial goods included artefacts associated with Sámi cultural heritage, such as a drum hammer and bronze rings, and the individual was interpreted as a noaidi, a Sámi shaman. The burial dates to the turn of the 16th and 17th centuries, when Kuusamo was home to the Kemi Sámi, an indigenous group who spoke a now-extinct southern Sámi language. Today, the area is occupied by Finns – Finnish immigration to the area started in the 17th century and the local Sámi-speaking communities disappeared in the 19th century. The individual is the only currently known pre-modern individual from Kuusamo, and his remains have drawn interest in both researchers and the public. Here, we studied the life history of the individual using archaeogenetics and isotopes of carbon, nitrogen, oxygen and strontium. Our results show that the individual's ancestry is consistent with his presumed connection to Sámi, and he likely represents the local Kemi Sámi group. Despite the genetic similarity, we found that present-day Sámi carry more West European ancestry than our studied individual does. Therefore, it is possible that Kemi Sámi differed from the more northern Sámi, or that the present-day Sámi received West European gene flow during the last centuries. We also compared the new genetic data to contemporary Finnish-speaking inhabitants of Kuusamo, but found no evidence of extensive Sámi-related contribution in them. The isotopes clarify the individual's lifetime mobility and livelihood and indicate that he was highly mobile during his lifetime. The strontium values representing early childhood are consistent with expected values for the bedrock of Finland, but values reflecting the individual's place of residence during adolescence are highly unusual for Finland. The low values of oxygen, together with dietary modelling, may hint towards the coast of the Arctic Ocean.

ABSTRACT HGP-026

Preliminary aDNA analysis of Viking Age collective grave in the Čunkāni – Dreņģeri cemetery from Latvia

Speaker: **Alise Pokšāne**
Latvian Biomedical Research and Study Centre, Latvia

Co-authors: Jānis Ķimsis[1], Alisa Kazarina[1], Elīna Pētersone-Gordina[2], Antonija Vilcāne[2], Guntis Gerhards[2], Renāte Ranka[1]

[1] Latvian Biomedical Research and Study Centre, Latvia
[2] University of Latvia, Latvia

Abstract:

Čunkāni Dreņģeri is one of the most widely excavated and researched archaeological sites corresponding to the Viking Age in Latvia, containing more than 700 burials. The aim of the research was to obtain and analyse endogenous genomic data from a collective grave in the Čunkāni – Dreņģeri cemetery (N=6). Because of limited availability of the osteological material from the site, in this study the authentic aDNA data was obtained from six individuals (four adults and two adolescents) and compared in order to investigate their possible kinship and genetic affiliation, taking into account the contemporaneous nature of the burial. The obtained information about the mtDNA and Y chromosomal haplotypes, as well as kinship estimation analysis, currently show no genetically detectable relationship between the buried individuals, thus suggesting that they were connected by other, probably social or cultural, factors. The origin of the buried individuals will be assessed in more detail when additional genomic information is obtained from comparable inhumation burials from Čunkāni – Dreņģeri. There was only one collective grave of this size in the whole site, thus pointing to the possibility that the individuals buried in it were of different origin and/or cultural affinity than others. This study was supported by FLPP lzp-2022/1-0059.

ABSTRACT HGP-027

The Genetic Legacy of Ancient Gaul: Insights into Social Organization and Human Mobility during the Roman Empire

Speaker: Mélanie Pruvost

Université de Bordeaux, France

Co-authors: Fanny Mendisco[1], Harmony de Belvalet[1], Lou Ferrapie[1], Anais Pavin[1], Hélène Barrand-Emam[2], Valérie Bel[3], Bruno Bosc-Zanardo[4], Lola Briceno[1], Madeleine Châtelet[3], Fanny Chenal[2,3], Sophie Desenne[3,5], Yves Gleize[3], Julie Grimaud[3], Noemie Gryspert[3], Mark Guillon[3], Jérôme Hernandez[3], Sophie Oudry[3,5], Estelle Pinard[3,5], Marie Rochette[3], Isabelle Souquet Isabelle[1,3], Sandrine Thiol[3], Benjamin Thomas[1,3]

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Abstract:

Spanning three continents for over five centuries from 27 BCE to 476 CE, the Roman Empire was a vast multi-ethnic and multicultural empire. France, known as Gaul during this period, was an important province within the vast Roman Empire due to its strategic location, as it provided a link between the Mediterranean and Northern Europe. During Roman rule, Gaul flourished with a thriving economy and rich cultural life thanks to the construction of roads, aqueducts, and public works that connected different parts of the province and facilitated trade and communication, enabling unprecedented human mobility across the region. This project analyzed genome-wide data from 170 individuals from 31 archaeological sites in present-day France, spanning the entire Roman Empire period. The genetic analyses, combined with archaeological and anthropological data, revealed various degrees of cosmopolitanism, some of which were associated with specific funerary practices. Although the genetic diversity was diverse overall, the high number of individuals analyzed allowed for the identification of a subtle regional structure. The continuity with Iron Age results suggests the lasting influence of previous populations. Despite the cultural heritage of Roman seen in the region’s art, architecture, language, and society, its impact on the genome of the Gaulish population appears modest. Through dense sampling of necropolises, this study provides insights into the social organization and human mobility of ancient Gaulish society.

ABSTRACT HGP-029

The Picenes and the Genetic Landscape of Central Adriatic Italy in the Iron Age.

Speaker: **Francesco Ravasini**
Sapienza University of Rome, Italy

Co-authors: Helja Niinemäe[1], Anu Solnik[1], Chiara Delpino[2], Stefano Finocchi[3], Pierluigi Giroldini[4], Elisabetta Cilli[5], Christiana Lyn Scheib[1,6], Fulvio Cruciani[7,8], Eugenia D'Atanasio[8], Beniamino Trombetta[7]

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Abstract:

Central Italy during the Iron Age (IA, approx. X-III century BCE) was characterized by the presence of several different cultural groups thoroughly studied from an archaeological perspective. Some of these groups have also been partially examined from a genomic point of view, starting to clarify population dynamics of the Italic IA. Although many studies concerning Central Italy have been performed, we still miss a comprehensive description of the genetic pool of the ethnic groups that lived along the mid-Adriatic coast. To better understand the evolution and history of IA Italic populations, we focused our attention on the Picenes, a civilization that thrived on the Adriatic coasts of Central Italy from the IX century BCE until the Roman colonization in the III century BCE and that seems to be composed of many local groups not necessarily ancestrally related. We analyzed DNA samples from 81 ancient individuals buried in three different IA necropolises located in Central Italy, two belonging to the Picene culture (Novilara and Sirolo-Numana, VIII-VII century BCE) and one Etruscan necropolis (Colle Val D'Elsa, VIII-VI century BCE). Our analysis reveals no major differences between the Picenes and other contemporary populations like the Etruscans, indicating a common genetic origin for the Central Italian IA ethnic groups. Nevertheless, in the Picenes we detected genetic influences from the Balkans and Northern Europe. These findings suggest genetic contacts across the Adriatic Sea and point out the role of the Apennine mountains in partially acting as a geographic barrier to gene flow. Moreover, we identified individuals that show a different genetic origin but that were buried within the Picenes, suggesting the existence of a multicultural society composed of people from different parts of Europe.

ABSTRACT **HGP-030**

Echoes from the last Green Sahara: a ghost population of cattle herders unveiled from joint whole modern genome analysis of Sahelian Fulani and ancient African individuals.

Speaker: **Flavia Risi**
Sapienza University of Rome, Italy

Co-authors: Eugenia D'Atanasio[1], Francesco Ravasini[2], Francesco Montinaro[3], Mogge Hajiesmaeil[2], Biancamaria Bonucci[4], Letizia Pistacchia[1], Daniel Amoako-Sakyi[5], Maria Bonito[2], Sara Onidi[2], Ornella Semino[6], Giovanni Destro Bisol[2], Paolo Anagnostou[2], Mait Metspalu[4], Kristiina Tambets[4], Beniamino Trombetta[2], Fulvio Cruciani[2]

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Abstract:

The Sahelian Fulani are the largest nomadic pastoral ethnic group. Their origins are still largely unknown and their Eurasian genetic component is usually explained by recent admixture events with northern African groups. However, it has also been proposed that Fulani may be the descendants of ancient groups settled in the Sahara during its last Green phase (12000-5000 BP), as also suggested by Y chromosome results.We produced 23 high-coverage (30 ×) whole genome sequences from Fulani individuals from 8 Sahelian countries, plus 17 samples from other African groups and 3 Europeans as controls, for a total of 44 new whole genome sequences. These data have been compared with published whole genomes from relevant populations, for a total of 814 samples. This modern dataset has been then analyzed together with relevant published ancient individuals (for a total of > 1800 ancient and modern samples). These analyses showed that the non-sub-Saharan genetic ancestry component of Fulani cannot be only explained by recent admixture events, but it is more ancient than previously reported and probably traces its origin to the last Green Sahara. According to our results, Fulani may be the descendants of Saharan cattle herders settled in that area during the last Green Sahara. The exact ancestry composition of such ghost Saharan population(s) cannot be completely unveiled from modern genomes only, but the joint analysis with the available African ancient samples suggested a similarity between ancient Saharans and Late Neolithic Moroccans.

ABSTRACT HGP-031

The genetic history of pre-Columbian Mesoamerica

Speaker: **Xavier Roca-Rada**
The University of Adelaide, Australia

Co-authors: Lars Fehren-Schmitz[1], Kalina Kassadjikova[1], Marie-France Deguilloux[2], Fanny Mendisco[2], Marie-Hélène Pemonge[2], Yassine Souilmi[3,4], João C. Teixeira[3,5,6], Cristina Santos[7], Assumpció Malgosa[7], Antonio González-Martín[8], Linda R. Manzanilla[9], Grégory Pereira[10], Bastien Llamas[3,4,5]

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[10] Archéologie des Amériques, France

Abstract:

We present one of the first few paleogenomic attempts to disentangle the genetic history of Mesoamerica during the first and a half millennium CE. Mesoamerica is a historically and culturally defined geographic area that comprises central and south Mexico, Belize, Guatemala, El Salvador, and the border regions of Honduras, western Nicaragua, and north-western Costa Rica. This region was home to several cultures connected by commerce and farming, harbouring ancient genetic diversity that was at least partly lost during Spanish conquest and colonial rule. Mesoamerica has a rich archaeological record and Indigenous cultural diversity which have regularly been interpreted as the result of a complex demographic history that could be unravelled with ancient DNA. However, paleogenomic research in Mesoamerica remains extremely limited. Here, we analysed 25 newly sequenced ancient genome-wide datasets from five archaeological sites located in the Basin of Mexico, the Michoacán state, and the Mayan region, spanning from the Classic to the Postclassic time periods (320-1,400 CE). Preliminary results suggest a high mitochondrial DNA diversity, with A2 being the most frequent haplogroup (48%). Nuclear genetic differences between ancient and contemporary individuals suggest a geographical correlation probably explained by isolation by distance. While the ancient individuals from the Basin of Mexico and Michoacán present equivalent genetic affinities to present-day central and southern Mexicans, the ancient Mayans show a higher genetic affinity to contemporary Mayans and ancient American individuals predating the settlement of Mesoamerica, including Anzick-1. In the future, additional analyses and further sampling across Mesoamerica will discern population structure, adaptation, and detailed demographic inferences that are essential for a comprehensive understanding of Indigenous history.

ABSTRACT HGP-033

The skull of a saint? A genetic analysis of the purported skeletal remains of Bishop Henry from the Cathedral of Turku, Finland

Speaker: **Elina Salmela**
University of Turku, Finland

Co-authors: Aki Arponen[1], Sanni Peltola[2], Kerttu Majander[3], Johannes Krause[4], Jussi-Pekka Taavitsainen[1], Päivi Onkamo[1]

[1] University of Turku, Finland
[2] University of Helsinki, Finland
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Abstract:

In 1924, a human skull was found carefully hidden in a wall niche in the main cathedral of Turku, Finland. Despite its unknown provenance, some claim the skull to have belonged to Bishop Henry who - according to legend - was an English-born bishop of Uppsala, Sweden, who arrived in Finland in the 1150s to baptize the natives and got murdered by a local peasant. He has traditionally been considered a saint (St. Henry, the patron saint of now-Lutheran Finland), even though his historicity remains unclear as no historical sources mention Bishop Henry. While mobility isotope data are pending, a radiocarbon analysis has dated the skull to 1020–1190 calAD, or 1030–1250 calAD when corrected for a marine reservoir effect (Taavitsainen, et al. Mirator 2015), thus in congruence with the legend of St. Henry. Here, we have produced ancient-DNA sequence data from the skull, yielding pseudohaploid genotypes for ca. 1.1 million single-nucleotide polymorphisms (SNPs) genome-wide. Intriguingly, the individual appears genetically distinct from other individuals from the same region and era both autosomally and by his Y-chromosomal haplogroup, showing pronounced affinity to Central and Northwestern Europe. We will present results of analyses attempting to pinpoint the individual's genetic ancestry on the map. Obviously, genetic results cannot prove or disprove the historicity of Bishop Henry; instead, they may illuminate the possible origins of the skull in question and, more generally, of Catholic relics in medieval Finland.

ABSTRACT HGP-034

Ancient DNA perspective on the origins and structure of a Merovingian population in Belgium

Speaker: **Stefania Sasso**
University of Tartu, Estonia

Co-authors: Lehti Saag[1,2], Alexander Lehouck[3], Katrien Van De Vijver[4], Kristiina Tambets[1], Maarten H. D. Larmuseau[5,6], Toomas Kivisild[1,6]

[1] University of Tartu, Estonia
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Abstract:

The Merovingian period was a time of political changes in western Europe, characterized by the scarcity of historical records and the prevalence of cremation practice. The locality of Koksijde (West Flanders) represents one of the earliest inhumation sites on the coast of Flanders with 53 burials uncovered in 2017. These individuals offer a unique opportunity to investigate the Late Merovingian community. Here we report whole-genome shotgun sequence data of 31 skeletal remains from the Late Merovingian site of Koksijde along with 21 genomes from two High Medieval sites in Belgium. We find two distinct ancestries with the majority of Late Merovingian genomes clustering with ancient Anglo-Saxon and present-day Germanic-speaking populations whereas a minor subgroup sharing ancestry with the ancient Gaulish genomes from Iron Age France. Joint analyses of isotope and genetic data support a model by which the burials represent a local coastal community that had incorporated migrants from local inland populations rather than the individuals with coastal isotope signatures being derived from a geographically distant Germanic-speaking area. Our analyses of genetic kinship revealed high modularity of distant relationships among large sub-group burials standing in contrast to a smaller number of individuals with mixed ancestry and fewer or no connections to the main group.

ABSTRACT HGP-035

When cultural insight of admixture does not match the genome ancestry: the case of the Cerny culture (Middle Neolithic, Northern France)

Speaker: **Juliette Sauvage**
Museum National d’Histoire Naturelle, France; Université Paris Cité - Paris, France

Co-authors: Maël Lefeuvre[1,2], Françoise Dessarps[1,2], Marine Delvigne[1,2,3], Sophie Lafosse[1,2], Marie-Claude Marsolier[1,2,4], Aline Thomas[1,2], Céline Bon[1,2]

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Abstract:

The spread of agriculture in Europe is an emblematic episode of proto-historic migrations. The archaeological and paleogenetic records highlight the arrival during the Early Neolithic of an exogenous culture and the diffusion of populations from Anatolia. Previous studies have evidenced various amount of genetic admixtures between Neolithic farmers and the local descendants of Mesolithic hunter-gatherers during the Neolithic. In the Paris Basin (North of France), the Middle Neolithic is characterized by the Cerny culture (4700-4300 BCE) that mixes an agricultural way of life with funerary features marked by references to hunting and the wild. Furthermore, several adult males, qualified as archers because of arrowheads in their graves, practiced archery intensively during their lifetime. This contrast could suggest a late acculturation of hunter-gatherers at the origin of the Cerny culture. We therefore tested if Cerny individuals exhibited a particularly high proportion of Mesolithic hunter-gatherer genomic ancestry. We sequenced the genomes of about twenty individuals from several Cerny necropolises, and found that these Cerny individuals do not present significantly larger proportion of Mesolithic ancestry compared with other Middle Neolithic populations, indicating that the funerary ideology was not linked to high genetic admixture with descendants of hunter-gatherers. If these cultural features were however linked to a phenomenon of “Mesolithic resurgence”, or late acculturation, this took place without strong admixture. We then replaced our study Cerny individuals within the Neolithic genetic diversity of France, by comparing them with published genomes corresponding to (i) non-Cerny populations from the Paris Basin, and (ii) other Cerny populations located outside the Paris Basin. Our preliminary results tend to show that for our individuals it is the geographic rather than the cultural proximity that translates into genetic proximity.

ABSTRACT HGP-036

Preliminary genetic results about Sarmatians from the Carpathian Basin

Speaker: **Oszkár Schütz**
Institute of Hungarian Research, Hungary

Co-authors: Zoltán Maróti[1], Emil Nyerki[1], Endre Neparáczki[2], Balázs Tihanyi[2], Bence Kovács[2], Kitti Maár[2], Gergely Varga[2], Alexandra Gînguță[2], Tibor Török[2]

[1] University of Szeged, Hungary
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Abstract:

The genetic composition of the Sarmatian groups living on the Russian Steppe have been relatively well studied in previous publications, while the tribes arriving on the Great Hungarian Plain are generally understudied, and their genetic origin and relations to their neighbours are still to be investigated. To fill this gap, we present preliminary genetic results from more than a 100 Sarmatian period individuals from the Carpathian Basin. We show that some our samples map closely to the Sarmatians from the Russian Steppe, however most of them are very different from this group. In contrast to the previously observed genetic homogeneity of the early Russian Sarmatians most of our studied genomes display clear genetic affinity to the local inhabitants of the Carpathian Basin, while several individuals have significant East Asian genetic affinity, indicating possible societal connection between the Sarmatians of the Carpathian Basin and the eastern Steppe.

ABSTRACT HGP-037

Genetic research into pre-colonial Trinidad

Speaker: **Eleni Seferidou**
Max Planck Institute for Evolutionary Anthropology, Germany

Co-authors: Zara Ali[1], Ashleigh Morris[2], Kathrin Nägele[3]

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[2] The National Trust of Trinidad and Tobago, Trinidad
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Abstract:

Recent genomic research into the Caribbean region has explored, among others, the complexity of past Caribbean populations, possible settlement routes and human movement into and between the islands. Successive dispersals from the mainland to the islands have been recognised and one of these dispersals originated from northern South America. The decorated ceramics associated with this dispersal heralded the Ceramic Age of the Caribbean, tracing a northward expansion into the islands of the Lesser Antilles, via Trinidad due to its geographic location. The extensive networks of communication between the inhabitants of the Caribbean islands and the mainland are evident through multiple lines of evidence, which span throughout the pre-colonial period. This study presents the preliminary results of genomic analysis of pre-colonial populations from Trinidad, with the aim of reconstructing their genomic histories. The two sites under investigation - Manzanilla and Red House - are found on opposite sides of the island, with the former located on the eastern shore and the latter, being the seat of the Parliament of the Republic of Trinidad and Tobago, near the western shore in the capital, Port Spain. These two sites were occupied during the Ceramic Age (Manzanilla: 1650 – 550 BP, Red House: 1830 – 550 BP) and have yielded assemblages associated with both the Saladoid and Arauquinoid (Guayabitoid) cultural series. Thus, they provide a valuable opportunity to study genetic connections between their inhabitants, and among them and neighboring, contemporaneous populations.

ABSTRACT HGP-038

Genomic and isotopic evidence for a Sarmatian individual in Roman Britain

Speaker: **Marina Silva**
The Francis Crick Institute, UK

Co-authors: Thomas Booth[1], Joanna Moore[2], Kyriaki Anastasiadou[1], Don Walker[3], Alexandre Gilardet[1], Christopher Barrington[1], Monica Kelly[1], Mia Williams[1], Michael Henderson[3], Alex Smith[3], David Bowsher[3], Janet Montgomery[2], Pontus Skoglund[1]

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Abstract:

The Imperial Roman period witnessed political and societal changes, fueled by road and maritime network development associated with military campaigns, governance and trade, resulting in an intensification of human movement across Western Eurasia, including long-range mobility (Martiniano, et al. Nature Communication 2016; Antonio, et al. BioRxv 2022). One such historically attested event was the deployment of Sarmatian cavalry from the northeastern borders of the empire to its western edge in Britain by Roman Emperor Marcus Aurelius in 175 CE, in the aftermath of the Marcomannic Wars (Richmond, JRS 1945). Here we generated a ~4.12x whole-genome (MQ>30) and measured isotope ratios of carbon and nitrogen from an Early-Mid Roman individual (95% confidence interval 126-228 cal. CE), whose remains were recovered by MOLA Headland Infrastructure from a rural farmstead near Offord Cluny, in Cambridgeshire, eastern England, UK. We identified the individual as karyotypically male (XY), and found he was an ancestry outlier, who did not harbour Western European Hunter-gatherer-related ancestry (p=1.65E-10). Instead, he was genetically closest to Roman-period populations from present-day Armenia, with additional ancestry from Sarmatian-related groups. Incremental stable isotope analysis indicates that his childhood diet included high levels of C4-plants, consistent with a Caucasus or Pontic-Caspian location, and at least two moments of dietary change linked to periods of mobility within his lifetime. Our results are consistent with this individual being contemporary with the historical deployment of Sarmatian cavalry in Britain in 175 CE (Richmond 1945). The archaeological context of the Offord Cluny individual allows for several possible explanations of how he arrived in Britain but primarily highlights how long-distance migration enabled by the Empire extended to rural areas of Roman Britain.

ABSTRACT HGP-039

Ancient Soqotri genomes over 1,000 years document a small, consanguineous, and genetically homogenous population with deep connections to the Arabian Peninsula

Speaker: **Kendra Sirak**
Harvard University, USA

Co-authors: Julian Jansen van Rensburg[1], Iosif Lazaridis[2], Bowen Chen[2], David Reich[2]

[1] PaleoWest, USA
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Abstract:

The island of Soqotra, situated at the mouth of the Gulf of Aden in the northwest Indian Ocean, is home to ~60,000 people subsisting through fishing and semi-nomadic pastoralism and speaking a unique Modern South Arabian language within the Semitic language family. Most of what is known about Soqotri history derives from writings of foreign traders who provided little detail about the local population. Here, we report ancient DNA data from 39 individuals who lived between ~650-1750 CE at six locations across the island. Genomic data attest to strong connections between Soqotra and the Arabian Peninsula, especially to the Hadramawt region of coastal South Arabia. Modeling the Soqotri gene pool requires a ~55% contribution from a Natufian-like source, while models with a Neolithic Levantine-related source do not fit. This Natufian-related source is also required to model the ancestry of present-day people from the Hadramawt, while other groups living in Arabia and the Levant often are mostly better modeled with a Neolithic Levantine-related proxy. These data suggest that Natufian-like ancestry was also present in the Arabian Peninsula and that later Levantine-related ancestry may not have permeated throughout the entirety of this region. Soqotra was home to a small and consanguineous population during the Medieval Period: long ROH at the level typical of offspring for second cousins in six out of 10 individuals of sufficient coverage likely reflects cultural preference for cross-cousin marriage. A longstanding question has been whether the Soqotri segregated burial tafoni by sex. We provide genetic evidence supporting the co-burial of males and females and document both matrilineal and patrilineal relationships evident in burial practices.

ABSTRACT HGP-040

Urbanization from a demographic and population history perspective in Thessaloniki between 300 BC and 1500 AD

Speaker: **Angelos Souleles**
Democritus University of Thrace, Greece

Co-authors: Maria Korelidou[1], Asterios Aidonis[1], Elissavet Ganiatsou[1], Panagiota Bantavanou[1], Tania Protopsalti[2], Stavroula Tzevreni[2], Krino Konstantinidou[2], Stella Vasileiadou[2], Laura Winkelbach[3], Jens Blöcher[3], Yoan Diekmann[3], Joachim Burger[3], Christina Papageorgopoulou[1]

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[3] Johannes Gutenberg University of Mainz, Germany

Abstract:

omic and cultural outputs. As cities expand, there is often immigration from other regions, shaping the city’s genetic structure. The changes in population density alter the strength of genetic drift, while the influx of new residents from different regions increases the gene flow and the genetic diversity of the city. In addition, urbanization creates new environmental conditions that lead to altered selection pressures. Up to now few studies explore these processes from a population genetic perspective especially in historic period urban centers. We study these phenomena in Thessaloniki, a metropole in northern Greece founded in 315 BC that formed a bridge between the Roman West and the Byzantine East and played a central role in Roman, Byzantine, and Ottoman Empire. We generated who le genome sequenced data from 55 individuals dated from 300 BC to AD 1500. We incorporated previously published genomic data from the Aegean, the Balkans and the Mediterranean. For analyzing the genomes, we applied state of the art methods such as PCA, ADMIXTURE, f-statistics and ROH analysis, together with IBD analysis on imputed phased genotypes. Our results demonstrate that during the transition from city’s foundation to the transformation into a metropolitan center, a genetic ancestry shift towards western Europe occurred whilst the genetic diversity of the city increases. There are also people with obvious origins from far away, indicating mixing of populations with different backgrounds, due to increased migration rates. Finally, despite the increased genetic variability, we found cases with high endogamy levels. This fact combined with the existence of shared IBD segments, suggests the presence of an underlying social structure, in contrast to the multicultural character of the city.

ABSTRACT HGP-041

Analysis of genetic connections between the medieval communities of the Dniester Valley and the Carpathian Basin

Speaker: **Bea Szeifert**
Research Centre for the Humanities, Hungary

Co-authors: Balázs Gyuris[1,2], Kristóf Jakab[1], Balázs Gusztáv Mende[1], Péter Langó[1,3], Attila Türk[3,1], Vitalij Sinika[4], Dániel Gied[5], Péter Major[6], Norbert Berta[6], Anna Szécsényi-Nagy[1]

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[4] Pridnestrovian State University named after T. G. Shevchenko, Moldova
[5] Museum, Szentendre, Hungary
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Abstract:

The Dniester Valley and Carpathian Basin are geographically distant regions of East-Central Europe. The early Hungarians’ 9-10th century history however connects them, as their last settlement area was in the Dniester Valley (so-called Etelköz) on their migration route from the Urals to the Carpathian Basin. Archaeological findings of the Subbotsi horizon can be attributed to early Hungarians north of the Black Sea and also indicate links with Volga-Ural region’s medieval cultures. The analysis of the first few generations of the Hungarian conqueror population, characterized by specific archaeological material can help determine the migrating group’s complex genetic origin. Here we present a new genome-wide dataset from cemeteries representing the first few generations after the Conquest of the Carpathian Basin (10th c. AD, 53 individuals), and from burials in Etelköz (9-10th c. AD, 14 individuals). In the case of Etelköz, our aim is to differentiate the Pecheneg and early Hungarian remains based on genetic, archaeological and radiocarbon information. For genomic-level analysis, we use whole genome data of other medieval populations from the Volga-Ural region and from other Carpathian Basin’s medieval burials. The studied group from the Dniester Valley shows a mixed genetic makeup with signals towards Central-Asia and Ural, but European genetic composition is also observed. The Hungarian conqueror community is also heterogeneous, with the dominance of European genomic ancestry. Our results suggest genetic link between individuals from the two study areas. We detected several intra-site family connections at an intensively studied site (Páty, Hungary), which along with distant relatedness analyses give an insight into the composition of the conqueror population. Our study provides new important information about the population history of medieval East-Central Europe.

ABSTRACT HGP-042

Integrating Multidisciplinary Methods to Investigate the Lives of Nonadults in Early Medieval Sites from North Eastern Croatia

Speaker: **Brina Zagorc**
University of Vienna, Austria

Co-authors: Magdalena Blanz[1], Anita Rapan Papeša[2], Hrvoje Vulić[2], Mario Novak[3], Andrea Rimpf[4], Zrinka Premužić[5], Mario Carić[3], Tajana Trbojević Vukičević[6], David Reich[7,8,9], Maria Ivanova Bieg[1], Ron Pinhasi[1]

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[4] Ilok Municipal Museum, Croatia
[5] Independent researcher
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[7] Harvard University, USA
[8] Harvard Medical School, USA
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Abstract:

This paper presents a comparative study of two Late Avar sites in North Eastern Croatia, Nuštar and Šarengrad Klopare, to gain insights into the lives of the nonadult populations. We utilise an interdisciplinary approach, combining paleogenetic, palaeodietary, osteological, and paleopathological methods to provide a comprehensive understanding of the upbringing and overall health of the nonadult population. In our study, 36 nonadults and adults from Nuštar and 18 nonadults from Šarengrad Klopare were analysed for kinship and molecular sex using established ancient DNA pipelines and protocols. For stable isotope ratio analysis ($\delta^{13}C$ and $\delta^{15}N$), we analysed bone collagen from both sites using the same individuals as in the previous analyses, in addition to 10 animal bones from Nuštar as dietary references. Furthermore, to enhance our understanding of the dietary habits at the sites, we also included additional samples of adults, resulting in a total of 55 nonadults and adults from Nuštar and 86 nonadults and adults from Šarengrad Klopare. Our findings shed light on questions of kinship, molecular sex, and diet, and provide a deeper understanding of the relationships between these factors and mortality rates, disease, and preferential sex-related treatment at the mentioned sites. The comparison between the two sites enhances our understanding of the time period and area, providing valuable insights into how populations lived, how they were impacted by external factors, and how they responded to these impacts.

ABSTRACT HGP-043

Archaeogenetic analysis of burials associated with Early Slavic state of Moravia, Czechia

Speaker: **Denisa Zlámalová**
Masaryk University, Czech Republic; Max Planck Institute for Evolutionary Anthropology, Germany

Co-authors: Ilektra Schultz[1,2], Renáta Přichystalová[3], Petr Dresler[3], Guido Alberto Gnecchi-Ruscone[4], Luca Traverso[4], Jiří Macháček[3], Daniel Wegmann[1,2], Zuzana Hofmanová[3,4]

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[2] Swiss Institute of Bioinformatics, Switzerland
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[4] Max Planck Institute for Evolutionary Anthropology, Germany

Abstract:

With the development of NGS methods and increased throughput, it is now possible to study whole burial sites, thus potentially investigating in detail topics related to biological relatedness, population structure, change and mobility. In the region of East Central Europe, one of the problems that can be approached with archaeogenetic methods and can only be investigated with large sample sizes is the impact of migrations that predate the formation of the first Slavic states in the region. Traditionally accepted scientific consensus is that the populations using the Slavic languages migrated from East Europe into the rest of the continent in the 5th or 6th century AD. There is, however, an ongoing debate that questions this narrative and suggests that the arrival of Slavic languages in the region was not necessarily connected to population movement. To describe these processes in more detail, we focused on an archaeologically well-defined region that used to be the territory of an early medieval state of Moravia (Czechia) in which, according to written historical sources and material culture, the Slavic language has been used. In this region, skeletal remains also from preceding occupation are present and available for comparison to those populations. The whole-cemetery approach allowed for investigating biological relatedness patterns in the studied community. We analyze the genetic relationship of specific groups from Moravia to each other and known reference data in the wide region, including newly generated data predating the period in question, to observe potential population change that would indicate a large migratory event.

ABSTRACT HGP-044

Mixed Turkic and Mongolic ancestry reveals complex history and origin of the Tu and other Chinese populations

Speaker: **Daniel Tabin**
Harvard University, USA

Co-authors: Nick Patterson[1,2], TianChen Zeng[1], David Reich[1,2,3]

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Abstract:

Turkic and Mongolic speakers have had a long and complex history of interaction with each other and with other neighboring populations. Due in part to this complex history, there is debate about whether or not the two groups share a common linguistic origin. We provide new genetic evidence regarding these patterns by leveraging the fact that Turkic and Mongolic peoples have differential sources of both West and East Eurasian ancestry, which we show can be used to disentangle Turkic and Mongolic ancestry in admixed populations. We find variable proportions of Turkic and Mongolic associated ancestry in modern Chinese Turko-Mongolic ethnic minorities including the Salar, Bonan, Dongxiang, Daur, Mongola, and Tu. Most have ancestry from both groups with notable exceptions such as the Salar who are consistent with having no Mongolic ancestry. While Chinese connections to and interactions with the Eurasian Steppe can be seen as early as the Shang Dynasty, genetic dating of the most recent wave of admixture suggests that the modern mixture of ancestries present in this populations were formed during the heyday of the Mongol empire. A plausible scenario is that these groups were formed by Turkic and Mongolic speakers, possibly soldiers, settling and admixing with Chinese and Tibetan peoples. Many of these admixed populations would have then undergone a language shift towards the Mongolic prestige language. This scenario would be consistent with the joint genetic, linguistic, and historical evidence. Additionally, we believe our methodology of distinguishing Turkic and Mongolic ancestry should benefit any future analyses of the history of the Eurasian steppe.

ABSTRACT HGP-045

East of the wall: aDNA in the Tisza region through the first phases of the Migration Period

Speaker: **Luca Traverso**
Max Planck Institute for Evolutionary Anthropology, Germany

Co-authors: Guido Alberto Gnecchi-Ruscone[1], Zsófia Rácz[2], István Koncz[2], Levente Samu[2], Tivadar Vida[2,3], Johannes Krause[1], Zuzana Hofmanová[1,4]

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[2] Eötvös Loránd University, Hungary
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[4] Masaryk University, Czech Republic

Abstract:

Historical sources record shifts in political power in the Eastern Carpathian Basin during the first phases of the Migration Period. Indeed, they report that in those centuries a number of new groups succeeded one to the other with the expansion of the Hunnic domination first and then the emergence of the Gepid Kingdom, which, after rising between the 5th and 6th century, played a key role in the historical developments of eastern Carpathian Basin and as a major actor interacting with both the Langobard Kingdom and the Eastern Roman Empire. Some of these shifts are associated with changes in archaeological material and in settlement structure. In the context of the HistoGenes project, we investigate whether these changes were brought upon by mobility of a few elite individuals - therefore as result of cultural assimilation, or if they are associated with larger shifts affecting whole communities. To this aim, we apply an ancient DNA sampling strategy targeting whole cemeteries to fully encompass the diversity at the cemeteries and explore the degrees of genetic diversity between the individuals buried there. These were selected in a time-transect fashion from archaeologically well analyzed Sarmatian- and Gepid-associated sites, densely covering the entire time period. We analyze more than 500 individuals buried in 8 sites on the Tisza river in the Carpathian Basin, archaeologically dated to between the 3rd to the 6th century. We infer genetic connectivity within and between sites based on direct inter-individual relatedness, allowing us to provide a measure of how the connections in material culture and burial costumes are mirrored in biological relatedness. We observe overall a large genetic shift in the population across the region, likely connected to reported historical events during and after the fading of the Danube Limes at the end of the 4th century.

ABSTRACT HGP-046

The dawn of Middle Age: a comprehensive archeogenetic analysis of the late antiquity site of Forum Sempronii in Central Italy.

Speaker: **Eugenia D'Atanasio**
Institute of Molecular Biology and Pathology, Italy

Co-authors: Francesco Ravasini[1], Toni de-Dios[2], Elisabetta Cilli[3], Pietro Gobbi[4], Oscar Mei[4], Chiara Delpino[5], Christiana L. Scheib[2], Beniamino Trombetta[1]

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[2] University of Tartu, Estonia
[3] University of Bologna, Italy
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Abstract:

The 5th and 6th centuries CE were characterized by major social and demographic changes in Western Europe and, in particular, in the Italian peninsula. On one hand, the shift in the political balance towards the east from the later Imperial period onwards led to a greater genetic influx from the Near East in the city of Rome (Antonio, et al. Science 2019). On the other hand, people from central Europe, like Goths, arrived in the Italian peninsula and replaced the weak political powers to form their own kingdoms. In addition to these major political changes, the Italian population was also affected by the Justinianic plague, caused by Yersinia pestis, in the VI century. In order to understand how these events affected the Italian peninsula outside the city of Rome, we analyzed the funerary area of the Roman city of Forum Sempronii (V-VI cc. CE, Marche, Italy), as a case-study. This site was first associated with Goths and is characterized by burials that gradually become hastier, possibly suggesting a pandemic event. In this study we performed a comprehensive archaeogenetic analysis on 21 individuals buried in Forum Sempronii. The genetic ancestry of these individuals is in line with samples from the same period from the city of Rome, suggesting that the Near Eastern influx was not restricted to the capital city and possibly rejecting the hypothesis of a non-local origin for this population. Moreover, by analyzing these samples we identified traces of the presence of Yersinia pestis, possibly confirming the hypothesis of the First Pandemic affecting the people in Forum Sempronii.

ABSTRACT HGP-047

The Genetic Legacy of the Roman Imperial Rule in northern Italy

Speaker: **Orhan Efe Yavuz**
University of Tübingen, Germany

Co-authors: Ella Reiter[1], Zita Laffranchi[2], Irene Dori[3], Brunella Bruno[4], Giulia Pelucchini[4], Maria Giovanna Belcastro[5], Marco Milella[2], Cosimo Posth[1]

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Abstract:

During the Roman Imperial period, the extension of Mare Nostrum to the entire Mediterranean Sea allowed Rome to strengthen its cultural, political, and economic hegemony over the surrounding provinces. The tightened interaction with the east brought many migrants to the Empire’s capital. Supporting these historical accounts, a genomic time-transect in the city of Rome clearly documented a shift in genetic ancestry towards eastern Mediterranean populations during the Imperial period. A following study expanded on this finding by showing that the shift was not unique to Rome but also affected the central Italian region of Etruria. However, how much further north along the Italian peninsula this incoming ancestry spread remains to be addressed. Here, we generated genome-wide data of 32 individuals from six sites in northern Italy archaeologically dated to the Imperial period. Principal Component Analysis reveals that all individuals fall on an admixture cline stretching from the placement of preceding Iron Age groups towards modern-day Near Easterners. While this trend mirrors the results obtained for the city of Rome and Etruria, the proportion of eastern Mediterranean ancestry varies considerably. Most of the newly studied individuals derive three-quarters of their genetic profile from the local population and one-quarter from contemporaneous groups in the Near East. However, the latter contribution is around half of what was observed for central Italy at the same time. Compared to present-day northern Italians, we could then model an additional 20% gene flow from northern European ancestries, possibly influenced by migrations into Italy during the Early Middle Ages. To conclude, while northern European ancestries left a similar genetic imprint into present-day populations from central and northern Italy, the demographic shift connected with the Roman Empire was diluted moving northward, but its genetic legacy still survives until today.

ABSTRACT HGP-048

Paleo-Pathological Studies at Pachacamac, Peru: Challenges and Preliminary Results

Speaker: **Nathalie Suarez Gonzalez**
Université Libre de Bruxelles, Belgium

Co-authors: Gontran Sonet[1], Peter Eeckhout[2]

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Abstract:

Ancient DNA (aDNA) analysis can be a useful tool for sex determination, general mitochondrial lineage (haplogroup) and disease diagnosis in human remains. However, non-endogenous DNA contamination of archaeological material is a recurrent problematic, since excavation, handling and storage usually don't fit with the precautions recommended for ancient DNA analysis. Here, we present preliminary aDNA results from several human individuals recovered by the Ychsma Project (ULB) from the monumental archaeological site of Pachacamac, Peru, a corpus dating from 500 to 1400 AD where a high proportion of diseases is suspected. Our objectives are to complete the demographic information and to characterize the health status of the population buried in this pilgrimage site dedicated to the eponymous healing god. Our preliminary results show that, despite an important modern human-DNA contamination, a strict selection of DNA reads based on short sizes and deamination damage patterns that are typical for ancient DNA, allow us to determine the genetic sex of 70% of the individuals. The challenging detection of ancient DNA form human pathogens requires additional precautions. By multiplying negatives and environmental controls and data analysis strategies, our preliminary results suggest that our approach is appropriate for the detection of paleopathological conditions in this major archaeological corpus.

ABSTRACT KSSP-001

Genome-wide analysis of a collective grave from Mentesh Tepe provides insight into the population structure of early neolithic population in the South Caucasus

Speaker: **Perle Guarino-Vignon**
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Co-authors: Maël Lefeuvre[1], Amélie Chimènes[1], Aurore Monnereau[2], Farhad Guliyev[3], Laure Pecqueur[1,4], Bertille Lyonnet[5], Céline Bon[1]

[1] Muséum National d'Histoire Naturelle, France
[2] University of York, UK
[3] Institut National de Recherches Archéologiques Préventives, France
[4] The National Academy of Sciences of the Republic of Azerbaijan, Azerbaijan
[5] Proche-Orient – Caucase langues, archéologie, cultures, France

Abstract:

Despite the localisation of southern Caucasus at the outskirt of the Fertile Crescent, the Neolithisation process started there only at the very beginning of the 6th millennium with the Shomu-Shulaveri culture. To better understand the role of human migrations into the diffusion of Neolithic in the southern Caucasus, we present here genome-wide data for three new individuals from Mentesh Tepe in Azerbaijan, dating back to the beginnings of the Shomu-Shulaveri culture. We evidence that two juveniles buried embracing each other were brothers. We show that Mentesh Tepe Neolithic population is the product of a recent gene-flow between Anatolian farmer-related population, and Caucasus/Iranian population, with an impulse from a Mesopotamian-related group, demonstrating that recent population admixture was at the core of the development of agriculture in the South-Caucasus. These results are in agreement with the archaeological record that suggests technical transfers with neighboring regions such as Southern Anatolia, Pre-Halafian and Halafian culture of northern Mesopotamia and Zagros. By comparing Bronze Age individuals from South Caucasus with Neolithic individuals from the same region, including Mentesh Tepe, we also evidence that new gene flows between Pontic Steppe populations and Mentesh Tepe-related groups contributed to the make-up of the Late Bronze Age and modern Caucasian populations. Our results show that the high cultural diversity during the Neolithic period in the South Caucasus deserves a detailed genetic analysis.

ABSTRACT KSSP-002

Archaeogenomic research of Kamenice, a prehistoric Albanian tumulus (1600-500 BCE)

Speaker: **Xiaowen Jia**
Max Planck Institute for Evolutionary Anthropology, Germany; Max Planck Harvard Research Center for the Archaeoscience of the Ancient Mediterranean (MHAAM), Germany; Ludwig Maximilian University of Munich, Germany

Co-authors: Eirini Skourtanioti[1,2], Lorenc Bejko[3], Maria Grazia Amore[3], Skender Aliu[3], Iris Pojani[3], Harald Ringbauer[1,2], Johannes Krause[1,2], Philipp Wolfgang Stockhammer[1,2,4]

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Abstract:

Situated in southeastern Albania at the interface of the Aegean and the Adriatic, the Tumulus of Kamenice was used for inhumations continuously from 1600 to 500 BCE. We generated genome-wide SNP data for ca. 200 individuals from Kamenice that span the full time transect, providing the unique and first possibility for insights into, on one hand, genetic continuities and changes of Late Bronze Age and Iron Age Albania, on the other hand, biological relatedness and demography of a single large tumulus. We identified a genetically homogeneous population throughout the respective time in contrast to all societal transformations in the wider region. Our results indicate that populations from Albania, the northern Aegean and Dalmatia form a joint cluster, which differs from the southern Aegean regarding the Neolithic Caucasus-like gene flow, but also from further inland Balkan in terms of hunter-gatherer ancestry. Moreover, we found evidence for a patrilineal society, within which all the males' Y chromosomes belong to two distinct sub-groups of R1b1a1b (M269). We identified the biological relatedness up to 10th degree both inside of the tumulus and with neighboring sites using IBD analysis. The amount of intra-site relatedness raised after 750 BCE. We also detected a signature of an effective population size decrease around 750 BCE using HapROH, which coincides with the prevalence of Y chromosome lineage R1b1a1b1b3 and a new way of grave construction. Overall, all the ancient DNA evidence support a local population bottleneck event.

ABSTRACT KSSP-003

Genetic population structure of the Xiongnu Empire at imperial and local scales

Speaker: **Juhyeon Lee**
Seoul National University, Republic of Korea

Co-authors: Bryan K. Miller[1,2], Jamsranjav Bayarsaikhan[1,3], Erik Johannesson[4], Alicia Ventresca Miller[1,2], Christina Warinner[5,6], Choongwon Jeong[7]

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Abstract:

The Xiongnu established the first nomadic imperial power, controlling the Eastern Eurasian steppe from ca. 200 BCE to 100 CE. Recent archaeogenetic studies identified extreme levels of genetic diversity across the empire, corroborating historical records of the Xiongnu Empire being multiethnic. However, it has remained unknown how this diversity was structured at the local community level or by sociopolitical status. To address this, we investigated aristocratic and local elite cemeteries at the western frontier of the empire. Analyzing genome-wide data from 18 individuals, we show that genetic diversity within these communities was comparable to the empire as a whole, and that high diversity was also observed within extended families. Genetic heterogeneity was highest among the lowest status individuals, implying diverse origins, while higher status individuals harbored less genetic diversity, suggesting that elite status and power was concentrated within specific subsets of the broader Xiongnu population.

ABSTRACT KSSP-004

Palaeogenomics of Stone Age Hunter-Gatherers at Lake Baikal

Speaker: **Ruairidh Macleod**
University of Cambridge, UK

Co-authors: Matthew Collins[1], Andrzej Weber[2], Eske Willerslev[1,3]

[1] University of Cambridge, UK
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Abstract:

The Lake Baikal region represents an archaeological focal point of mid-Holocene hunter-gatherer populations, from the period broadly spanning the Neolithic and Bronze Age cultures (8000-4000 BP). Extensive archaeological investigation of a number of hunter-gatherer cemeteries has been undertaken by the Baikal Archaeology Project, providing a wealth of new insights about spatiotemporal variation in the region's mid-Holocene adaptive strategies. Here, we report on the results of ongoing palaeogenomic analyses undertaken in collaboration with the Baikal Archaeology Project, with a focus on regional and local-scale population dynamics among these groups, aided by rich archaeological contextual information. Through shotgun ancient genome data for >100 individuals, we describe how biological relatedness and identity-by-state analyses reveal intra- and inter-population dynamics, in particular focusing on implications for hunter-gatherer lifeways and connectedness through space and time. Specific focus will be placed on a case study of the Shamanka II cemetery, which was intensively used in the Early Neolithic, and revisited in the Early Bronze Age to inter members of a kinship group showing a very rare instance of unusually high perimortem lethal violence.

ABSTRACT KSSP-005

Demographic change and social interactions during the Early Islamic period in Northern Iberia: the case of the Plaza del Castillo Necropolis

Speaker: **Iñigo Olalde**
University of the Basque Country, Spain

Co-authors: Vanessa Villalba-Mouco[1,2,3], Patxuka de-Miguel-Ibáñez[4,5,6], Roberto Risch[7], Concepción de la Rúa[8], Montserrat Hervella[8], Raffaela Bianco[1,2], Nadin Rohland[9], Swapan Mallick[9,10], Michael McCormick[2,11], Philipp W. Stockhammer[1,2,12], Carles Lalueza-Fox[13,14], Johannes Krause[1], David Reich[9,10,15]

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[15] Broad Institute of MIT and Harvard, USA

Abstract:

711 CE marks the onset of the Islamic Period in the Iberian Peninsula. This period has been intensively studied using archaeological and scrappy historical evidence, which from the perspective of funerary archaeology manifests itself in the widespread adoption of Muslim burial customs (right lateral decubitus bodies with the head facing East and absence of grave goods). Whether these acculturation processes went hand in hand with major demographic changes and how incoming groups and local populations interacted at the early stages of the Islamic conquest are controversial issues. We generated human genome-wide data using in-solution enrichment from 79 individuals from the Plaza del Castillo (Pamplona, northern Iberia) burial ground, one of the earliest Islamic cemeteries in Iberia dated to the first half of the 8th century CE. Despite the homogeneity of the Muslim burial rite, we identify a mix of ancestry profiles, highlighting local ancestry as well as Middle Eastern and North African ones. The preliminary results obtained from the reconstructed pedigrees at the site suggest that this cemetery represents the first few generations of intermarriage between predominantly North African/Near Eastern men and local women, as well as between local men and local women, shedding new light on the social processes at play at the beginning of Islamic rule in Northern Iberia.

ABSTRACT KSSP-007

Two sides of kinship structure in Bronze Age burial mounds of the North Caucasian Bronze Age

Speaker: **Sabine Reinhold**
German Archaeological Institute, Germany

Co-authors: Ayshin Ghalichi[1], Andrey Belinskiy[2], Svend Hansen[3], Wolfgang Haak[1]

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[3] German Archaeological Institute, Germany

Abstract:

Biological relatedness is closely interlinked with social kinship organisation and the exchange of mating partners. In social sciences, it is discussed as a crucial mechanism which shapes and maintains social relations in and between groups. Large burial mounds (kurgans), which are common form of funerary architecture in Bronze Age West Eurasia are highly and widely visible symbols in ancestral landscapes. Containing the graves of sometimes several dozens of individuals, they were understood as manifestation of genealogies and consequently as reflecting genetic or social kin relations over time. However, these ideas have never been systematically tested. Improved archaeogenetic wet and dry lab methods now provide the opportunity to study many individuals from the same site, which in turn allow intra-site analyses of biological relatedness and inferences about kinship structures and social organisation. Here, we present new genomic data from burial mounds the North Caucasus, which reveal a much more complex structure of biological relatedness or the lack thereof than anticipated previously. These kurgans can be viewed as micro-transects through time in which the degree of genetic connectedness seems to correspond to the distinct genetic ancestry profiles found in this region at the time: Steppe-, and Caucasus-related ancestry. By comparing a number of case studies, we discuss examples of closely and remotely biologically related individuals, inbreeding and reduced effective population sizes, which provides the first insights into the social organisation of the cultural groups using these monuments. In particular, the lack of biological relatedness with certain temporal horizons is challenging the interpretation of the data as genealogies and calls for new models to understand the social structure of the different genetic groups.

ABSTRACT METP-001

Assessing antimicrobial peptides, resistance genes, and functional gene clusters in ancient microbial DNA

Speaker: **Jasmin Frangenberg**
Leibniz Institute for Natural Product Research and Infection Biology - Hans Knöll Institute, Germany

Co-authors: James A. Fellows Yates[1,2], Anan Ibrahim[1], Louisa Perelo[3], Moritz E. Beber[4], Christina Warinner[1,2], Pierre Stallforth[1]

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[2] Max Planck Institute for Evolutionary Anthropology, Germany
[3] University of Tübingen, Germany
[4] Unseen Bio ApS, Denmark

Abstract:

Genome-mining of ancient DNA (aDNA) is a powerful strategy to discover new bioactive natural products and to study their evolution and structural diversity. Paleofeces is rich in microbial aDNA, which allows to gain insight into the composition of the ancient human microbiome and unravels an untapped diversity of functional genes. Microbial sequences are mined for different types of functional genes using bioinformatic annotation tools. However, the diversity in computational platforms, accessibility, scalability, and heterogeneous reporting of results hampers the effectiveness and usability of such analysis tools. Here, we present nf-core/funcscan (Frangenberg, et al. Zenodo 2023), a Nextflow pipeline for the screening of functional and biosynthetic genes from assembled contigs. We demonstrate this functionality on a dataset of aDNA from paleofeces, taking the additional challenge of short aDNA sequence fragments into account. We especially investigate antibiotic resistance determinants which are critically affecting the global antibiotic resistance crisis and have also been found in the past microbial pangenome (D'Costa, et al. Nature 2011). nf-core/funcscan currently provides 12 tools to simultaneously predict antimicrobial peptides, antibiotic resistance genes, and biosynthetic gene clusters. It is simple to install, executable across multiple platforms from personal laptops to HPCs, highly reproducible via the use of software containers, and offers both graphical and command-line interfaces. The pipeline further provides summaries of the outputs of all featured bioinformatic tools, which facilitates the rapid evaluation and visualization of the results by the user. Thus, nf-core/funcscan allows researchers of different scientific fields and backgrounds to efficiently screen genomic data for functional genes.

ABSTRACT METP-002

µBiocodicology: studying ancient animal skin microbiomes through the analysis of historical parchment documents

Speaker: **Guillermo Rangel-Pineros**
University of Copenhagen, Denmark

Co-authors: Luisa Fernanda Sacristán-Carrillo[1], Matthew Teasdale[2], Sarah Fiddyment[2], Laura Cristina Viñas-Caron[3], Alejandro Reyes[1], Matthew Collins[2]

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[2] University of Cambridge, UK
[3] University of Copenhagen, Denmark

Abstract:

Parchment is a writing support made from the hides of livestock such as cows, sheep and goats, and represents an invaluable source of historical and cultural information from different societies throughout history. In addition to the document features commonly inspected by codicologists, the analysis of biomolecules present within the parchment provides further historical details about the documents. Among these, the study of microbial DNA could provide a snapshot of the skin microbiome of the animals used as the source for the parchment and offer the opportunity to recover the genomes of ancient skin pathogens affecting livestock. Here, we have shotgun-sequenced the DNA extracted from a set of parchment documents and employed kmer-based taxonomic profilers to identify the different bacterial taxa present in each sample. Draft genomes were recovered for bacterial species detected at high coverage depths, and the corresponding sequence reads were subjected to standard aDNA a uthentication methods. Our preliminary results demonstrate that the sampling method applied to the parchment has a profound influence on the range of microbial taxa that are detected with the applied taxonomic profiling methods. In addition, we recovered the genomes of some animal skin pathogens, such as Erysipelothrix rhusiopathiae and Vagococcus fluvialis. The results presented here further showcase the potential that parchment microbiome analysis has for uncovering ancient animal skin pathogens and studying the effects of historical events on livestock microbiome.

ABSTRACT METP-003

Benchmarking tools for the detection, reconstruction and phylogenetic analysis of ancient viral genomes

Speaker: **Yuejiao Huang**
University of Copenhagen, Denmark

Co-authors: Jonas Niemann[1], Hannes Schroeder[1], Martin Sikora[1]

[1] University of Copenhagen, Denmark

Abstract:

With the advent of high-throughput sequencing, ancient DNA (aDNA) analysis has opened up new avenues for investigating the emergence and spread of viral agents of disease. However, the reconstruction and analysis of ancient pathogen genomes are often challenging, due to high fragmentation, low pathogen DNA content, and the presence of contamination within ancient samples. Although many software tools have been developed for studying pathogen evolution, they are not generally optimized for ancient DNA. We conducted a comprehensive benchmarking study to evaluate the performance of various workflows on simulated aDNA metagenomic datasets. To do so, we first simulated aDNA reads by incorporating the detected composition of three ancient samples, which encompassed the reads of target viral species and other representative species, such as human, bacteria, etc. We then evaluated different metagenomic classifiers (Kraken2, KrakenUniq and MALT) based on their computational consumption and classification accuracy in terms of false positive, false negative, and true positive hits. In addition, we tested the performance of different alignment tools (BWA-aln, Bowtie2, minimap2, and vg) and the effect of using different reference genomes (linear and variation graph), and variant callers (GATK, bcftools, and ANGSD SNPs calling) on the sensitivity and precision of alignment and variant calling. Lastly, we compared the performance of four phylogenetic placement tools, namely pathPhyder, UShER, App-SpaM, and EPA-ng, in correctly assigning the query sequence to the corresponding node of a tree. Based on these experiments, we present best practices for improving the detection accuracy of ancient viral pathogens and optimising the genome recovery from ancient metagenomic datasets.

ABSTRACT METP-004

Leveraging High-Throughput Metagenomic Screening for the Identification of Human Parasitic Protozoa

Speaker: **Megan Michel**
Max Planck Institute for Evolutionary Anthropology, Germany

Co-authors: Alexander Herbig[1], Johannes Krause[1,2]

[1] Max Planck Institute for Evolutionary Anthropology, Germany
[2] Max Planck-Harvard Research Center for the Archaeoscience of the Ancient Mediterranean, Germany

Abstract:

Parasitic protozoa, including the agents of Chagas disease, leishmaniasis, malaria, and trypanosomiasis, contribute significantly to the burden of infectious disease in modern human populations. Recent methodological advancements have made it possible to retrieve genome-wide data from a variety of human bacterial and viral pathogens; however, significant challenges remain regarding the genomic characterization of parasitic protozoa from ancient humans. While demographic and burial patterns provide clues for identifying epidemic disease in the archaeological record, many protozoan infections are chronic, making it difficult to pinpoint individuals, regions, and/or time periods likely to be impacted by specific disease agents. Furthermore, as many parasites exhibit complex life cycles with infective stages distributed across multiple tissues, it is unclear which skeletal elements to select when targeting specific pathogenic species. Finally, compared to viruses and bacteria,parasitic protozoa have larger genomes characterized by frequent rearrangements and repetitive elements, increasing the likelihood of false-positive species identifications. To combat these challenges, we present a high-throughput metagenomic screening approach targeting parasitic protozoa of interest. Using the Heuristic Operations for Pathogen Screening (HOPS) pipeline (Hübler, et al. Genome Biol. 2019), we screened 11,430 previously produced shotgun-sequenced ancient DNA datasets against a custom database including both target species and taxa that may generate false-positive identifications in ancient datasets. Our expanded sample size spans a large geographic and temporal range and includes a variety of skeletal elements, making it possible to evaluate patterns of parasite DNA preservation across contexts. Piloting approaches to identify ancient protozoan infections constitutes an important first step in exploring the evolutionary history and historical relevance of these underexplored pathogenic taxa.

ABSTRACT METP-005

Parasites lost: Parasite detection in ancient and modern metagenomic datasets

Speaker: **Jonas Niemann**
University of Copenhagen, Denmark

Co-authors: Liam T. Lanigan[1], Arve Lee Willingham Grijalba[2], Martin Sikora[1], Hannes Schroeder[1]

[1] University of Copenhagen, Denmark
[2] Institut Pasteur, France

Abstract:

Parasites represent a major disease burden for human populations. The detection of parasites in archaeological remains can shed light on the health status of past human populations and the prevalence of human parasites in the past. Recent advances in ancient genomics have enabled the identification of parasite DNA in archaeological remains, such as coprolites, mummies, and latrine sediments. However, the detection of parasites using high-throughput sequencing is challenging due to the incompleteness of reference databases and the presence of contamination in published reference genomes. These can result in false negative and false positive assignments, respectively. To address this issue, we decontaminated over 600 endoparasite and eukaryotic pathogen reference genomes and used a metagenomic screening pipeline for species-level identification of parasites in ancient samples. We tested the workflow using the original and decontaminated databases against published and unpublished ancient and modern metagenomic datasets and found that the removal of contaminant DNA significantly reduces the rate of false positive identifications. Our study highlights the issues related to contaminated reference genomes in ancient metagenomics and presents a bioinformatic pipeline that enables the reliable detection of parasites in ancient metagenomic datasets.

ABSTRACT METP-006

Optimization of host and pathogen DNA recovery from archived tuberculosis wet tissue specimens

Speaker: **Teresa Zeibig**
Max Planck Institute for Evolutionary Anthropology, Germany

Co-authors: Jan Schinköthe[1], Kirsten I. Bos[2]

[1] Leipzig University, Germany
[2] Max Planck Institute for Evolutionary Anthropology, Germany

Abstract:

Tuberculosis (TB) is the primary cause of worldwide mortality by a single bacterial pathogen. Lungs are commonly affected, though other organ systems are also susceptible. After infection, well-structured lesions called granulomas develop as part of an orchestrated immune response that aims to contain and eliminate Mycobacteria. Granulomas can be harvested during necropsy of deceased animals for diagnostic purposes and are often featured in teaching collections of veterinary colleges. While morphological, macroscopic, and histological assessments can diagnose the disease and the involved pathogen, they do not provide a strain-level identification and cannot inform on distinct genetic features. To increase diagnostic resolution, we tested the feasibility of DNA extraction methods in 15 mammal specimens from the late 19th to mid-20th centuries with the goal of recovering M. tuberculosis complex DNA. We used 15 specimens, of which 14 were confirmed TB infections in accordance with macroscopic, histologic, histochemical, and immunohistologic evaluation. We show that it is possible to extract host-derived DNA from granulomas of historic animal wet specimens utilizing a chemical and mechanical-based lysis method. Through an analysis of metagenomic data we evaluate the applicability of our methods and demonstrate greatest success in pathogen DNA retrieval for tissues that show acid-fast Mycobacteria during histological assessment.

ABSTRACT METP-007

The skeletal proteome: mapping proteome variation between cortical and trabecular bone

Speaker: **Ragnheiður Diljá Ásmundsdóttir**
University of Copenhagen, Denmark

Co-authors: Jakob Hansen[1,2], Gaudry Troché[1], Maria Saña Segui[2], Frido Welker[1]

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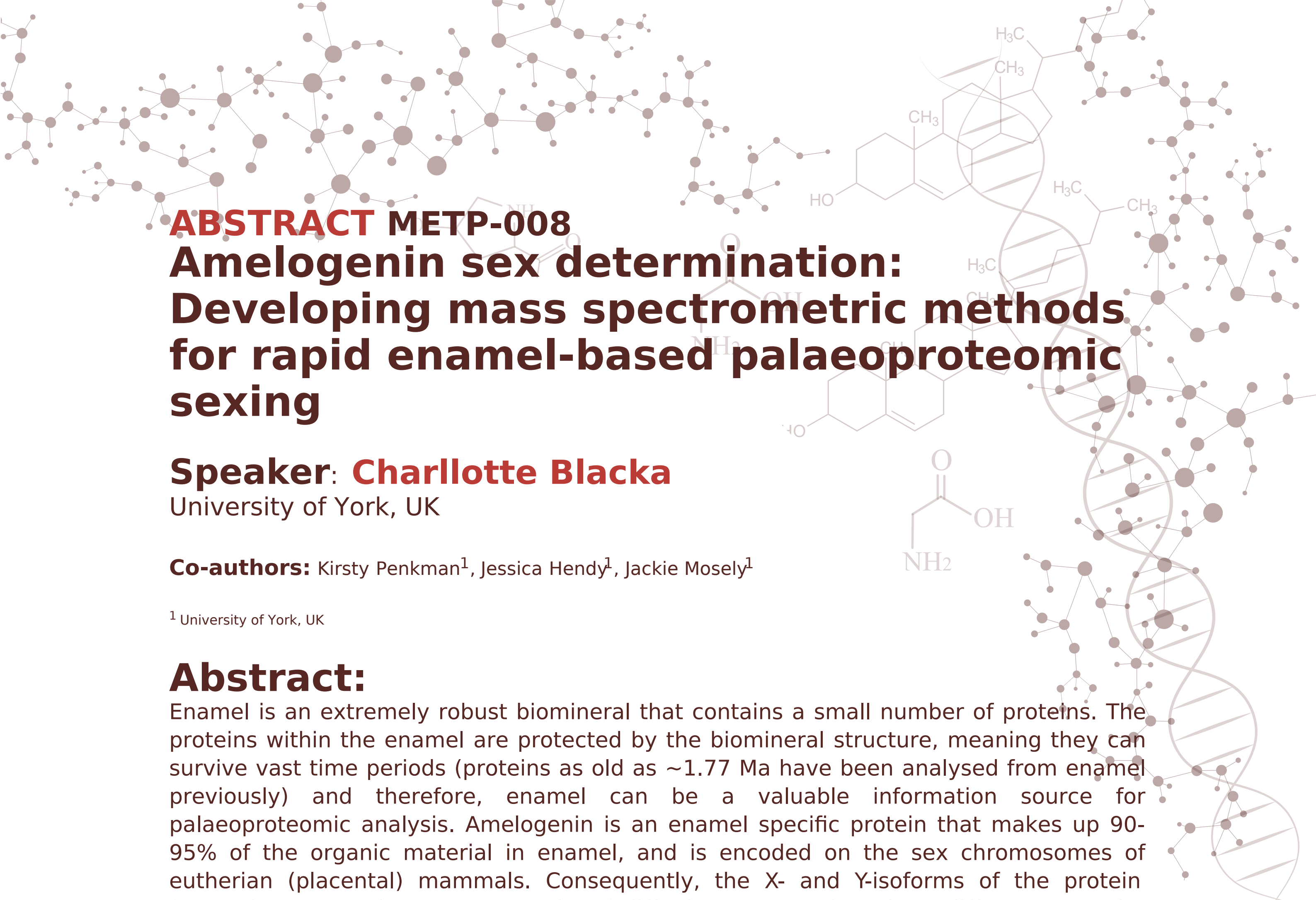
Abstract:

The field of palaeoproteomics, the analysis of ancient proteins, is fast growing, however, sampling strategies of archaeological material for protein extraction have not been extensively studied before, especially in connection with the biological processes that form the skeleton. The bony tissues of the skeleton are formed through two ossification processes, endochondral and intramembranous ossification. Additionally, bones are composed of two types of bones, cortical and trabecular, which have differences in function and in structure. Moreover, trabecular bone is metabolically more active, with much higher turnover rate per year than what is observed in cortical bone. If and how the proteome composition varies between cortical and trabecular bone is largely unknown. Here we explore the proteomic composition variation within cortical and trabecular bone from six herbivore ribs from La Draga, an Early Holocene site in Spain, using liquid chromatography tandem mass spectrometry (LC-MS/MS). The cortical and trabecular bone proteomes vary in terms of composition, e.g. different protein groups identified, and size, e.g. the number of peptides and proteins identified. Furthermore, our analysis allows comparison of rates of protein degradation between cortical and trabecular bone. These results presented here give unique insight into the skeletal biology of archaeological remains as well as aid in optimising sampling strategies to get the most information from highly precious specimens.



ABSTRACT METP-008

Amelogenin sex determination: Developing mass spectrometric methods for rapid enamel-based palaeoproteomic sexing

Speaker: **Charllotte Blacka**
University of York, UK

Co-authors: Kirsty Penkman[1], Jessica Hendy[1], Jackie Mosely[1]

[1] University of York, UK

Abstract:

Enamel is an extremely robust biomineral that contains a small number of proteins. The proteins within the enamel are protected by the biomineral structure, meaning they can survive vast time periods (proteins as old as ~1.77 Ma have been analysed from enamel previously) and therefore, enamel can be a valuable information source for palaeoproteomic analysis. Amelogenin is an enamel specific protein that makes up 90-95% of the organic material in enamel, and is encoded on the sex chromosomes of eutherian (placental) mammals. Consequently, the X- and Y-isoforms of the protein (termed AMELX and AMELY, respectively) differ in many species. These differences can be exploited to give a palaeoproteomic sex determination method, which possesses some advantages over aDNA sex determination methods, such as the ability to be applied to geochronologically older samples, in which the aDNA has degraded.Currently, the most widely used method to analyse amelogenin is a liquid chromatography tandem mass spectrometry method developed by in 2017; although useful, this method is hindered by long analytical run times (~60 minutes) and therefore high costs. More recently, a low-cost amelogenin analysis method, utilising flow injection analysis and quadrupole ion trap mass spectrometry, that also has a much higher sample throughput (run times of ~1 minute). While these methods are promising, there are still further analytical modifications that can be considered. Emerging analytical technology has been explored to optimise rapid amelogenin analysis, and preliminary comparisons of different mass spectrometers and preparation methods provide interesting results to assess the applicability of techniques to palaeoproteomic sex determination. Here, the results from these preliminary experiments are presented.

ABSTRACT METP-010

Going de novo? The suitability of de novo sequencing for ancient proteins

Speaker: **Yun Chiang**
University of Copenhagen, Denmark

Co-authors: Matthew Collins[1,2]

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Abstract:

Mass spectrometry-based approaches have been widely used in archaeology to elucidate phylogeny, palaeodiet, ancient disease and the diagenetic processes of ancient proteins. However, despite their wide applications, a large fraction of tandem mass spectra (MS2) consistently fail to be sequenced, because they are outside a significant false discovery rate (FDR). This ‘dark proteome’ seems to be predominant in archaeological experiments where MS2 matching is constantly low (Warinner, et al. Chem. Rev. 2022). One could only speculate about the sources of these undetected queries; they could be uncanonical variants, damaged peptides containing unknown post-translational modifications (PTMs), non-tryptic contaminants from the environment or complex cross-linkers plus glycoproteins derived from interactions between proteins, carbohydrates and lipids. Conventional database search engines, for example MaxQuant and Mascot, may not be suitable for these analytical challenges. The reasons are threefold: firstly, ancient proteins are complex mixtures that may not be fully captured in even curated databases; secondly, using an entire Swiss-Prot database for matching may result in long processing time, increased false positives and a bias towards model organisms; lastly, ancient proteins could be extensively modified, and these complex PTMs may not be detected, as search engines generally assign one modification to a single amino acid residue. These issues of the dark proteome, the search for comprehensive databases and the detection of PTMs are shared in modern metaproteomics, cancer research, the design of therapeutic antibodies and ageing studies (Beslic, et al. Brief Bioinform. 2023). One common strategy is leveraging deep learning models such as transformers to shed light on all acquired MS2 spectra. We have explored de no sequencing and ground truthed it using a combination of open-source algorithms. The suitability of this de novo-centric approach will be discussed in my talk.

ABSTRACT METP-011

Proteomic characterisation of the impact of cooking and burial on experimental food crusts and ceramics

Speaker: **Miranda Evans**
University of Cambridge, UK

Co-authors: Manon Bondetti[1], Jasmine Lundy[1], Richard Hagan[1], Łukasz Kowalski[2], Jarosław Wilczyński[3], Penny Bickle[1], Kamil Adamczak[2], Oliver E. Craig[1], Harry K. Robson[1], Matthew Collins[4,5], Jessica Hendy[1]

[1] University of York, UK
[2] Nicolaus Copernicus University, Poland
[2] Polish Academy of Sciences, Poland
[4] University of Cambridge, UK
[5] University of Copenhagen,Denmark.

Abstract:

Proteomic analysis of ceramics and their residues is becoming a popular method for interpreting ancient diet and culinary practice. While proteomics has the advantage of providing taxonomically and tissue specific evidence - revealing ingredients and even food preparation practices in the past - it is becoming apparent that the identification of proteins and peptides present in ancient samples are not perfectly representative of fresh ingredients, and we remain ignorant of the ways in which behavioural and taphonomic actions impact the presence, abundance and nature of proteins identified in ancient samples. In this study, we characterised and scrutinised proteomic results from experimental ceramics, foodcrusts and cheesemaking residues, to explore the impact of food preparation practices and burial on their composition. The results from these modern analogues have implications on the way in which proteomic results derived from ancient foodcrusts and ceramics are interpreted.

ABSTRACT METP-012

Fast and quantitative mass spectrometric assay for biological sex determination from dental enamel.

Speaker: **Claire Koenig**
University of Copenhagen, Denmark

Co-authors: Ana Martinez-Val[1], Enrico Cappellini[1], Jesper V. Olsen[1]

[1] University of Copenhagen, Denmark

Abstract:

Biological sex is one of the key feature archaeologists need to characterize human remains. Yet, it is not always possible to morphologically retrieve this information due to degradation, partial recovery of remains or pre-pubertal individuals. Biological sex can be assessed through a dental enamel specific protein: amelogenin - and its two sex-specific isoforms (AMELX and AMELY). Traditionally, biological sex identification was carried out by analyzing amelogenin-derived peptides by liquid chromatography tandem mass spectrometry (LC-MS/MS) using extensive chromatographic separation (i.e., >=1 hour) with a semi-stochastic acquisition mode (DDA). Peptides were identified by matching resulting MS/MS spectra against a protein sequence database with manual interpretation of the search outputs. Whilst the detection of AMELY-specific peptides confirmed a male identification, the absence of AMELY-specific peptides cannot unambiguously confirm female identification. This legacy workflow was time consuming, expensive, and required proteomics expertise, making it inaccessible for most archaeological studies. Here, we present an alternative approach to streamline the proteomics-based sex identification of archeological remains with higher throughput and confidence. Enamel proteins were extracted using acid etching and peptides were directly loaded on Evotips for subsequent LC-MS/MS analysis using an Evosep One chromatographic system with a pre-defined 200SPD (Sample Per Day) gradient. Using a targeted approach (PRM), a pre-defined set of peptides were measured on an Exploris 480 mass spectrometer, providing both increased throughput and sensitivity. Downstream automatized data analysis enabled MS2-based quantification of the selected peptides. As a result, true female samples were assigned through a combination of two factors: absence of AMELY-specific peptides and high AMELX-specific peptides abundance, making large-scale sexing accessible.

ABSTRACT METP-013

A monk or a nun? The story of a partial dental element from an ascetic in-chain buried in a Christian Women’s cemetery in Jerusalem area during Byzantine time

Speaker: **Paula Kotli**
Weizmann Institute of Science, Israel

Co-authors: Yossi Nagar[1], Zubair 'Adawi[1], Kfir Arbiv[1], David Morgenstern[2], Elisabetta Boaretto[2]

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[2] Weizmann Institute of Science, Israel

Abstract:

We present here a straightforward and rapid peptidomics-based methodology for identifying sex, antiquity, and site-specific post-translational modifications (PTMs) from ancient remains, using small sample quantities and minimal damage to the remains. We applied this method to a partial human dental element from a Byzantine ascetic individual found in Israel, for which aDNA or osteological analysis was not feasible. Our methodology is based on Stewart, et al. RSC Adv. 2016 and Stewart, et al. Proc. Natl. Acad. Sci. 2017. Using peptidomics we analyzed native peptides of amelogenin (AMELs) –X and –Y isoforms, comparing the archaeological sample to extracts from modern teeth. Based on peptide spectral (PSMs) counting of AmelX and AmelY we show the sample belongs to a female. PTM specific analysis of the data shows increasing oxidation and deamidation of the remains compared to current samples, with >10 fold oxidation and >1.4 deamidation in the archaeological sample. The pepitdes extracted from the archaeological samples are also much shorter (10.4 vs 15.7 AA long compared to the current samples, most probably due to hydrolysis. Taken together, we demonstrate our ability to provide multi-attribute information using a rapid and simple analytical method, causing the minimal degree of damage to a precious sample. We are sure this method will be usable for similarly scarce and precious samples, including those who suffered from adverse conditions. Reference: Nagano, et al. J. Dent. Res. 2009

ABSTRACT METP-014

Potential of ancient proteins analysis of sheep and goats’ bones to shed light on past human economy during the Italian Bronze Age

Speaker: **Marlisa Mazzola**
University of Bologna, Italy

Co-authors: Claudio Cavazzuti[1], Elisabetta Cilli[1], Antonio Curci[1], Jacopo De Grossi Mazzorin[2], Beatrice Demarchi[3], Anna Depalmas[4], Elena Maini[5], Claudia Minniti[2], Marco Pacciarelli[6], Giulia Recchia[5], Andrea Cardarelli[5]

[1] University of Bologna, Italy
[2] University of Salento, Italy
[3] University of Turin, Italy
[4] University of Sassari, Italy
[5] Sapienza University of Rome, Italy
[6] University Federico II of Naples, Italy

Abstract:

Discriminating between the remains of morphologically similar species, most famously sheep and goats, has always been a great challenge for archaeozoologists. However, this distinction is paramount for understanding different aspects of past economies, such as the exploitation of primary and secondary products. The HERDS project (“Animal Husbandry and its Economic Role in the Development of Central Mediterranean Protohistoric Societies”, progetto Miur - PRIN 2020 prot. 2020EP24PP, 2022-25) investigates the socio-economic transformations that took place in Italy during the Bronze Age, through the study of sheep and goat remains, integrating classical archaeozoology methods and biomolecular techniques such as the analysis of aDNA, isotopes and ancient proteins. These different methodologies aim to shed light on aspects such as the breeding techniques, the selection of ovicaprid breeds and the subsistence and mobility of human communities that managed the flocks. The ZooMS (Zooarchaeology by Mass Spectrometry) method exploits the differences in the amino acid sequence of type I collagen between distinct species, reflected in shifts in the mass of peptides, which can be used as “biomarkers”. This difference can be detected by MALDI-TOF mass spectrometry, thus obtaining the fingerprint of the taxon of interest. This method is particularly useful in this study, as it allows us to distinguish between goat and sheep (Buckley, et al. J. Archaeol. Sci. 2010) using a small amount of material and at low cost. The data obtained by ZooMS on a selection of morphologically identified sheep/goats will allow us, in addition to the reconstruction of the subsistence strategies, to test the different morphological criteria for the distinction of ovicaprids and therefore the development of a protocol as reliable as possible for their identification using a traditional approach.

ABSTRACT METP-015

Assessment of intra-crystalline enamel amino acid and proteins to understand enamel closed system model

Speaker: **Fazeelah Munir**
University of York, UK

Co-authors: Adam Dowle[1], Marc Dickinson[1], Samantha Presslee[1], Jane Thomas-Oates[1], Kirsty Penkmana[1]

[1] University of York, UK

Abstract:

Major tooth enamel proteins are trapped within intracrystalline sites. This makes enamel a potentially closed system in which proteins could be preserved for long periods of time, as protein degradation products such as amino acids and peptides remain within the closed system. Studying closed system peptides is important to help us understand the interaction between proteins and tooth biominerals which in turn will help us in tracking preserved peptides for the purpose of sex identification or taxa identification over time. To study this in detail, bleaching experiments on three modern taxa (Equus caballus, Bos taurus, Capra hircus) were conducted. Bleaching is thought to remove those intercrystalline amino acids and peptides not trapped within the enamel crystalline structure. These samples were analysed by two different techniques; reversed-phase high performance liquid chromatography (RP-HPLC) which can be used to calculate amino acid concentrations and compositions, racemisation, and peptide bond hydrolysis, and liquid chromatography with tandem mass spectrometry (LC-MS/MS), which yields peptide sequence information. Upon bleaching, it was noted that there was differential preservation of peptides from the same protein across the three taxa demonstrating different protein structures of the same protein among taxa. Peptides recovered from enamel proteins from these taxa will potentially enable us to identify those peptides involved in mineral interaction - they would be expected to be preserved by those interactions. Such studies will also enable us to determine whether species and sex specific peptides will be preserved into deep time.

ABSTRACT METP-016

Comparison of magnetic beads (SP3), glass beads (SP4) and suspension trapping (S-trap) approaches for proteomics studies of ancient human dental calculus.

Speaker: **Fallen K.Y. Teoh**
University of Turin, Italy

Co-authors: Federica Dal Bello[1], Rosa Boano[1], Beatrice Demarchi[1]

[1] University of Turin, Italy

Abstract:

Dental calculus, also called dental tartar, is the hard calcified bacterial plaque commonly found on ancient human adult teeth. It has received much attention in biomolecular archaeology during the last decade, because of its potential for yielding well-preserved biomolecules. It allows researchers to access important information not only on food consumption in the past, but also on other activities that may result in the incorporation of particles in dental plaque, and on oral health and potential diseases affecting the individual. In paleoproteomics, sample preparation is a key step affecting the quality of the data recovered, therefore testing novel methodologies is paramount. We compare the well-established single pot, solid phase-enhanced sample preparation (SP3) and newly described solvent-precipitation SP3 (SP4) and suspension trapping (S-trap) approaches, in order to evaluate their protein trapping/enrichment efficiency on mediaeval dental calculus samples from Alba, Italy. SP3 employs carboxylate-modified magnetic beads in the presence of an organic solvent to promote protein binding to the beads, requiring extensive washing to eliminate contaminants while SP4 employs glass beads and captures the protein aggregates by centrifugation, providing a minimalistic, low-cost protein clean up approach. S-trap utilises a three-dimensional porous derivatized silica as a filter medium and traps particulate protein suspensions with the subsequent depletion of interfering substances and in-filter digestion. All the proteins recovered from the experiments were enzymatically digested with trypsin and analysed by nanoHPLC-MS/MS using an Orbitrap Fusion Tribrid Mass Spectrometer. Overall, the protein recovery yield for all three of the methodologies tested was good, with SP3 outperforming SP4 and S-trap; SP4 and S-trap have comparable performance in recovering proteins from dental calculus.

ABSTRACT METP-017

Ancient metagenomics and synchrotron microtomography of ancient dental calculus - an interdisciplinary approach to studying health and diet in archaeological populations

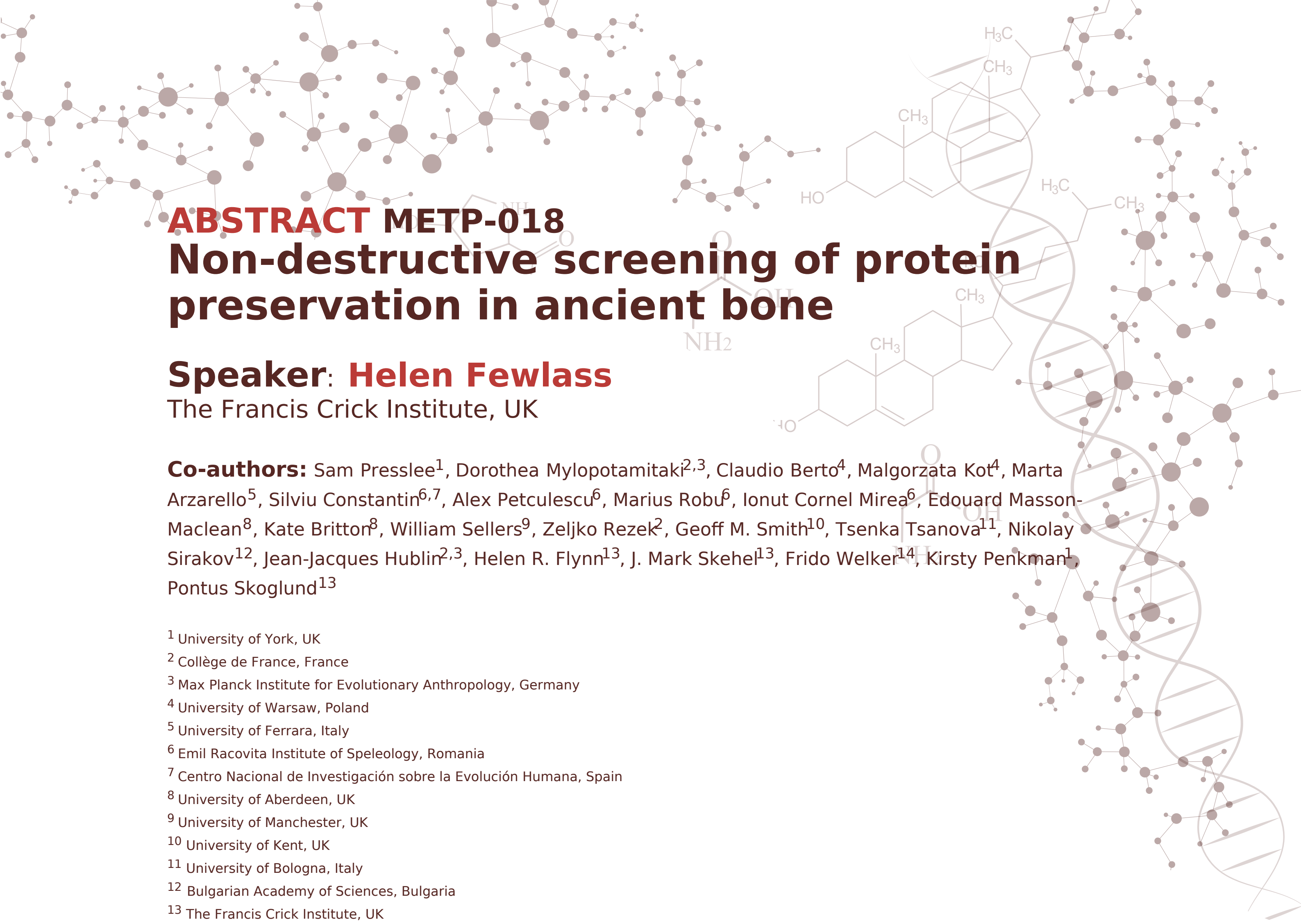
Speaker: **Sierra Blunt**
University of Bordeaux, France

Co-authors: E. Andrew Bennett[1], Elsa Garot[2], Yves Gleize[2], Adeline Le Cabec[2], Mélanie Pruvost[2], Eric Pubert[2], Alexander Rack[3], Nicolas Vanderesse[2], Clément Zanolli[2]

[1] Chinese Academy of Sciences, China
[2] Université de Bordeaux, France
[3] European Synchrotron Radiation Facility, France

Abstract:

In the past decade, dental calculus has been established as a robust material in the study of archaeological populations. However, the sampling methods used in both biomolecular and microscopic analyses involve destroying the calculus to varying degrees. Some exploration is still required to improve sampling strategy, limit contamination, and ensure specimen preservation. Dissolution-based microscopy and histological thin-sections can isolate dietary microfossils like starch grains, fibers, and phytoliths. These permanently alter the calculus and can damage other fragile inclusions. On the other hand, novel approaches such as synchrotron radiation micro-computed tomography allow for the non-invasive observation of the internal structure of calculus, in addition to dietary inclusions like seeds and other plant remains. When combined with biomolecular methods, dietary proteins, health and disease-associated microbes, and even population dynamics can be detected. Here, we apply an experimental and interdisciplinary approach to the study of an abnormally large calculus deposit from one individual from the Clarensac cemetery near present-day Nîmes, France (8th-10th centuries AD). Using metagenomics, metaproteomics, functional analysis of the oral microbiome, and synchrotron imaging, we investigate microbial composition, host-microbiome interactions, calculus structure, taphonomic alterations, and dietary inclusions. These preliminary results provide valuable information concerning health, diet, and lifestyle in Medieval Southern France. Finally, by comparing invasive and non-invasive methods, we hope to highlight the importance in preserving specimens through 3D scanning prior to destructive analyses. This is not only useful in preserving calculus for future research by ensuring traceability prior to destructive studies, but also for selecting intact regions for sampling, decreasing contamination risk and ensuring higher-quality results from biomolecular analyses.



ABSTRACT METP-018

Non-destructive screening of protein preservation in ancient bone

Speaker: **Helen Fewlass**
The Francis Crick Institute, UK

Co-authors: Sam Presslee[1], Dorothea Mylopotamitaki[2,3], Claudio Berto[4], Malgorzata Kot[4], Marta Arzarello[5], Silviu Constantin[6,7], Alex Petculescu[6], Marius Robu[6], Ionut Cornel Mirea[6], Edouard Masson-Maclean[8], Kate Britton[8], William Sellers[9], Zeljko Rezek[2], Geoff M. Smith[10], Tsenka Tsanova[11], Nikolay Sirakov[12], Jean-Jacques Hublin[2,3], Helen R. Flynn[13], J. Mark Skehel[13], Frido Welker[14], Kirsty Penkman[1], Pontus Skoglund[13]

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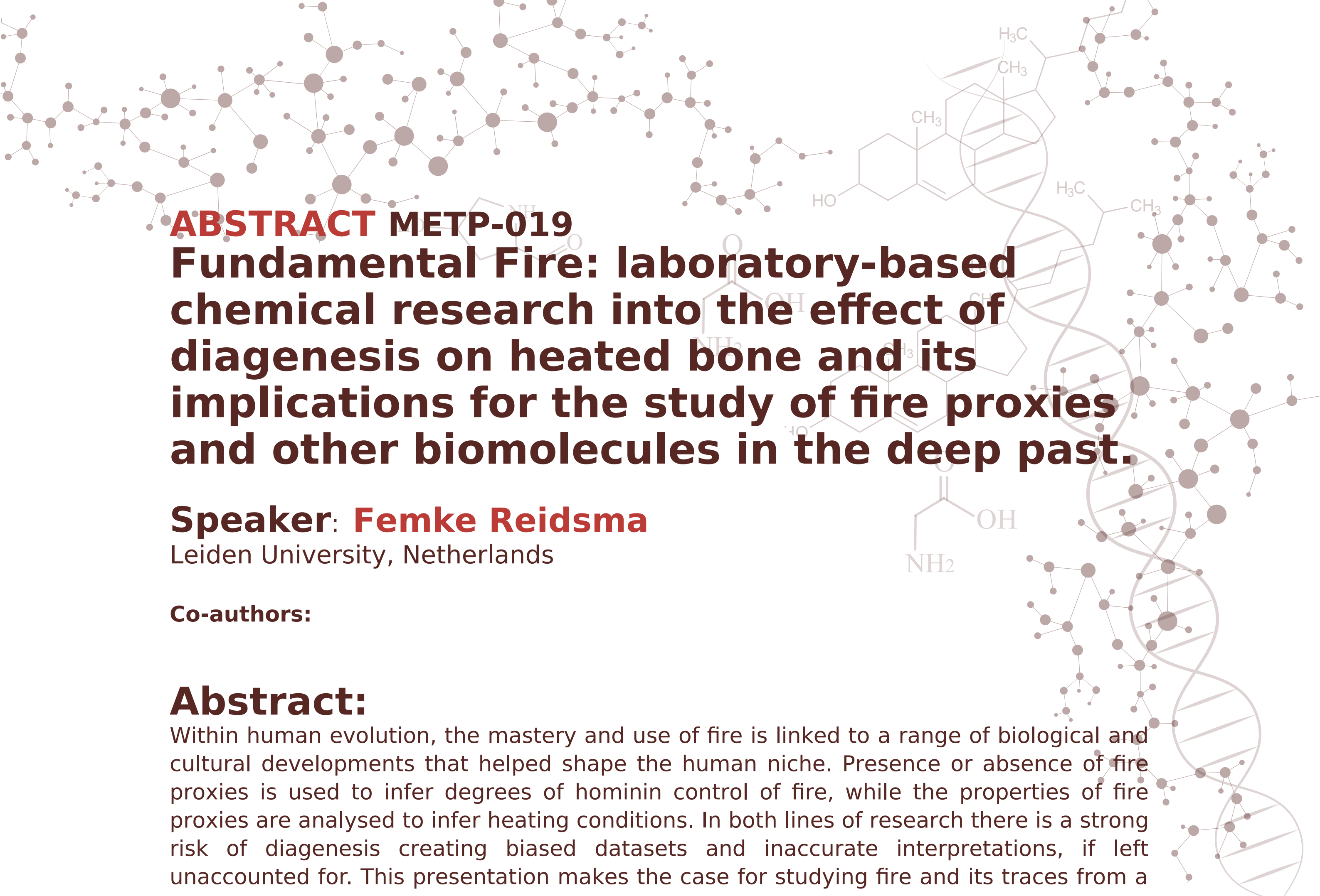
[2] Collège de France, France
[3] Max Planck Institute for Evolutionary Anthropology, Germany
[4] University of Warsaw, Poland
[5] University of Ferrara, Italy
[6] Emil Racovita Institute of Speleology, Romania
[7] Centro Nacional de Investigación sobre la Evolución Humana, Spain
[8] University of Aberdeen, UK
[9] University of Manchester, UK
[10] University of Kent, UK
[11] University of Bologna, Italy
[12] Bulgarian Academy of Sciences, Bulgaria
[13] The Francis Crick Institute, UK
[14] University of Copenhagen, Denmark

Abstract:

Protein preserved in ancient bone provides us with phylogenetic, chronological and behavioural insights that are crucial for understanding human prehistory. Yet given the destructive nature of these analyses it is beneficial to determine the preservation of each fossil bone prior to analysis in order to limit destructive sampling where chances of successfully retrieving data are low. A range of methods are used to assess organic preservation in ancient skeletal material prior to sampling for aDNA, proteomic, isotopic or 14C dating (e.g. Kontopoulis, et al. PLoS One 2020; Presslee, et al. J. Prot. 2021), but these methods generally require destructive sampling of small amounts of material (several milligrams) and exportation to a lab. Recently, near infra red (NIR) spectroscopy has been shown to be a useful method or assessing bulk collagen content of bone prior to extraction for isotopic or 14C analysis (Sponheimer, et al. Sci. Rep. 2019). NIR pre-screening is fast, the instruments are transportable and, crucially, scanning is completely non-destructive. In this study, we analysed an extensive set of bones and teeth from different sites (modern to >1 Ma) using NIR, chiral amino acid analysis, fourier transform infrared spectroscopy (FTIR) and liquid chromatography tandem mass spectrometry (LC-MS/MS) to test the potential of NIR as a pre-screening method for bones prior to palaeoproteomic analysis, covering the full range of protein preservation. Here, we compare the accuracy of the screening methods and NIR prediction models for LC-MS/MS. The ultimate aim of the study is to ensure responsible sampling of precious skeletal material.



ABSTRACT METP-019

Fundamental Fire: laboratory-based chemical research into the effect of diagenesis on heated bone and its implications for the study of fire proxies and other biomolecules in the deep past.

Speaker: **Femke Reidsma**
Leiden University, Netherlands

Co-authors:

Abstract:

Within human evolution, the mastery and use of fire is linked to a range of biological and cultural developments that helped shape the human niche. Presence or absence of fire proxies is used to infer degrees of hominin control of fire, while the properties of fire proxies are analysed to infer heating conditions. In both lines of research there is a strong risk of diagenesis creating biased datasets and inaccurate interpretations, if left unaccounted for. This presentation makes the case for studying fire and its traces from a chemical perspective; understanding the chemical properties of the fire proxies that enter the archaeological record, as well as the chemical changes they endure after burial. Results are presented of extensive laboratory-based experimental research into the effect of pH on the physical and chemical properties of heated bone (Reidsma, et al. Sci. Rep. 2022). Experiments included bone samples created under different heating conditions (20-900 °C; charred vs. combusted), and incubation in three pH solutions (pH 3, 7, 12). Samples were analysed using different analytical techniques (TGA, XRF, XRD, FTIR, py-GCMS) and results compared to reference data on unexposed heated bone. Diagenetic changes were visible at all scales of analysis, including in the molecular signature and crystallinity of the heated bones. This has direct implications for the preservation of heated bone, as well as for the reliability of the chemical techniques used to reconstruct past heating conditions. To mitigate this, a toolkit and best-practice approach is also be presented. Finally, the controlled nature of the experiments makes the toolkit and reference data relevant for heated bone from any time period and context, as well as for our understanding of the effect of diagenesis on certain other isolated biomolecules.

ABSTRACT METP-020

Best practices for Neanderthal segment detection in time-series data using tree-sequence-based ancestry tracking

Speaker: **Alba Refoyo Martinez**
University of Copenhagen, Denmark

Co-authors: Martin Petr[1], Fernando Racimo[1]

[1] University of Copenhagen, Denmark

Abstract:

The study of the regions in human genomes highly likely inherited from Neanderthal can be very informative for identifying loci affected by positive selection (Marciniak, et al. Nature Reviews Genetics 2017). Recent studies have also investigated large regions depleted of neanderthal ancestry, likely from negative selection against Neanderthal-like alleles (Vernot, et al. Science 2016). Here, we present a set of best practices for Neanderthal segment detection in large imputed ancient datasets, which allows us to understand better the effect of introgressed variation from archaic humans in the human gene pool across time and space. We will introduce a new functionality in the R package slendr to trace and record simulated introgressed alleles through time and use that information to benchmark an existing method, IBDmix, to detect archaic tracts in time-series data. Finally, we investigated the archaic proportions using ancient genomes spanning the past 40,000 years.

ABSTRACT METP-021

New methods to detect archaic introgression in early modern human genomes with low-coverage data

Speaker: **Jiaqi Yang**
Max Planck Institute for Evolutionary Anthropology, Germany

Co-authors: Benjamin Peter[1]

[1] Max Planck Institute for Evolutionary Anthropology, Germany

Abstract:

As a result of the gene flow from Neandertals and Denisovans, 2-3% of non-Africans' genomes can be traced back to Neandertals. In addition, Denisovan ancestry is present in East Asians and Americans (at low levels) and Oceanians (at higher levels). This Denisovan ancestry is only distantly related to the sole sequenced Denisovan, making detection in modern human genomes hard. Identifying genomic regions with these archaic ancestries in ancient DNA data remains even more difficult because most methods either require high-quality, phased data or require Neandertal and Denisovan reference genomes that are representative of introgressing populations. Here, we present two approaches for detecting archaic ancestry from low-to-intermediate coverage ancient DNA with and without using Neandertal or Denisovan data. The first method is an extension of a previously described hidden Markov model (Skov, et al. PLoS Genetics 2018) to genotype likelihoods. We utilize an unadmixed outgroup to enrich for only variants that are private to the introgressing archaic lineage, and use genotype likelihoods to incorporate the uncertainty of genotypes due to low coverage, degraded ancient DNA or contamination. In simulations, we find that the extended model works for ancient DNA samples with as low as 5~7X coverage, and we then test the model on published early modern genomes. The second approach is based on a reference-based method (Peter bioRxiv 2020), where we find that combining Neandertal and Denisovan ancestry into a single panel is an effective strategy to detect introgression from populations that are highly divergent from any reference population, if they are but fall within the variation of sampled Neanderthal or Denisovan individuals. Taken together, our new approaches allow us to study introgression without perfect sequencing or complete reference data, as is common when studying early modern humans.

ABSTRACT METP-022

The Limits of Ancient DNA Analysis in Resolving Recent Human Genetic History

Speaker: **Matthew Williams**
Pennsylvania State University, USA

Co-authors: Pavel Flegontov[1], Christian Huber[2]

[1] University of Ostrava, Czech Republic
[2] Pennsylvania State University, USA

Abstract:

Since the mid-2000s, paleogenomics has made remarkable progress in uncovering the genetic history of prehistoric human populations through the analysis of ancient DNA (aDNA) via an array of statistical tools such as ADMIXTURE, principal component analysis (PCA), and a suite of methods based on f-statistics (e.g. qpWave, and qpAdm). Over the last decade, published ancient human samples have steadily shifted toward the more recent past whereby aDNA is increasingly used to address archaeological and historical-guided questions surrounding the relationships amongst human groups, many of which may be separated by short periods of isolation and descend from a complex history of migration and population structure. The extent to which commonly used methods in aDNA, such qpWave/qpAdm and their underlying f-statistics, are suited to resolving recent complex human history remains under-explored. To address this we simulated a range of demographic models of varying complexity, each constructed to assess relationships between specific parameters of human demography, such as population divergence and complex admixture events, and the performance of aDNA methods for inferring the true admixture history. Our results indicate that under demographic models that do not violate the assumptions of qpAdm, both f-statistics and qpAdm perform most optimally by the time levels of genetic differentiation amongst groups reach that observed in West Eurasian Paleolithic and Neolithic populations as measured by pairwise FST. As the levels of population differentiation decrease, we observe a gradual decline in statistical performance such that under divergence approximating the median levels of differentiation observed in Bronze Age West Eurasian populations it becomes rare to uniquely identify the true admixing source populations. Our research serves as a crucial reference point for assessing the performance of commonly utilized methods studying recently-diverged complex admixture histories.

ABSTRACT METP-023

Caution! Contents were hot: experiments exploring the suitability of novel high-temperature lipid biomarkers detected in Mediterranean neolithic pottery

Speaker: **Adrià Breu Barcons**
Koç University, Turkey

Co-authors: Ayla Türkekul-Bıyık[1], Cafer Çakal[2], Mehmet Fırat İlker[1], Rana Özbal[3]

[1] Boğazici University, Turkey
[2] Hacettepe University, Turkey
[3] Koç University, Turkey

Abstract:

The study of ancient fats trapped inside pottery has demonstrated exciting potential to understand the role ceramic vessels played amongst societies which invented or started using this type of container for the first time. Researchers have frequently studied the effects of vessel exposure to fire in order to better understand the origins and uses of pottery in different regions and times. This is because the effects of protracted heating (i.e >100ºC) to lipid residues can be used to identify cooking activities and help better understand the purpose of the multiple vessel shapes appearing in the repertoires of the earliest pottery productions. Advancing the understanding of the molecular species formed under these conditions is therefore key to understand pottery use and, ultimately, the role this widespread artefact had in human societies throughout the world. Based on three unreported groups of lipid compounds detected as pottery residues from the earliest farming societies in the Mediterranean, this talk will present the results of archaeological analyses and heating experiments exploring the conditions leading to their formation, their suitability and limitations as high-temperature biomarkers, and their potential to affect current interpretations on how pottery might have been used. These are: - The ketonic decarboxylation of saturated fatty acids and dicarboxylic acids yielding very long chain fatty acids with a ketonic group. - The cyclisation of monounsaturated fatty acids yielding saturated fatty acids with five-membered rings, ω -(o-alkylcyclopentyl)alkanoic acids. - The elimination reactions affecting long chained alcohols yielding even chained alkenes. By presenting the characteristics of the above-mentioned compounds, our results will facilitate their detection in further studies and explore their potential in case studies from the Mediterranean Neolithic.

ABSTRACT METP-024

Increasing the sensitivity of cereal detection in pottery using LC-Q-Orbitrap MS

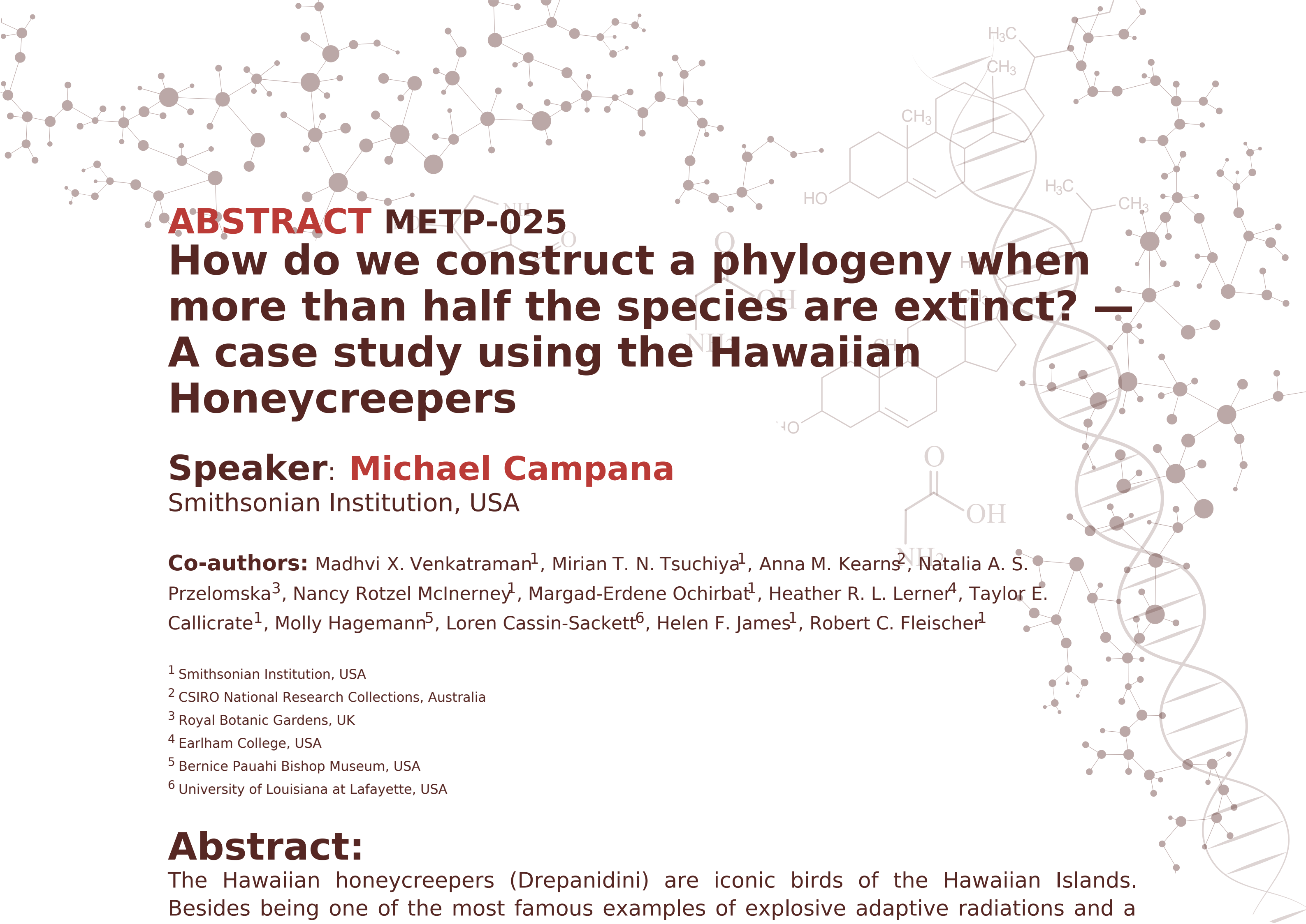
Speaker: **Jonica Ella Doliente**
University of York, UK

Co-authors: Swen Langer[1], Alexandre Lucquin[1], Miriam Cubas[2], Andre Colonese[3], Oliver Craig[1], Kirsty Penkman[1]

[1] University of York, UK
[2] University of Alcalá, Spain
[3] Universitat Autònoma de Barcelona, Spain

Abstract:

Alkyresorcinols (ARs) are cereal-specific biomarkers characterised by a nonpolar odd-numbered alkyl chain attached to a polar resorcinol ring. Recently, they have been recovered from potsherds dating from the Neolithic and Early Bronze Age demonstrating their potential for investigating prehistoric pottery use. Their detection in archaeological contexts is valuable as it can help determine the spread of cereal exploitation by prehistoric communities. Due to ARs' inherently low content in cereals, their detection becomes difficult resulting in an obvious lack of cereal presence in analysed Neolithic ceramics. The current gas chromatography-mass spectrometry (GC-MS)-based methods used for AR analysis have limitations including long sample preparation and analysis times, and insufficient sensitivity. Meanwhile, liquid chromatography (LC)-MS-based methods offer superior resolving capabilities, high sensitivity and selectivity, minimal sample preparation (no sample derivatisation required), and fast scan speed. Here we report the development, validation, and application of a LC-MS method for the detection and identification of low-concentration ARs in modern cereal grains and archaeological pottery. The method comprises a purification step and used an ultra-performance liquid chromatography (UPLC) separation system connected to an orbitrap mass analyser. The achieved LOD was found to be 250- and 10-times lower than the values obtained from GC-MS and GC-Q-TOF-MS. The developed UPLC-Q-Orbitrap MS method was then applied in the analysis of purified Must Farm and Swifterbant total lipid extracts (TLEs), and the results indicated that emmer grain was the main source of ARs extracted from Must Farm pots. Unfortunately, no ARs were detected in Swifterbant TLEs. Overall, the described method offers a highly sensitive approach and robust alternative to GC-MS for the detection and identification of AR homologues in archaeological pottery.



ABSTRACT METP-025

How do we construct a phylogeny when more than half the species are extinct? — A case study using the Hawaiian Honeycreepers

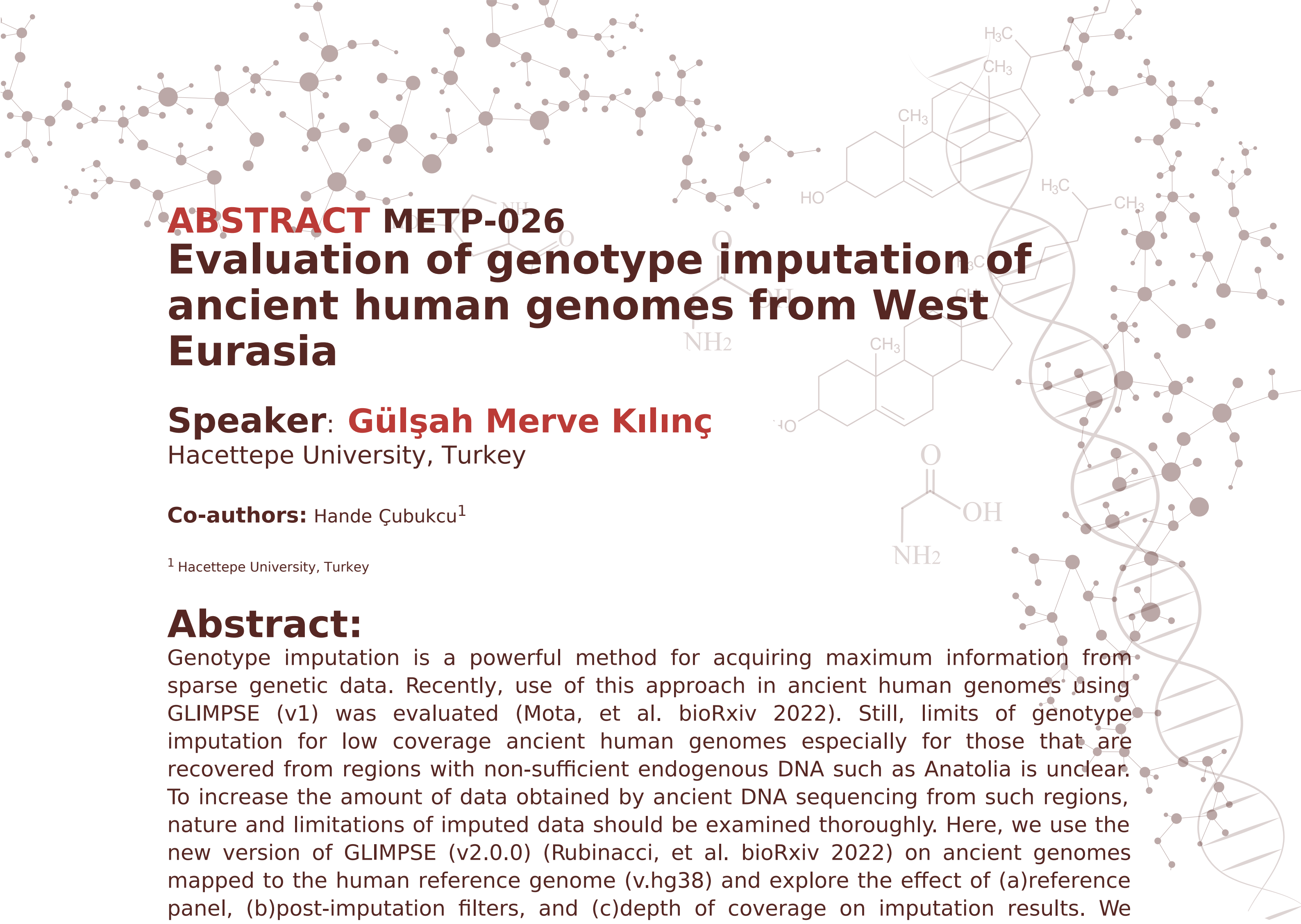
Speaker: **Michael Campana**
Smithsonian Institution, USA

Co-authors: Madhvi X. Venkatraman[1], Mirian T. N. Tsuchiya[1], Anna M. Kearns[2], Natalia A. S. Przelomska[3], Nancy Rotzel McInerney[1], Margad-Erdene Ochirbat[1], Heather R. L. Lerner[4], Taylor E. Callicrate[1], Molly Hagemann[5], Loren Cassin-Sackett[6], Helen F. James[1], Robert C. Fleischer[1]

[1] Smithsonian Institution, USA
[2] CSIRO National Research Collections, Australia
[3] Royal Botanic Gardens, UK
[4] Earlham College, USA
[5] Bernice Pauahi Bishop Museum, USA
[6] University of Louisiana at Lafayette, USA

Abstract:

The Hawaiian honeycreepers (Drepanidini) are iconic birds of the Hawaiian Islands. Besides being one of the most famous examples of explosive adaptive radiations and a symbol of the islands, the honeycreepers play critical roles in Native Hawaiian culture. Unfortunately, since the arrival of humans to the islands, more than half of the honeycreepers have gone extinct. Here we describe our methods for the reconstruction of the complete Hawaiian honeycreeper phylogeny. Constructing an accurate phylogenetic tree is one of the key steps in genomic inference. Ancient DNA data are frequently used to fill in the phylogeny when taxa are extinct or endangered. However, accurately constructing phylogenomic trees using ancient DNA data, especially when the majority of the taxa are extinct, is more challenging than frequently assumed. Missing-data-derived long-branch attraction and batch effects have been insufficiently addressed for ancient-DNA-based phylogenies. We address these challenges using combined DNA capture and whole genome sequencing along with supertree reconstruction methods to optimize the phylogenetic placement of each component taxon. Our methods are suitable for a wide-range of ancient DNA analyses and will be broadly employable in archaeogenomic analyses seeking to understand past phylogenomic relationships.



ABSTRACT METP-026

Evaluation of genotype imputation of ancient human genomes from West Eurasia

Speaker: **Gülşah Merve Kılınç**
Hacettepe University, Turkey

Co-authors: Hande Çubukcu[1]

[1] Hacettepe University, Turkey

Abstract:

Genotype imputation is a powerful method for acquiring maximum information from sparse genetic data. Recently, use of this approach in ancient human genomes using GLIMPSE (v1) was evaluated (Mota, et al. bioRxiv 2022). Still, limits of genotype imputation for low coverage ancient human genomes especially for those that are recovered from regions with non-sufficient endogenous DNA such as Anatolia is unclear. To increase the amount of data obtained by ancient DNA sequencing from such regions, nature and limitations of imputed data should be examined thoroughly. Here, we use the new version of GLIMPSE (v2.0.0) (Rubinacci, et al. bioRxiv 2022) on ancient genomes mapped to the human reference genome (v.hg38) and explore the effect of (a)reference panel, (b)post-imputation filters, and (c)depth of coverage on imputation results. We perform imputation on ten downsampled ancient genomes (coverage of 0.1x,0.25x,0.5x and 1x) from Anatolia, Caucasus, Iran, Central Asia, and Europe using GLIMPSE (v2) and two distinct reference panels i.e. Panel1-1000 Genomes Project Phase 3 (TGP) and Panel2-TGP merged with the Human Genome Diversity Project (HGDP-TGP). Panel2 slightly improved accuracy for Iran-Caucasus samples. Imputation of variants with MAF>5% reached 75% accuracy after GP>80% filter even at 0.1X coverage. PCA revealed that genetic affinity of imputed samples toward reference panel populations increases explicitly in data with depth of 0.1x filtered with GP>99%. Our results suggest that imputed data with depth above 0.25X and filtered with GP of 80% and above can be used for population genetics analysis such as PCA instead of pseudohaploidized data. F4-statistics revealed that imputed data has a lower degree of reference bias compared to pseudohaploidized data especially in samples outside of Europe. Our results suggest that since most of the data from challenging regions such as Anatolia are low coverage, imputation can be a better alternative to genotype calling.

ABSTRACT METP-027

Assessing the Daicel Arbor Biosciences Prime Plus enrichment bias: implications for the future of accessible ancient DNA research

Speaker: **Roberta Davidson**
The University of Adelaide, Australia

Co-authors: Matthew P Williams[1], Xavier Roca-Rada[2], Kalina Kassadjikova[3], Ray Tobler[2,4], Lars Fehren-Schmitz[3], Bastien Llamas[2,4,5]

[1] The Pennsylvania State University, USA
[2] The University of Adelaide, Australia
[3] University of California, USA
[4] Australian National University, Australia
[5] Telethon Kids Institute, Australia

Abstract:

In-solution hybridisation enrichment of genetic variation is a valuable methodology in human paleogenomics. It allows the enrichment of endogenous DNA in the sample by targeting a set of genetic markers that are comparable between sequencing libraries. Many studies have used the 1240k reagent—which enriches for 1,237,207 genome-wide SNPs—since 2015, though access was restricted to some research groups. In 2021, Twist Biosciences and Daicel Arbor Biosciences independently released commercial enrichment kits that finally enabled all researchers to perform enrichments for the same 1240k SNPs. We used the Daicel Arbor Biosciences Prime Plus enrichment kit to enrich hundreds of ancient samples from four continents for unrelated projects in different laboratories. We identified a systematic assay bias that increases the genetic similarity between enriched samples and that cannot be explained by batch effects. Here, we present the impact of the bias on population genetics inferences (e.g., Principal Components Analysis, ƒ-statistics) and genetic kin relatedness (READ). We also compare the Prime Plus bias to that of the legacy 1240k enrichment assay, confirming the previous report by Rohland et al. 2022. In ƒ-statistics, we find that all Prime-Plus-generated data exhibit artefactual excess shared drift, to the extent that within-continent relationships cannot be correctly determined. In PCA analyses, the first PCs may capture the Prime Plus bias rather than the underlying genetic structure. In READ the bias is more subtle, though still misleading interpretations of results in specific contexts. We expect the bias may affect analyses we have not yet tested. Our observations support previously reported concerns about the integration of different data types in ancient DNA. We also caution that technological solutions to generate 1240k data might necessitate a thorough validation process before their wide adoption in the paleogenomic community.

ABSTRACT METP-028

Duplicates, duplicates: Reducing ancient DNA sequencing cost by avoiding jumping DNA molecules

Speaker: **Marianne Dehasque**
Centre for Palaeogenetics, Sweden

Co-authors: J. Camilo Chacón-Duque[1], Peter D. Heintzman[1], Love Dalén[1]

[1] Centre for Palaeogenetics, Sweden

Abstract:

Optimizing sequencing efficiency remains a major challenge in palaeogenomic research. Sequencing duplicates are a major concern, as they can drastically inflate sequencing costs. Many methods aim to minimize duplicates originating from PCR amplification. However, duplicates originating from “jumping” DNA molecules on patterned Illumina flowcells are an often-overlooked source of duplicates. These duplicates are associated with underloading flowcells and can severely affect sequencing efficiency. Overloading flowcells, on the other hand, is associated with lower sequencing quality. To test the effect of loading concentration on final sequencing efficiency of ancient DNA, we sequenced ancient DNA library pools at four different loading concentrations using Illumina sequencing technology. We found a positive correlation between loading concentration and sequencing efficiency, even when accounting for DNA quality. To minimize sequencing costs, we therefore advise to use loading concentrations of 400 to 500 pM for ancient DNA studies using patterned Illumina flowcells.

ABSTRACT METP-029

Typical qpAdm protocols are not robust to false detection of genetic admixture

Speaker: **Pavel Flegontov**
University of Ostrava, Czech Republic; Harvard University, USA

Co-authors: Eren Yüncü[1], Ulaş Işıldak[1], Matthew P. Williams[2], Christian D. Huber[2], Piya Changmai[1]

[1] University of Ostrava, Czech Republic
[2] Pennsylvania State University, USA

Abstract:

Just a few methods for reconstructing population history gained universal popularity in archaeogenetics: PCA; ADMIXTURE; formal tests for admixture such as f3-statistics and D-statistics; and qpAdm, a tool for fitting two-component and more complex admixture models to groups or individuals. The popularity of these methods is explained by their modest computational requirements and ability to analyse data of various types and qualities. Despite their popularity, protocols relying on qpAdm that screen alternative models of varying complexity and find “fitting” models (considering both estimated admixture proportions and p-values as a composite criterion of model fit) remain untested on complex simulated population histories in the form of random admixture graphs. We analysed high-quality and low-quality genotype data extracted from such simulations and tested various types of qpAdm protocols (“rotating” and “non-rotating”, with/without temporal stratification of target groups and proxy ancestry sources, with/without a “model competition” step). We argue that these protocols are not appropriate for exploratory analyses since their false discovery rates on our simulated data invariably exceeded 20% (i.e., >20% of fitting two-way admixture models imply gene flows that were not simulated). Especially high false discovery rates above 50% were demonstrated by a rotating qpAdm protocol with no temporal stratification of targets and proxy sources. We argue that qpAdm protocols are robust to false detection of admixture only if very specific assumptions about admixture graph topology are valid, such as the absence of gene flows directed from the target or proxy source private lineages to “outgroups” and strict cladality of the proxy and true sources. Robustness of screens for admixture can be radically improved by combining rotating and non-rotating qpAdm protocols (with targets post-dating or contemporaneous with both proxy sources) with an unsupervised ADMIXTURE analysis.

ABSTRACT METP-030

Exploring allele frequency dependencies of F4-statistics for investigating fine-scale population structure

Speaker: **Lei Huang**
Max Planck Institute for Evolutionary Anthropology, Germany

Co-authors: Stephan Schiffels[1]

[1] Max Planck Institute for Evolutionary Anthropology, Germany

Abstract:

Various statistical methods have been developed in human archaeogenetics to identify population structure. One traditional approach is F4-statistics (Reich, et al. Nature 2009), which measures the average correlation in allele frequency differences between two pairs of populations. Although F4-statistics are widely applied in human archaeogenetics studies, the SNP panels involved are often based on common variation, without covering the entire allele frequency spectrum. Here we explore how allele frequency dependencies affect the significance of F4-statistics in a new family of F4 tests (RAS-F4) and develop a new tool for computing F-statistics with flexible ascertainment on allele frequencies. We find, even for widely used SNP panels based on common variation, there is a strong dependency on allele frequency, with up to 2-fold differences in Z scores for rare variants than for common variants. The effect is much stronger in dense genotyping datasets, such as 1000 Genomes. We test RAS-F4 on published data from early medieval individuals from England (Gretzinger et al. Nature 2022) and find that their F4 values correlate much better with estimates of continental Northern European ancestry from supervised clustering when ascertaining variants that are rare in modern Europeans but absent in Africans. With similar ascertainments, those ancient English individuals with different ancestries are more clearly distinguished, as reflected by the increasing Z scores of F4-statistics involving two English and two distinct modern European populations. Taking advantage of that, we further find possible ways to improve RAS-F4 estimates under high levels of SNP missingness, and explore ways to use RAS-F4 statistics to derive ancestry proportions. In sum, our method can provide new ways to identify and model population structure, allowing us to understand the more subtle relationships among populations in the recent human past.

ABSTRACT METP-031

A standardized comparative analysis of ancient DNA kinship estimation methods, using "BADGER" (Benchmark Ancient DNA GEnetic Relatedness): a high-fidelity ancient DNA pedigree simulations pipeline.

Speaker: **Maël Lefeuvre**
Musée de l’Homme, France

Co-authors: Marie-Claude Marsolier[1,2], Céline Bon[1]

[1] Musée de l’Homme, France
[2] Service de Biologie Intégrative et Génétique Moléculaire, France

Abstract:

Paleogenetics provides for the first time a direct estimation of close genetic kinship ties from archaeological remains, as a means of deciphering the social structure of past societies. Consequently, many specialized statistical methods now claim their ability to provide users with precise estimates of genetic relatedness from extremely low-coverage ancient DNA (aDNA). However, these newly published methods can be in practice quite difficult to implement in routine analyses, and may carry a high degree of uncertainty in the result they provide, especially when working with highly degraded samples and/or poorly characterized populations. Thus, gaining a firm grasp on the predictive power, applicability, and biases of each method is an essential cautionary measure to safely interpret their results. Here, we present "BADGER" : a scalable Snakemake pipeline designed to benchmark several aDNA kinship estimation methods. BADGER leverages whole-genome pedigree simulations using randomly selected present-day individuals from the 1000g dataset, and mimics raw aDNA sequencing data for each individual. BADGER then pre-processes the data by following best-practices, and finally attempts to estimate kinship within each pedigree, using our candidate methods. We applied our benchmark in hundreds of replicates and under five scenarios of sequencing depths, ranging from 0.01 to 1X, to obtain comparable sensitivity, specificity and general performance estimates for each method. Our study thus provides with general guidelines and best-practices when attempting kinship analyses, and confirms that confidently estimating kinship with as few as 1700 overlapping SNPs remains a feasible prospect under specific conditions. Finally, BADGER was designed with reusability in mind, and can be easily fitted to the specific parameter space of a given aDNA analysis, thus providing researchers with a workflow-agnostic framework to assess confidence in the results provided by kinship analysis.

ABSTRACT METP-032

Assessing ancestry through Principal component analysis

Speaker: **Francesco Montinaro**
University of Bari, Italy

Co-authors: Luciana de Gennaro[1], Ludovica Molinaro[2], Alessandro Raveane[3], Luca Pagani[4], Mario Ventura[1]

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[3] Human Technopole, Italy
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Abstract:

Evaluating the ancestral components of human populations is crucial not only to fully characterise the history of our species but also for the efficient development and design of Translational and medical studies and treatment. Although many methods aiming to infer the different sources of admixed populations have been recently developed, most of them have scarce reliability when samples analysed are characterised by a high missingness rate, as is the case for genetic data extracted from ancient specimens.It has been recently shown that Principal components are correlated to f-statistics, the fundamental unit of an important method assessing ancestry using the qpAdm method. Here we developed, tested and assessed ASAP (Assessing ancestry through Principal component analysis), a non-negative least square-based method based on Principal Components for estimating ancestry in genotype data characterised by missing data. Our results show that ASAP has high accuracy and reliability, similar to that obtained with qpAdm.

ABSTRACT METP-033

Mapache: a flexible pipeline to map ancient DNA

Speaker: **Samuel Neuenschwander**
University of Lausanne, Switzerland; Swiss Institute of Bioinformatics, Switzerland

Co-authors: Diana I. Cruz Dávalos[1], Lucas Anchieri[1], Bárbara Sousa da Mota[1], Davide Bozzi[1], Simone Rubinacci[1], Olivier Delaneau[1], Simon Rasmussen[2], Anna-Sapfo Malaspinas[1]

[1] University of Lausanne, Switzerland
[2] University of Copenhagen, Copenhagen, Denmark

Abstract:

Mapping of sequencing reads to a reference genome is a fundamental step in genomic analyses. Compared to modern data, ancient DNA is highly challenging as data is sparse, contaminated and shows damage, such as fragmentation and deamination. Here, we introduce mapache, a lightweight pipeline designed to map both ancient and present-day DNA sequences to one or multiple reference genomes while generating reports with summary statistics to inspect the quality of the mappings. Mapache is implemented in the workflow manager Snakemake and it thus inherits its flexibility, scalability, and reproducibility. Snakemake is based on Python allowing users to easily adapt the code or to combine the workflow with other Snakemake workflows. Moreover, unlike other tools, mapache efficiently manages temporary files, keeping the necessary storage space small. Furthermore, mapache can map sequences to more than one genome in parallel and the pipeline can be used on modern clusters with queuing systems. Finally, mapache has an additional module to allow for genotype imputation of low-coverage genomes with GLIMPSE, a step that may become quite common in ancient DNA.

ABSTRACT METP-034

HaploCart: Human mtDNA Haplogroup Classification Using a Pangenomic Reference Graph

Speaker: **Joshua Rubin**
Technical University of Denmark, Denmark

Co-authors: Nicola Vogel[1], Shyam Gopalakrishnan[2], Peter Sackett[1], Gabriel Renaud[1]

[1] Technical University of Denmark, Denmark
[2] University of Copenhagen, Denmark

Abstract:

Current mitochondrial DNA (mtDNA) haplogroup classification tools map reads to a single reference genome and perform inference based on the detected mutations to this reference. This approach biases haplogroup assignments towards the reference and prohibits accurate calculations of the uncertainty in assignment. We present HaploCart, an mtDNA haplogroup classifier which uses VG's pangenomic reference graph framework together with principles of Bayesian inference (Rubin, et al. bioRxiv 2022; Hickey, et al. Genome Biol. 2020). We demonstrate that our approach significantly outperforms available tools by being more robust to lower coverage or incomplete consensus sequences and producing phylogenetically-aware confidence scores that are unbiased towards any haplogroup. HaploCart is available both as a command-line tool and through a user-friendly web interface. The program written in C++ accepts as input consensus FASTA or FASTQ files, and outputs a text file with the haplogroup assignments along with confidence estimates. Our work considerably reduces the amount of data required to obtain a confident mitochondrial haplogroup assignment. HaploCart is available as a command-line tool at https://github.com/grenaud/vgan and as a web server at https://services.healthtech.dtu.dk/service.php?HaploCart.

ABSTRACT METP-035

Poseidon – Powerful and FAIR archaeogenetic genotype data management

Speaker: **Clemens Schmid**
Max Planck Institute for Evolutionary Anthropology, Germany

Co-authors: Thiseas C. Lamnidis[1], Ayshin Ghalichi[1], Dhananjaya Athanayaka[1], Wolfgang Haak[1], Stephan Schiffels[1]

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Abstract:

The increase in ancient human DNA data requires robust yet flexible solutions to store and distribute it. While raw sequencing data is generally shared in large archives (e.g. ENA or SRA), no such standard exists for derived genotype data and contextual, spatiotemporal information. This raises concrete issues: - Ancient individuals only constitute meaningful observations if their spatiotemporal provenience is known. Current practice renders it difficult to maintain the connection between archaeological context and sampled genomic data. - Specific results can only be reproduced with genotypes. Current practice does not include their publication. - Meta-analyses involving large amounts of data require tedious curation. Available public datasets have high key-person-risk, lag behind and are not well machine-readable. To tackle these issues we present 'Poseidon', a computational framework including an open data format, software, and community-maintained archives to enable standardised and FAIR handling of archaeogenetic data. A Poseidon "package" bundles genotypes in industry-standard formats with human- and machine-readable context data, storing sample-wise information on spatiotemporal origin and genetic data quality. Through collective effort we already prepared 100+ packages for published studies in an open online repository. In our talk we want to specifically highlight two components of the framework: 1. A computational platform to process raw sequencing data directly from archive data (e.g. ENA), with a public interface for package curators to control processing parameters. Infrastructure will be provided by MPI-EVA, with community access and continuous integration provided via GitHub. 2. Command line software for package validation, manipulation and analysis. Validating structural integrity is a core task to honour the FAIR promise. The reliable structure then allows for advanced stream processing and co-analysis of genomic and contextual information.

ABSTRACT METP-036

New data on Twist Bioscience’s target enrichment efficiency on poorly preserved aDNA samples

Speaker: **Nicoletta Zedda**
University of Ferrara, Italy

Co-authors: Laura Winkelbach[1], Jens Blöcher[1], Barbara Bramanti[2], Joachim Burger[1]

[1] Johannes Gutenberg University Mainz, Germany
[2] Department of Environmental Sciences and Prevention, University of Ferrara, Italy

Abstract:

In the last 15 years, the analysis of ancient DNA from bioarchaeological remains has undergone tremendous development thanks to the introduction of new sequencing technologies that can be used to produce almost complete genomes from prehistoric skeletal remains. However, the analysis of extremely bio-molecularly degraded material presents some difficulties that can only be overcome by capture enrichment approaches. Twist-Bioscience produces reagents specifically suited for the enrichment of ancient human DNA. The Twist Ancient DNA capture baits are built on approximately 1.4 M SNPs, and their enrichment performance was recently tested with optimal results (Rohland, et al. Genome Res. 2022). We present new results after testing the Twist reagent for its enrichment power and its sensitivity. Experiments were performed on human skeletal samples with known low endogenous DNA content (1-12 %) of different (pre)historical origins. The aim was to adjust the published enrichment protocol to our protocols for aDNA extraction and library preparation (Zegarac, et al. Sci. Rep. 2021) and to define the optimal protocol for samples with low endogenous DNA content. We compared the results of enriching library pools of different complexity for each sample, comparing 2 vs. 4 libraries from 1 vs. 2 independent DNA extracts. For better comparison, our evaluation is based on the 1,240k SNPs for which a larger reference data set is available. We were able to retrieve 981.665-1.174.646 SNPs in 7 samples with an average depth of 2,80X using 2 libraries per sample, and between 1.107.393-1.225.654 SNPs with an average depth of 6,80X using 4 libraries from 2 independent extracts per sample. Thus, we find that increasing the complexity of enriched pooled libraries leads to an increase in the depth of coverage, but the number of captured SNPs is only slightly positively affected, as the Twist reagent performed with high sensitivity for all samples even with low complex pooled libraries.

ABSTRACT METP-037

A comparison of DNA extraction methods to develop a rapid, on-site test for sedimentary ancient DNA

Speaker: **Nihan D. Dagtas**
Tel Aviv University, Israel

Co-authors: Viviane Slon[1]

[1] Tel Aviv University, Israel

Abstract:

The retrieval of DNA from archaeological sediment samples has been shown to be a promising approach to study ancient genomes. Yet, sampling sediments for DNA analyses is far from being a common practice in the field; so far, this approach has been applied to relatively few archaeological sites. As the exact source of the ancient DNA fragments in sediments and the factors that lead to their long-term preservation remain elusive, sampling strategies tend to be mostly haphazard, relying on ‘gut-feeling’ as to where to collect the samples. Then, as the procedure to generate sequencing data from such samples is lengthy, after sampling at an archaeological site, it usually takes several months until the results of the initial screening for DNA preservation are available. By then, the archaeological site in question may not be available for further sampling - either until the next dig season, or in the case of salvage excavations, ever again. Therefore, implementing the best sampling strategy in the first step of the process - in the field - is crucial for the smooth flow of any project. Here, with the overreaching goal of developing a method that allows for the rapid, on-site detection of preserved sedimentary ancient DNA, we tested the performance of several rapid DNA extraction methods. We compared a method commonly used in the laboratory for sedimentary ancient DNA research (Rohland, et al. Nature Protocols 2018) to methods developed for specimens of non-sediment origin. We evaluated the methods in terms of time and handling required, the amount of genetic material extracted, and their applicability in the field. The results will contain information about how to quickly extract DNA from sediment samples in the field using minimal equipment – a first step to more efficient field sampling for sedimentary ancient DNA research.

ABSTRACT METP-038

New methods for the discrimination and recovery of faunal taxa from sedaDNA libraries based on the study of Paleolithitic Sediments from El Mirón Cave, Spain.

Speaker: **Pere Gelabert**
University of Vienna, Austria

Co-authors: Victoria Oberreiter[1], Florian Brück[1], Stefan Franz[1], Manuel Ramon González Morales[2], Lawrence Straus[3], Ron Pinhasi[1]

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[2] University of Cantabria, Spain
[3] University of New Mexico, USA

Abstract:

Sediment DNA (sedaDNA) NGS sequencing and analyses have gained momentum during the last years after the publication of several studies that have evidenced the capacity to recover and study human and mammalian DNA from Pleistocene sediments, some up to 2 million years old. The recovery of sedaDNA allows for the identification of taxa and, in the cases with enough DNA, the performance of phylogenies and population genetic analyses. Although the primary focus of sedaDNA analysis has been the study of human DNA, most of the recovered sequences are of another animal. Nevertheless, the study of mammalian DNA from sediment faces important challenges, including a) the presence of multiple taxa in the same sample, and in most cases DNA from multiple individuals from the same taxa b) the limited number of published Pleistocene mammalian genomes to compare with. We screened 26 sedaDNA samples from the archaeological site of El Mirón Cave in Cantabrian Spain. The filtered samples span both the Middle and Upper Paleolithic occupation phases of El Mirón (Mousterian-Initial Magdalenian, 46,000-21,000 cal BP). We have recovered large quantities of animal DNA in 22 of 26 samples and human DNA traces in six. We estimate that more than 90% of the mammalian reads are lost through the existing pipelines for species identification due to the limited discrimination capacities between closely related taxa. To overcome this limitation, we introduce a new integrated methodology that enables the discrimination of faunal DNA at the species level and increases the number of sequences correctly classified, enabling the identification of taxa at the species level and the reconstruction of consensus sequences.

ABSTRACT METP-039

Benchmarking tools for ancient metagenome assembly - Current state and challenges

Speaker: **Louis Kraft**

Technical University of Denmark

Co-authors: Gabriel Renaud[1]

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Abstract:

Studying genomes of ancient microbes in metagenomic samples enables reconstructing biogeochemical cycles, the history of humans as host organisms, microbial diversity and evolutionary trajectories of microbial species. Sequencing ancient metagenomic samples results in large volumes of data, comprising varying abundances of numerous (extinct) species from different kingdoms such as bacteria, fungi and plants.Ancient DNA degrades with time, resulting in extremely short fragments and deaminated nucleotides that cause spurious signals of mismatches between DNA fragments. The assembly of ancient metagenomes is therefore a challenging task. During the assembly process the sequenced fragments should be reconstructed to the longest possible contiguous sequences (contigs).Here we present an overview of different assemblers and their performance of assembling various ancient metagenomic datasets. We also benchmarked different parameter settings for each assembler. The assembly quality was evaluated using different metrics such as correctness of assembled contigs (accuracy), percentage of genomes covered by the contigs (sensitivity) and usage of computational resources. Our benchmark shows that while existing tools do assemble a proportion of genes with sufficient quality, the corrupted nature of ancient sequences is reducing the fraction of sequences that can be properly reconstructed.

ABSTRACT METP-040

A new method of extract-pooling for sediment ancient DNA analyses

Speaker: **Victoria Oberreiter**
University of Vienna, Austria

Co-authors: Pere Gelabert[1], Florian Brück[1], Olivia Cheronet[1], Evelyn Zelger[1], Sophie Szedlacsek[1], Fernanda Tenorio Cano[1], Susanna Sawyer[1], Ron Pinhasi[1]

[1] University of Vienna, Austria

Abstract:

In recent years, the field of aDNA has taken a promising new direction towards extracting DNA from archeological sediments (Gelabert, et al. Curr. Biol. 2021). However, the screening of sediment samples from archeological sites can be time consuming and expensive as a high number of these samples need to be analyzed in order to identify those with detectable aDNA signals (positives), especially if the target is human aDNA. We are proposing a high throughput method that facilitates the fast and efficient analysis of sediment samples by applying a pooled testing approach. By pooling multiple extracts together we are able to parallelize lab procedures while screening for potentially positive samples. Positives can then be analyzed in further detail while negatives are discarded. We successfully applied this method to several Middle and Upper Paleolithic sediment samples from European cave sites and one open-air site and show that up to five samples can be pooled, maintaining a detectable signal of aDNA and enabling specific taxa determination. This high throughput pooling method will allow for large scale sediment analyses for aDNA preservation with great reductions in costs and time.

ABSTRACT METP-041

Assessing ancient DNA sampling strategies for natural selection inference with time-series data

Speaker: Lucas Anchieri

University of Lausanne, Switzerland; Swiss Institute of Bioinformatics, Switzerland

Co-authors: C. Eduardo Amorim[1], Samuel Neuenschwander[2,3], Anna-Sapfo Malaspinas[1,2]

[1] California State University Northridge, USA
[2] University of Lausanne, Switzerland
[3] Swiss Institute of Bioinformatics, Switzerland

Abstract:

With the increasing availability of genomic data from ancient human individuals, it has become possible to measure allele trajectories across time (time-series data). These allele trajectories can be used to estimate natural selection at specific loci. Several methods have been developed to that effect and were validated with simulations using mostly large sample sizes. However, in reality, genomic data of ancient humans typically include a small number of individuals per time point, making estimations of selection parameters such as time of onset, selection coefficient, and dominance, challenging. Here, we compared the performance of three methods (ApproxWF, Slattice, and Sr) through extensive simulations. We used SLiM to simulate allele trajectories under realistic parameters for human populations and tested the methods using time-series data sampled from these simulations. We investigated several sampling schemes (for example, fixing sample size and varying the dates of the samples, or the opposite) as well as different strengths of selection to get a sense of the best sampling strategy and approach to recover the simulated values. We show that the performance of the methods is very variable and that the selection coefficient used for the simulations has a large impact. Depending on the sampling scheme, the methods do not perform well if selection is either too high or too low. Furthermore, the methods perform better with homogenous sampling schemes and some thought should therefore be given to avoiding uneven time-series data when estimating selection.

ABSTRACT METP-043

Tracing changes in the human genome left by the process of adaptation

Speaker: **Mikołaj Danielewski**
Poznan University of Medical Sciences, Poland

Co-authors: Jan Nowak[1], Jarosław Walkowiak[1], Karolina Wielgus[1]

[1] Poznan University of Medical Sciences, Poland

Abstract:

With the development of Next Generation Sequencing and, subsequentially, new protocols for isolating highly degraded DNA, fully sequencing ancient genomes became a possibility. As a result, in the last decade, a staggering amount of achievements has been reported in the field of paleogenetics. This kind of genomic data allows to not only research the demographic history of species but also to identify ancient gene variants and to analyse changes in frequencies of variants in populations. Consequentially, it may be possible to detect and analyse effects of selective processes which are responsible for adaptation to changes in the environment. In our study, we plan to compare two populations: hunter-gatherers and agrarians, in order to ascertain whether their differing life-styles had any impact on their genomes. As both geographical distance and time frame separating these populations were relatively small, the only differing factor between them is their way of life, which makes it a perfect set up for our research purposes. Of particular interest for our study are methylation levels, as the epigenome, in contrast to the genome, adapts to the changing of environmental factors at a much more rapid pace. While analysing methylation in ancient genetic material is very challenging, some methods based on inferring patterns of methylation from post-mortem damage are rather promising for highly degraded samples.

ABSTRACT METP-044

A systematic review of database research engines using a controlled, degraded single protein

Speaker: **Matthew Collins**
University of Copenhagen, Denmark

Co-authors: Yun Chiang[1,2], Bharath Nair[1], Ismael Ismael Rodriguez Palomo[3], Benjamin Dartigues[4], Miranda Evans[3], Ruairidh Macleod[3], Jan Dekker[1,5]

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[2] Université Côte d'Azur, France
[3] University of Cambridge, UK
[4] University of Bordeaux, France
[5] University of York, UK

Abstract:

Palaeoproteomics is a rapidly evolving discipline, and practitioners are constantly developing novel strategies for the analyses and interpretations of complex, degraded protein mixtures. As a community, we began by using well-established approaches to sequence and interrogate our data to ensure that we achieve the expected norms of good proteomics practice. This includes the consideration of an increasingly wide array of post translational modifications (PTMs), well-represented databases which encompass every potential constituents of samples, defensible rules on identification of peptides/proteins and statistically significant false discovery rates (FDRs). So far there have been limited attempts to justify these standardised approaches in the study of ancient proteins. There is also no systematic evaluation of different database search engines. Bovine beta-Lactoglobulin was targeted here since it is one of the most robust and ubiquitous proteins in the archaeological record. Using a controlled model system - the experimental degradation of this single purified protein treated at neutral pH and 95 oC for 0, 4 and 128 days respectively - we have explored (1) the performance of FASTA database choices (published, targeted and annotated dairy vs whole bovine genome databases), (2) enzymatic digestion (tryptic vs semi-tryptic vs non-specific options), (3) the efficiency of open search that allows for wide precursor mass tolerance and global identification of PTMs, as well as (4) the suitability of various database searching packages and algorithms such as PEAKS, Mascot, MaxQuant (Andromeda), Alphapept (X!Tandem), MSGF+, Comet, Sage, Metamorpheus, pFind and Fragpipe. In this talk we report on the performance of these different strategies in accurately surfacing peptides from samples which have undergone either mild (4 days + tryptic digestion) or severe (128 days, without digestion) degradation. The starting point (0 day) was included as a positive control.

ABSTRACT METP-045

Improved methylation detection in ancient DNA

Speaker: **Susanna Sawyer**
University of Vienna, Austria

Co-authors: Benjamin Yakir[1], Alejandro Llanos Lizcano[2], Eran Meshorer[1], Liran Carmel[1], Ron Pinhasi[2]

[1] The Hebrew University of Jerusalem, Israel
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Abstract:

Changes in gene regulation are strongly associated with changes in epigenetic marks, which modify how the genome works without involving direct changes in the DNA sequence. A key epigenetic mark in vertebrates is cytosine methylation (5mC). 5mC has been heavily studied in modern DNA, primarily measured using bisulfite treatment. However, the damage to ancient DNA (aDNA) has not allowed for a successful measure of 5mC using bisulfite treatment. Rather, computational methods have been developed to reconstruct premortem DNA methylation of ancient samples (Gokhman, et al. Science 2014). This method requires high-coverage of ancient samples, which is expensive and only applicable to well-preserved samples that were shotgun sequenced or captured to high coverage.We have developed a new and reduced-cost method to measure 5mC in ancient samples. The method makes use of an enzymatic-based methylation treatment, NEBNext Enzymatic Methyl-seq (EM-seq™), which has been shown to work for small amounts of DNA (Vaisvila, et al. Genome Res. 2021). Our aDNA-optimized method allows for orders of magnitude more information to be used for 5mC analyses in ancient DNA. The reduced cost, combined with the increased power, opens the door for groundbreaking discoveries in the ancient DNA field, where large numbers of samples can be epigenetically studied to provide inferences on evolutionary adaptations, and on the impact of environmental factors such as diet, disease and cultural practices of past populations.

ABSTRACT METP-046

Ancient Epigenomics of Cattle and Aurochs

Speaker: **Ciarán O'Connor**
Trinity College Dublin, Ireland

Co-authors: Victoria Mullin[1], Conor Rossi[1], Valeria Mattiangeli[1], Dan Bradley[1]

[1] Trinity College Dublin, Ireland

Abstract:

The fields of bioarchaeology and ancient DNA (aDNA) have developed rapidly in recent years, greatly advancing our understanding of early animal domestication events and the effects of human interference on the biology of domesticates. However, the focus has primarily been on sequence-specific changes, with a lack of research in the epigenomics of ancient domesticates. Ancient epigenomics is a powerful tool that can leverage the difference in post-mortem cytosine deamination rates of methylated and unmethylated CpG sites in aDNA, enabling the reconstruction of ancient methylomes. Key information such as the sex, castration status, and age-at-death of individuals can be deduced from methylation profiles. Using high-coverage ancient genomes from sites across Europe and Asia, we have generated methylation data for ancient aurochs and domestic cattle. We have developed an elastic net regression model trained on these methylation patterns, selecting for genomic windows centred on CpG sites that are the most predictive of sex. Here we present the preliminary results of this machine learning model, utilising the fraction of methylated CpG sites within informative windows to infer the sex of ancient bovines.

ABSTRACT NOVP-001

Reconstructing ancient microbial genomes from the wine ferments of the Roman biblical king Herod

Speaker: **Maxime Borry**
Max Planck Institute for Evolutionary Anthropology, Germany; Leibniz Institute for Natural Product Research and Infection Biology and Hans Knöll Institute, Germany

Co-authors: Tziona Ben Gedalya[1,2], Alexander Herbig[3], Christina Warinner[3,4,5]

[1] Ariel University, Israel
[2] Hebrew University, Israel
[3] Max Planck Institute for Evolutionary Anthropology, Germany
[4] Friedrich-Schiller University, Germany
[5] Harvard University, USA

Abstract:

The fortress of the Herodium, built towards the end of the first century BCE on the orders of Herod the Great, Roman client king of Judea, attests the expansion of Roman influence in the eastern Mediterranean. During archeological excavations of the Herodium in 2017, a winery was discovered on the ground floor of the palace, with an assortment of clay vessels in situ, including large fermentation vessels each capable of fermenting up to 300-400 L of wine. Analyzing organic material consistent with grape pomace at the bottom of these vessels, we extracted and sequenced DNA using shotgun metagenomics and targeted capture, aiming for enrichment of DNA from fermentation associated microbes. While the analysis of the sequencing data first revealed a partial degradation of the overall microbial communities, we could successfully control for contaminant microbes using soil samples from the fortress and a differential abundance analysis approach. After de novo assembly and binning of the remaining fermentation bacteria genomes, we analyzed the reconstructed high-quality de novo metagenome-assembled genomes (MAGs) from a phylogenetic and functional standpoint. The phylogenetic signal of these ancient fermentation bacteria confirmed both their ancient origin and their affiliation to bacteria associated with wine fermentation. Gene functional analysis of the reconstructed fermentation-associated MAGs revealed both beneficial genes involved in malolactic fermentation and diacetyl production, as well as genes involved in the production of wine spoilage compounds, especially in species typically viewed today as spoilage bacteria. Overall, our analysis brings a new appreciation of winemaking in Roman Judea and enriches our understanding of Roman accounts of flavoring wine with different herbs and aromatics, which may have been performed in part to mask the off-flavor compounds produced by bacterial wine spoilage genes.

ABSTRACT NOVP-002

Diversity of bacteriophages in the ancient human microbiome

Speaker: **Remi Denise**

University College Cork, UK

Co-authors: Alexander Hübner[1], Irina Marie Velsko[1], Colin Hill[2], Christina Warinner[1], Andrey Shkoporov[2]

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[2] APC Microbiome Ireland, Ireland

Abstract:

While recent work has begun to shed light on the microbiota, which includes the trillions of bacteria and phages that inhabit our body, our understanding of its evolution throughout human history is limited. To answer research questions regarding the development of the human microbiota over time, researchers have begun to sequence ancient DNA from well-preserved fecal and dental samples to understand their bacterial community composition. However, an important group of the microbiota, bacterial viruses (or bacteriophages), which play a large role in influencing bacterial community structure and can affect human health and disease, are often understudied in these ancient samples. Using an integrative and collaborative approach, we used sequencing data of ancient paleofeces and dental calculus to study the oral and gut microbiome from a variety of time periods. This allowed us to identify viruses in ancient samples and found some similarities with modern samples regarding phage composition. We were also able to identify some phage/host pairs that helped us understand the evolution of the relationship between the phages and their bacterial host, how they evolved in the context of human lifestyle, and the geographic distribution of human populations.

ABSTRACT NOVP-003

Investigating the Ancient Oral Microbiome as a Marker of Frailty in Middle Eastern Populations Over Time

Speaker: **Abigail Gancz**
Pennsylvania State University, USA

Co-authors: A. Sołtysiak[1], L. Weyrich[2,3]

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[2] The Pennsylvania State University, USA
[3] University of Adelaide, Australia

Abstract:

Noncommunicable diseases, while common in modern industrialized individuals, are extremely challenging to describe in past populations. However, research has indicated that the oral microbiome (the community of microorganisms inhabiting the oral cavity) is intricately associated with conditions including cardiovascular disease, diabetes, obesity, rheumatoid arthritis, and psychological disorders. Additional investigations have demonstrated that the oral microbiome can be directly linked to morbidity and mortality indicators. As such, the reconstructed ancient oral microbiome may provide a critical analytical tool for understanding the origins of the noncommunicable diseases of the present. Specifically, this approach may well provide useful insights into how and why the human microbiome may have shifted over time in relation to diet, social, and lifestyle changes in specific populations in ways that led to differential disease outcomes. To investigate the utility of this approach in a specific region, we sampled individuals from the Neolithic to the Modern periods in the Middle East, specifically from Egypt, Syria, Israel, and Iran. First, we authenticated ancient DNA signatures from the dental calculus and assessed contamination in the samples. In addition, we tested for oral geography and processing biases and incorporated all those discovered into downstream analyses. Next, we tested for associations between skeletal morbidity indicators and the oral microbiome, and assessed whether similar associations were found in this ancient population as have been documented in modern studies. Finally, we evaluated whether and how the Middle Eastern ancient oral microbiome shifted with major human lifeway transitions and major historical events. While in early stages, this research has important implications for our understanding of how the oral microbiome relates to human health and how this relationship may have shifted over time to lead to modern day health outcomes.

ABSTRACT NOVP-005

aMeta:an accurate and memory-efficient ancient Metagenomic profiling workflow

Speaker: **Nikolay Oskolkov**

Lund University, Sweden

Co-authors: Zoe Pochon[1], Nora Bergfeldt[1], Emrah Kirdök[2], Mario Vicente[1], Claudio Mirabello[3], Per Unneberg[3], Love Dalen[1], Anders Götherström[1]

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Abstract:

Analysis of microbial data from archaeological samples is a rapidly growing field with a great potential for understanding ancient environments, lifestyles and disease spread in the past. However, high error rates have been a long-standing challenge in ancient metagenomics analysis. This is also complicated by a limited choice of ancient microbiome specific computational frameworks that meet the growing computational demands of the field. Here, we propose aMeta, an accurate ancient Metagenomic profiling workflow designed primarily to minimize the amount of false discoveries and computer memory requirements. Using simulated ancient metagenomic samples, we benchmark aMeta against a current state-of-the-art workflow, and demonstrate its superior sensitivity and specificity in both microbial detection and authentication, as well as substantially lower usage of computer memory. aMeta is implemented as a Snakemake workflow to facilitate use and reproducibility.

ABSTRACT NOVP-006

Bacteriophages in ancient human gut metagenomes

Speaker: **Piotr Rozwalak**
Adam Mickiewicz University, Poland

Co-authors: Jakub Barylski[1], Yasas Wijesekara[2], Andrzej Zielezinski[1], Bas E. Dutilh[3,4]

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[3] Utrecht University, the Netherlands
[4] Friedrich Schiller University Jena, Germany

Abstract:

Bacteriophages (phages), viruses that infect bacteria, are highly diverse and abundant everywhere on Earth. Recent advances in metagenomic sequencing and computational analysis have made it possible to explore the vast genomic diversity of phages and study their evolution and ecology. However, most studies only sample present-day phages, so they lack a long-term perspective on their evolution. In this study, we present the de novo assembly of 298 ancient phage genomes from publicly available ancient human gut metagenomes dated up to 5300 years before present. We authenticated their ancestral origin based on DNA deamination patterns. Next, we analyzed their relationships to modern viruses from the gastrointestinal tract and predicted hosts with cutting-edge tools. Our analysis revealed ancient representatives of known virus families and genera, as well as ancient phages that were unclassified or only distantly related to known viruses. We also discovered a genome of Mushuvirus mushu, a phage that infects Faecalibacterium prausnitzii, and other commensal bacteria in the human gut ecosystem. Despite 1300 years of evolution on different continents, modern and ancient Mushuvirus genomes share 97.7% nucleotide identity and suggest a long-term mutualistic relationship between the prophage and its host. Overall, our results demonstrate the feasibility of reconstructing high-quality ancient phage genomes and offer new insights into phage-bacteria interactions, expanding our understanding of the virosphere.

ABSTRACT NOVP-007

Biomolecular perspectives on the uses of birch bark tar in prehistoric Europe

Speaker: **Anna White**
University of Copenhagen, Denmark; University of York, UK

Co-authors: Tabea Koch[1,2], Theis Jensen[3], Jonas Niemann[3], Renate Ebersbach[4], Christian Harb[5], Renata Huber[5], Léonard Kramer[6], Michel Mauvilly[6], Aimee Little[2], Martine Regert[1], Nathan Wales[2], Hannes Schroeder[3]

[1] Université Côte d’Azur
[2] University of York
[3] University of Copenhagen
[4] Landesamt für Denkmalpflege Baden-Württemberg, Germany
[5] Amt für Denkmalpflege und Archäologie Zug, Switzerland
[6] Service Archéologique de l’Etat de Fribourg, Switzerland

Abstract:

Birch bark tar has been widely used since the Middle Pleistocene in Europe for hafting stone tools or, later, for repairing ceramics. Pieces of birch tar are often found with tooth imprints indicating that they were chewed. However, the exact uses of birch tar and why it was chewed remain debated. Ancient DNA analyses provide a new way of analysing ancient birch tar that can provide new insights into its uses in the past. Here we combined GC-MS analyses with shotgun DNA sequencing to characterise the composition of archaeological birch bark tar from Neolithic contexts in Europe and to explore its uses. The GC-MS analysis enables the identification of natural compounds including betulin and lupeol and their degradation markers that are characteristic of birch bark and are thought to have antibacterial properties, while the DNA analyses enable us to determine whether or not the pieces were chewed and to identify potential additives, which can shed light on how it was used or why it was chewed. In addition, the human DNA from the tar enables us to determine the genetic sex of the individuals who chewed the tar, giving fascinating insights into gendered practices of tool use and manufacture in the past. Our results highlight how combining GC-MS analysis with ancient genomics can provide new insights into the uses of birch bark tar artefacts and the technological choices of prehistoric communities.

ABSTRACT NOVP-008

Exploring the temporal limits of RNA preservation in historical and ancient biological material

Speaker: **Vincent Geyer**
Max Planck Institute for Evolutionary Anthropology, Germany

Co-authors: Lukas Bokelmann[1], Michael Boyle[1], Tessa Zeibig[1], Johannes Krause[1], Janet Kelso[1], Matthias Meyer[1]

[1] Max Planck Institute for Evolutionary Anthropology, Germany

Abstract:

Although DNA is the primary source of information in paleogenetic research, several studies have shown that, despite having a lower biochemical stability than DNA, RNA may also be preserved in ancient or historical biological material e.g. in historical medical tissue collections or ancient seeds. Notably, the recovery of ancient RNA was also reported from permafrost tissue samples from the late Pleistocene (Smith, et al. PLOS Biol 2019) demonstrating that RNA can survive in ancient biological material for many millennia under favorable conditions. This finding suggests that ancient RNA is an understudied source of genetic information and that more systematic evaluations are warranted to explore the temporal limits of RNA preservation in different types of material. To date, most ancient RNA studies have used traditional RNA library preparation methods. These methods are not ideally suited for highly degraded sample material because they either involve size-selective purification steps that are prone to the loss of short molecules or mask the native termini of sequences, resulting in information loss in both cases. To address this problem, we adapted a single-stranded DNA library preparation method that is widely used in ancient DNA research (Meyer, et al. Science 2012) for use with RNA. We are currently testing the suitability of this method for recovering RNA from formalin-fixed historical tissue samples and are investigating the possibility of RNA preservation in Pleistocene skeletal remains.

ABSTRACT NOVP-009

Ancient protein analysis of a Roman sealed jar: an intriguing palaeoproteomic case study

Speaker: **Jessica Hendy**
University of York, UK

Co-authors: Miranda Evans[1,2], Samantha Presslee[1], Birgit Schwahn[3], Peter Fasold[3], Carsten Wenzel[3]

[1] University of York, UK
[2] University of Cambridge, UK
[3] Archäologisches Museum Frankfurt, Germany

Abstract:

Palaeoproteomics can be a powerful tool for the characterisation of organic archaeological materials. Here we present a case study which reveals the presence of possible fetal tissue in a 3rd century AD sealed Roman jar. Excavations at the Roman site of Nida in modern-day Frankfurt uncovered an intact, sealed jar in the tomb of a subadult. After x-ray analysis confirmed the presence of material inside the jar, protein analysis was performed in order to characterize the vessel's contents. This analysis revealed a high number of identified proteins with over 350 confidently matching to the human proteome, and therefore suggesting the presence of human tissue. Using the Human Protein Atlas and GO terms, we compared this identified proteome to RNA expression data from a range of tissues revealing that many of the most abundant proteins (based on peptide counts and sequence coverage) had nonspecific tissue expression, although many were associated with extracellular matrix organization in epithelial cells. We also searched our protein lists for protein markers diagnostic of particular tissues and organs based on published medical and forensic literature, but found little to indicate the presence of a single organ or tissue type. Given the size of the vessel, its context and the abundance of proteins with low tissue specificity, we believe the most plausible explanation is the presence of fetal tissue. However, we welcome suggestions for further analyses and interpretations. This study demonstrates the preservation of proteins in this unique artefact type and makes advances in understanding Roman funerary practices in the absence of skeletal remains.

ABSTRACT NOVP-010

Using simulations to assess the power and limits of evolutionary inference based on ancient protein sequences.

Speaker: **Ioannis Patramanis**
University of Copenhagen, Denmark

Co-authors: Enrico Cappellini[1], Fernando Racimo[1]

[1] University of Copenhagen, Denmark

Abstract:

Ancient proteins from fossil material can preserve longer than DNA and in less favorable environmental conditions. When recovered, these ancient proteins have been used to reconstruct the phylogenetic histories of extinct organisms that lived several millions of years in the past. Although the temporal and geographic horizons for recovering these proteins are slowly broadening, the amount of genetic information obtained from them remains fairly limited: only a few gene trees are often available, and the sequences from which these are inferred are sometimes plagued with missing data. Furthermore, only amino acid changing mutations are visible to researchers. Finally, due to the functional importance of the proteins under study, they often tend to be highly conserved, further reducing the number of informative polymorphisms. Although these factors have been acknowledged before, the full extent and the manner in which they can potentially hinder the accuracy and precision of phyloproteomic analyses is still unknown. To investigate this, we used forward genetic simulations to simulate protein sequence data from different ancient and present-day hominids, emulating the idiosyncracies of some of the most commonly preserved proteins currently under study in palaeoproteomics. We then applied commonly used population genetic and phyloproteomic tools on the simulated sequence data, and assessed how well the various inferred gene trees and consensus phylogenies reflected the true simulated population history. Our analysis serves to evince the potential and limitations of palaeoproteomic analyses in providing information about deep population history.

ABSTRACT NOVP-011

Multi-omic analyses of palaeofaeces from Viking Age Ribe, Denmark

Speaker: Liam T. Lanigan

University of Copenhagen, Denmark

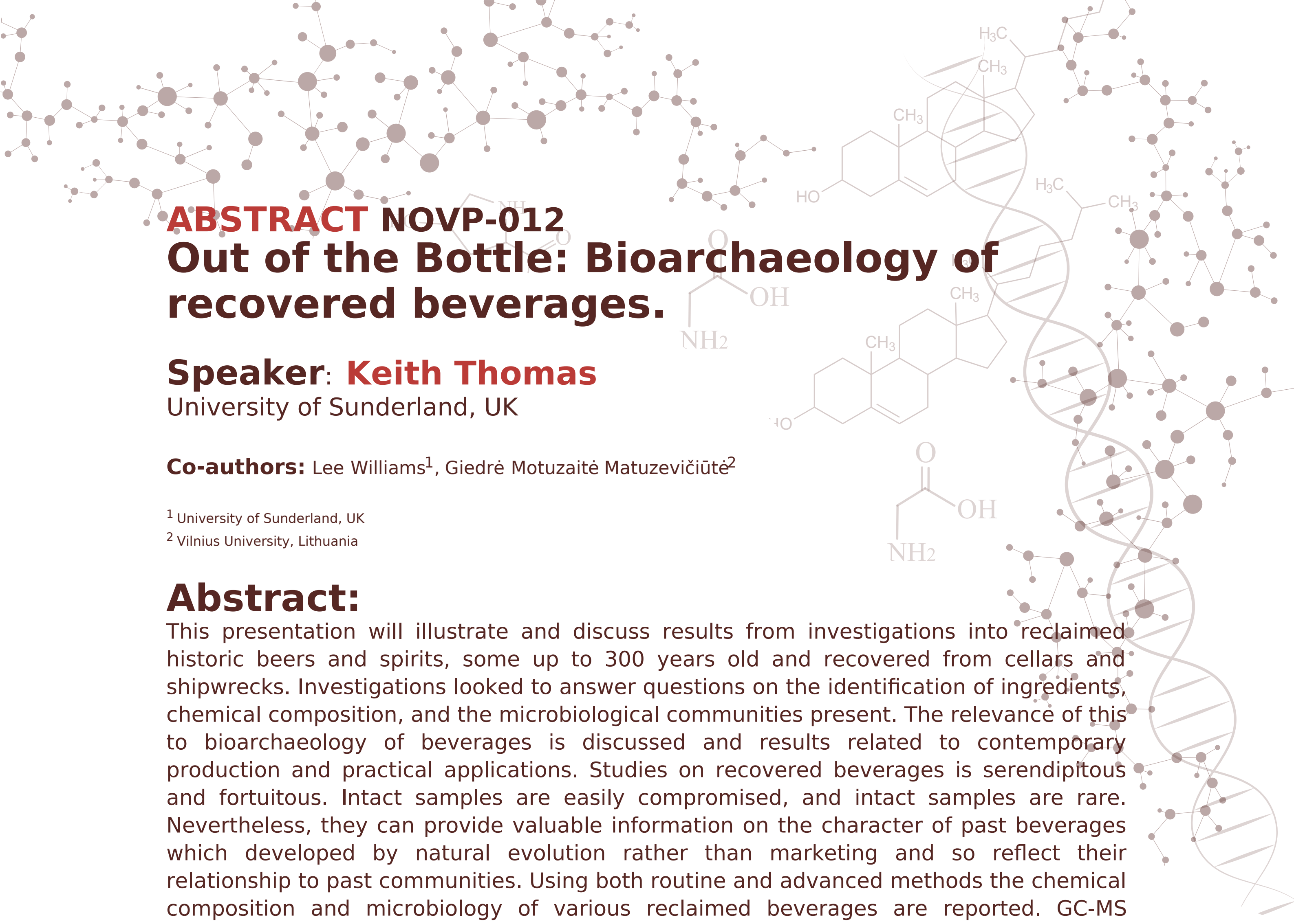
Co-authors: Jonas Niemann[1], Sarah Croix[2], Ainara Sistiaga[1], Hannes Schroeder[1]

[1] University of Copenhagen, Denmark

[2] Aarhus University, Denmark

Abstract:

The study of preserved faeces from archaeological contexts has a relatively long history, and has recently benefited from the advances in biomolecular approaches, but often single techniques in isolation. These ecofacts form a unique and singular depositional unit that have the potential to inform us at a very micro-scale about the individual's diet, microbiome, health, behaviour, and environment. Here we combine lipid analysis with shotgun metagenomics and proteomics on palaeofaeces recovered from occupation layers of the Northern Emporium site, Ribe, Denmark - the earliest urban community in Scandinavia. These different techniques can not only retrieve complementary types of information, but also provide parallel lines of evidence to yield more robust results. We discuss the possibilities and limitations of these three techniques, and how a combination provides more nuanced insights into past activities.



ABSTRACT NOVP-012

Out of the Bottle: Bioarchaeology of recovered beverages.

Speaker: **Keith Thomas**
University of Sunderland, UK

Co-authors: Lee Williams[1], Giedrė Motuzaitė Matuzevičiūtė[2]

[1] University of Sunderland, UK
[2] Vilnius University, Lithuania

Abstract:

This presentation will illustrate and discuss results from investigations into reclaimed historic beers and spirits, some up to 300 years old and recovered from cellars and shipwrecks. Investigations looked to answer questions on the identification of ingredients, chemical composition, and the microbiological communities present. The relevance of this to bioarchaeology of beverages is discussed and results related to contemporary production and practical applications. Studies on recovered beverages is serendipitous and fortuitous. Intact samples are easily compromised, and intact samples are rare. Nevertheless, they can provide valuable information on the character of past beverages which developed by natural evolution rather than marketing and so reflect their relationship to past communities. Using both routine and advanced methods the chemical composition and microbiology of various reclaimed beverages are reported. GC-MS provides a chemical listing and signature which can be compared to contemporary beverages and also to pure extracts of botanics. Metagenomic analysis of recovered aDNA allows a profiling of the microorganisms present. In a few cases surviving microorganisms may be recovered. These show promise in fermentation and biotechnology applications as they may reflect different characteristics to strains in culture collections and may have microbiome benefits. The presentation will focus on two investigations. In one, samples of beer from an 1895 shipwreck provided live cultures of yeast with unexpected identifications. Metagenomic analysis of the beer also indicated a range of bacteria while chemical analysis allowed a recipe to be recovered. A second investigation analysed samples of five 1730 spirits from a Lithuanian monastery cellar. Metabolomic profiling indicated differences of these to contemporary spirits but allowed identification of potential botanicals. The recovery of further samples is time sensitive as their deterioration progresses.

ABSTRACT NOVP-013

Collagen sequencing and peptide mass fingerprinting for the marine historical ecology of groupers (Epinephelidae) in the eastern Mediterranean.

Speaker: **Rachel Winter**
University of Groningen, Netherlands

Co-authors: Willemien de Kock[1], Meaghan Mackie[2,3,4], Max Ramsøe[2], Elena Desiderà[5], Matthew Collins[2,6], Paolo Guidetti[5], Alberto Taurozzi[2], Canan Çakirlar[1]

[1] University of Groningen, Netherlands
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[3] University College Dublin, Ireland
[4] University of Turin, Italy
[5] Stazione Zoologica Anton Dohrn, Italy
[6] University of Cambridge, UK

Abstract:

Groupers are large-bodied, solitary predatory fishes found globally in marine coral and rocky reef ecosystems. Within the Mediterranean Sea they are ecologically and commercially important, with high ubiquity in archaeological contexts. There are six species of groupers indigenous to the Mediterranean, with four species belonging to the Epinephelus genus. While the dusky grouper, Epinephelus marginatus, is the best studied and most emblematic species in the Mediterranean, data regarding species abundance and distribution prior to the commercialised fishing of the 20th century is largely unknown. In this study we have set out to test the viability of using Zooarchaeology by Mass Spectrometry (ZooMS) for intra-genus, species level identifications to inform the past biogeography of Mediterranean groupers. Using LC-MS/MS data, collagen type I amino acid sequences were reconstructed for four Epinephelus spp. and subsequently species-specific collagen peptide biomarkers were identified and validated. Our novel biomarkers were applied to a case study of Middle to Late Holocene grouper bones (n=23) from the archaeological site of Kinet Höyük located in the northeastern corner of Iskenderun Bay, Turkey. ZooMS analysis was combined with osteometrics to demonstrate that in the past the white grouper, Epinephelus aeneus, grew up to ca. 30 cm larger than previously documented. The successful application of ZooMS revealed a past abundance and dominance of this same species, E. aeneus, in Iskenderun Bay which is consistent with the current grouper species abundance in the region. Due to the small home ranges of groupers, this finding suggests millenia long, local population persistence of E. aeneus. This case study illustrates the potential for nuanced insight into the ecology and ecohistory of ichthyofauna that is possible with the species-level identifications provided by ZooMS.

ABSTRACT NOVP-014

The impact of taphonomy on post-translational modifications on the Middle Palaeolithic assemblages of Hohle Fels: a combined ZooMS and zooarchaeological study

Speaker: Fei Yang

University of Tübingen, Germany

Co-authors: Samantha Brown[1], Keiko Kitagawa[1], Britt Starkovitch[1], Nicholas Conard[1]

[1] University of Tübingen, Germany

Abstract:

Morphologically unidentifiable bone fragments have long played a role in zooarchaeological studies of breakage patterns, taphonomy, and site formation processes. Over the past decade, Zooarchaeology by Mass Spectrometry (ZooMS) has become an avenue to taxonomically identify these assemblages. In addition, ZooMS has been used to identify glutamine deamidation which occurs when the side chain of glutamine is converted into a carboxylic acid. It has been proposed that glutamine deamidation can be used to relatively date or identify intrusive collagenous material. However, additional factors that can affect the deamidation rate have been suggested, including different kinds of pre-depositional and depositional modifications (Welker, et al. STAR 2017; Brown, et al. J. Archaeol. Sci. 2021). We applied ZooMS to a Middle Palaeolithic fragmented bone assemblage from Hohle Fels, a UNESCO heritage site located in the Ach Valley of the Swabian Jura, SW Germany. We chose samples from a single excavation unit and across three consecutive layers in an attempt to identify any potential diachronic changes. For each sample, the deamidation rate was calculated and compared with their taphonomy and taxonomy. Our results shed new light on the ecology and subsistence of Neanderthals in the Ach Valley. Additionally, we highlight some of the challenges associated with studying glutamine deamidation through ZooMS data and explore its relationship with bone taphonomy.

ABSTRACT NOVP-015

A Complex Blend of West and East: An Organic Residue Analysis Study of Wine Manufacturing in Judea of the Early Roman Period

Speaker: **Tziona Ben-Gedalya**
Eastern R&D Center, Israel; Ariel University, Israel

Co-authors: Cynthianne Spiteri[1,2], Herodium Expedition[3]

[1] Università degli Studi di Torino, Italy
[2] Eberhard Karls University Tübingen, Germany
[3] Hebrew University of Jerusalem, Israel

Abstract:

The early Roman period winery discovered in 2017, in the fortress palace of King Herod at Herodium, provided the opportunity to systematically study organic remains of ancient winemaking. This study, which is a part of a wider interdisciplinary project, focuses on the results obtained after the application of organic residue and electron microscopy analyses. The Herodium is located on the margins of the Judean desert along the Dead Sea rift, within an earthquake prone region. The site combines well-defined archaeological evidence of a winery, the Judean desert climate, and contexts sealed by ancient episodes of collapse attributed to earthquakes. Hence, the Herodium winery is an excellent case study for optimising analytical techniques and exploring the preservation of ancient wine signatures in different substrates and archaeological artefacts. Wine production processes were studied by applying organic residue analysis to ceramic fermentation vessels and ancient grape pomace remains as well as control sediments. Using Gas Chromatography-Mass Spectrometry we observed well-preserved residues demonstrating evidence of wine and pine tar/resin, the latter probably used as a sealant as thick remnants were found adhering to the inner surfaces of the ceramic containers. Moreover, we further established a new approach to search for evidence of fermentation using scanning electron microscopy. We scanned the inner surface of the fermentation vessels and compared the patterns obtained with those observed in control vessels. Overall, our work contributes to discussions regarding the interpretation of wine in archaeological findings, enhances understanding of wine making traditions in the Mediterranean basin and informs on a culinary aspect of the vibrant Roman influenced glocalization processes in Judea at the end of the first century BCE.

ABSTRACT NOVP-017

Using a multi-pronged approach to the analysis of absorbed lipid residues to investigate chronological trends in pottery use from the Neolithic to the Iron Age in Saxony

Speaker: **Isabel Wiltshire**
University of Bristol, UK

Co-authors: Charlie Maule[1], Iman Abdelgani[1], Matthias Conrad[2], Matthias Halle[2], Isabel Hohle[3], Saskia Kretschmer[2], Germo Schmalfuß[2], Sabine Wolfram[4], Harald Stäuble[2], Melanie Roffet-Salque[1]

[1] University of Bristol,UK
[2] Landesamt für Archaeologie, Germany
[3] German Archaeological Institute, Germany
[4] Staatliches Museum für Archäologie, Germany

Abstract:

The analysis of lipids preserved in the clay pores of archaeological pottery is a powerful method for investigating pottery function and past diet. The use of state-of-the-art analytical methods allows for the identification and characterisation animal fats, plant oils and waxes that arise from the cooking of animal and plant products in ceramic vessels. Here we have employed a multi-pronged approach to the analysis of absorbed lipid residues including highly-sensitive tandem mass spectrometry for biomarker identification, both carbon and hydrogen isotopic analyses and compound-specific radiocarbon dating. Over 340 pottery fragments from 6 archaeological sites across Saxony were investigated spanning around four millennia of occupation, from the Early Neolithic (Linearbandkeramik) until the Iron Age. In a region where faunal remains are usually ill-preserved, lipid analyses of pottery sherds provide unique insight into the exploitation of wild and domesticated resources through time. Molecular and isotopic analyses of absorbed lipids show diachronic change in subsistence practices, herding strategies and pottery use, whilst freshwater resource exploitation is investigated through the targeted analysis of aquatic biomarkers, using a novel, highly-sensitive method. Furthermore, this study provides a stepping stone in the construction of regional climate records using hydrogen isotopic analyses from animal fats extracted from pottery and the direct 14C dating of pottery lipids.

ABSTRACT NOVP-018

Genomic exploration of private American diversity and its effect on ancient DNA analysis

Speaker: **Judith Ballesteros**
Max Planck Institute for Evolutionary Anthropology, Germany

Co-authors: Kathrin Nägele[1]

[1] Max Planck Institute for Evolutionary Anthropology, Germany

Abstract:

The lack of representation of genetic diversity is a topical fact and has consequences for genomics research. Especially when applying genomic methods to non-European ancestry population inferences such as risk predictions or population genetics, there are biased. This is particularly relevant for the case of the Americas. As a result of the population history, the overall genetic variation in American populations is lower compared to the worldwide variation. At the same time, most currently available arrays are accurate on worldwide populations but do not necessarily inform about the variation across the Americas, especially for ancient samples. Furthermore, recovering ancient endogenous DNA and enough analyzable markers can be challenging, and generally, researchers recover just around 1% of endogenous DNA. Population genetic analyses need several samples with enough informative markers, to reconstruct evolutionary history across populations. This study aims to understand the private genetic variation in ancient and present-day American individuals and assess how well this variation is represented in several widely used SNP arrays, specifically those designed for ancient DNA. Informed by this overview, the best strategy to add resolution to the human genetic history of the Americas can be discussed. References: Sirugo, et al. Cell 2019 Liu, et al. Cell 2022 Willerslev and Meltzer Nature 2021

ABSTRACT NOVP-019

An experimental approach: Exploring DNA preservation on archaeological ground stones

Speaker: **Alice Cao**
University of York, UK; University of Copenhagen, Denmark

Co-authors: Nathan Wales[1], Aimee Litlle[1], Tobias Richter[2], Mark Edmonds[1]

[1] University of York, UK
[2] University of Copenhagen, Denmark

Abstract:

Ground stone tools (GST) are abundant artefacts on many prehistoric archaeological sites, and evidence suggests prehistoric groups primarily used them to process plant tissues. In particular, phytoliths and starch grains are routinely sampled from GSTs. While the ubiquity of these microscopic plant structures on GSTs is well-established, it remains to be determined if other types of residues can be recovered from GSTs. The potential for genetic material to be embedded in the surface of GSTs is especially intriguing, as ancient DNA (aDNA) could provide a direct means for investigating GSTs usage and crop evolution in regions where archaeobotanical remains are only preserved by charring. Various sampling techniques (surface drilling, surface cleaning) and two extraction methods targeting DNA from plant tissues were tested on experimental replicas (e.g., handstones and slabs). DNA was successfully extracted and then analysed to test the efficiency of the methods. Archaeological samples were analysed from the Late Epipaleolithic and Early Neolithic at the Shubayqa 1 and 6 sites in Jordan. While the extraction of aDNA proved difficult on the Shubayqa materials, the experimental GSTs suggest that DNA can be preserved and extracted from ground stones. To further explore this hypothesis, GSTs from temperate regions (Ness of Brodgar in Scotland) from the Neolithic period are being investigated, leading to important insights on the range of conditions and periods which may be compatible with aDNA recovery from GSTs.

ABSTRACT NOVP-020

Complex analyses of ancient soil samples from burial context

Speaker: **Niall Cooke**
Max Planck Institute for Evolutionary Anthropology, Germany

Co-authors: Knut Rassmann[1], Jozef Bátora[2], Julia Gresky[1], Matthias Meyer[3], Benjamin Vernot[3]

[1] German Archaeological Institute, Germany
[2] Slovak Academy of Sciences, Slovak Republic
[3] Max Planck Institute for Evolutionary Anthropology, Germany

Abstract:

It has recently been demonstrated that ancient human nuclear DNA can be successfully retrieved directly from sediment samples. This breakthrough extends the possibility for ancient population genetic analyses to be conducted in regions or periods for which ancient materials (such as bones) are limited or unavailable for sampling. It also suggests that human DNA can be used to study not just the remains of deceased ancient individuals, but also used to trace their movement through the physical spaces in which they lived. To date, hominin nuclear DNA has only been successfully isolated and analysed from cave sediments, and used to investigate Paleolithic populations (Vernot, et al. Science 2021; Gelabert, et al. Cell 2021). However, most of human history has taken place outside of caves. Here, we present the first analysis of human nuclear DNA isolated from sediments from open-air Holocene settlements. Sediment samples were taken directly from house floors, or from alleyways between houses , at two early Bronze Age settlements in Slovakia, including the extensively studied and long-inhabited settlement of Vráble (Bátora et al. 2012). We find that these samples contain DNA from both humans and from domesticated species, with several samples containing sufficient human DNA to allow comparisons with skeletal data. We therefore additionally generated genome-wide data for eight individuals excavated from the cemetery at Vráble, and place the human DNA recovered from both sediments and bones into the wider context of ancient and present-day European variation. To investigate the relationships between the people who lived in the settlement with those buried in the cemetery, we performed direct comparisons of the sediment DNA to the excavated Vráble individuals. This study shows that ancient DNA derived from sediment samples can be used to study human history, and suggests that such an approach can facilitate an exploration of the living spaces of humans in Holocene settlements.

ABSTRACT NOVP-021

Potential use of bone-adhered soil as a novel source of host and environmental ancient DNA

Speaker: Toni de Dios

University of Tartu, Estonia

Co-authors: Jenna M. Dittmar[1], Sarah A. Inskip[2,3], John E. Robb[2], Christiana L. Scheib[2,4]

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[2] University of Cambridge, UK
[3] University of Leicester, UK
[4] University of Tartu, UK

Abstract:

In recent years sediments from cave environments have yielded inestimable data for the study of ancient hominids, but also for past fauna and flora reconstruction. Unfortunately, locations with favourable conditions for ancient DNA (aDNA) preservation in sediments are scarce. In this study we analysed a set of samples obtained from soil adhered to different human tissues and cavities originating from medieval sites in East Anglia, England. From them, we were able to recover aDNA sequences matching the genetic profile of the original individual. We also found genetic data corresponding to other animals, including members of the genus Canis, Ovis and Ascaris. Moreover, we have being able to retrieve the whole mitochondrial genome and a partial nuclear genome of a Black rat (Rattus rattus). Those sequences displayed damage typical of aDNA and when placed in a mitochondrial phylogeny, fell within other medieval Rattus rattus lineages. Our results demonstrate that material usually discarded, as it is soil adhered to human remains, could be used to get a glimpse of the environmental conditions at the time of the death of an individual.

ABSTRACT NOVP-022

Ancient human DNA from archaeological sediments: insights from sediments surrounding human bones and in settlements

Speaker: **Rikai Sawafuji**
University of Copenhagen, Denmark; The Graduate University for Advanced Studies (SOKENDAI), Japan

Co-authors: Ryohei Sawaura[1], Masaki Yokoo[2], Toshiaki Kumaki[3], Mikkel Winther Pedersen[4]

[1] Okinawa Prefectural Museum and Art Museum, Japan
[2] Yokoo, Uruma city board of education, Japan
[3] The University of Tokyo, Japan
[4] University of Copenhagen, Denmark

Abstract:

Ancient human bones degrade and disappear especially when buried in regions with acidic soils. Therefore, it remains challenging to obtain genetic information from past human populations in such regions. Over recent years, several studies have reported that hominin DNA including modern human can be recovered from cave sediments and calcites (Slon, et al. Science 2017; Sarhan, et al. Cell Press 2021; Vernot, et al. Science 2021). However, such caves are often located in karstic terrain and made of alkaline limestone and are not representative of all human populations. It is therefore fundamental to expand this research to study ancient human DNA from archaeological sediments in open-air sites. We, therefore, collected sediment samples surrounding two human burials from the Katsuren Castle in Okinawa, Japan, which dates from the 11-13th century CE as well as from the settlement Oshima 2 site in Hokkaido, Japan, dating from the 11-12th century CE. All samples were converted to Illumina libraries and subjec ted to target capture enrichment of human mitochondrial DNA. We found that ancient human mtDNA was obtained from sediments surrounding the burials, especially those close to rib bones, although rarely obtained in the sediment from the settlement site. Additionally, we show that the mitochondrial haplogroups obtained from the sediments were almost identical to that obtained from the human bones. Our results suggest that genetic information about past humans can be obtained directly from archaeological sediments in open-air sites, even in the absence of skeletal remains. Moreover, it can be a non-destructive alternative source of DNA to that obtained from bones and teeth. We also identified the optimal locations for obtaining ancient human DNA from burial sediment samples.

ABSTRACT NOVP-023

Ancient DNA from the Upper Paleolithic Mammoth Ivory of Hohle Fels, Germany

Speaker: **Kelsey Moreland**
University of Tübingen, Germany; Stockholm University, Sweden

Co-authors: Sibylle Wolf[1], Dorothée Drucker[1], Ella Reiter[1], Nicholas Conard[1], Cosimo Posth[1]

[1] University of Tübingen, Germany

Abstract:

Ivory is a material that has been highly valued by humans since the Upper Paleolithic. Hohle Fels, a cave in the Ach Valley of southwestern Germany, delivers an exceptionally rich and well-preserved Upper Paleolithic mammoth ivory assemblage, containing ivory artifacts such as some of the oldest known examples of human figurines and musical instruments. Despite its rich record, Hohle Fels ivory had never been screened for ancient DNA (aDNA) preservation before. Here, we genetically analyze 25 ivory pieces from Hohle Fels and successfully reconstruct twelve complete mitochondrial genomes (mtDNA). In our comparative analysis between dentin and cementum, cementum is revealed as the preferred sampling material for mammoth ivory for optimal, cost-effective aDNA retrieval. The inclusion of genetic sexing analyses also revealed that Upper Paleolithic humans collected tusks from both male and female mammoths for processing in Hohle Fels. Phylogenetic analysis of mammoth mtDNAs show ed that, despite the inclusion of ivory from three major archaeological cultures (Aurignacian [42–35 thousand years ago (kya)], Gravettian [35–28 kya], and Magdalenian [17–13 kya]), all sequences fell within the pre-Last Glacial Maximum (LGM) European mtDNA variation, contrasting previous work that showed a mtDNA clade shift in Europe during or right after the LGM (25–16 kya). However, direct radiocarbon dating on three Magdalenian layer specimens resulted in dates older than 30 kya, thus preceding the Magdalenian occupation. This prevented the testing of mtDNA replacement across the LGM at the site and provides further supporting evidence of erosion in the upper layers of Hohle Fels. Together, these results validate and optimize the use of Upper Paleolithic mammoth ivory as a source for a variety of biomolecular approaches, including mitochondrial and nuclear DNA analyses.

ABSTRACT NOVP-024

A Comparative Study of Taxonomic Assignment Methods for Palaeodietary Reconstruction using Shotgun Metagenomics

Speaker: **Aleksandra Laura Pach**
University of Copenhagen, Denmark

Co-authors: Jonas Niemann[1], Nicola Alexandra Vogel[2], Hannes Schroeder[1]

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[2] Technical University of Denmark, Denmark

Abstract:

Shotgun metagenomics has emerged as a powerful tool for palaeodietary reconstruction, allowing for the detection and characterization of eukaryotic organisms in archaeological samples such as ancient mastics and dental calculus. However, with the abundance of available software tools, it is crucial to evaluate their performance in accurately classifying eukaryotic reads. In this study, we assess the performance of different taxonomic classifiers for the classification of eukaryotic reads using both simulated metataxonomic ancient DNA data and experimental datasets from ancient mastics and dental calculus. We evaluated the overall performance in terms of false positive rates, true positive rates, the edit distance, evenness of coverage, last common ancestor calculations, ancient DNA damage detection as well as computational time and load. Finally, we highlight the potential of shotgun metagenomics for improving palaeodietary reconstruction through the identification of eukaryotic organisms in ancient samples.

ABSTRACT NOVP-027

Biochemical Preservation of Roman Leather Shoes

Speaker: **Gillian Taylor**
Teesside University, UK

Co-authors: C. Orr[1], R. Williams[1], H. H. Halldórsdóttir[1], E. Green[2]

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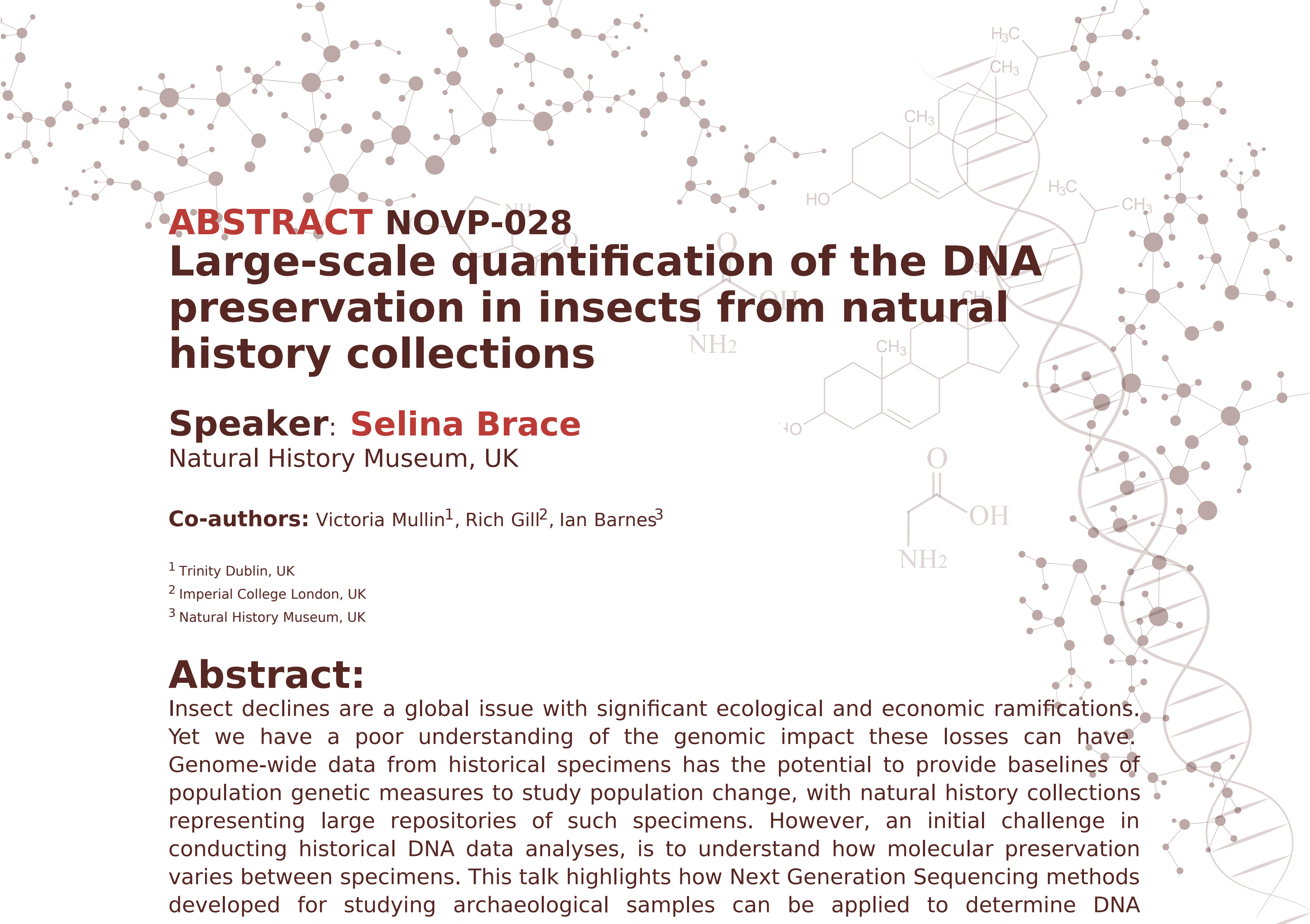
Abstract:

Leather is a versatile material, whose survival in archaeological contexts can yield valuable insight into past societies. Vegetable-tanned leather survives in wet soil environments common in Northern Europe and especially at the Roman Site of Vindolanda. Biochemical analysis, including FTIR-ATR, pXRF and MS analysis was applied to experimentally buried and archaeological leather. This poster summaries recent results obtained from FTIR-ATR, pXRF and MS analysis. Preliminary results indicate vegetable-tanning can impact on long-term preservation of leather in wet soil that could not be directly associated with the proportion of condensed to hydrolysable tannin, suggesting alternate paths of preservation processes. The results reflect a high degree of variability heterogeneity within the experimentally buried sample material.



ABSTRACT NOVP-028

Large-scale quantification of the DNA preservation in insects from natural history collections

Speaker: **Selina Brace**
Natural History Museum, UK

Co-authors: Victoria Mullin[1], Rich Gill[2], Ian Barnes[3]

[1] Trinity Dublin, UK
[2] Imperial College London, UK
[3] Natural History Museum, UK

Abstract:

Insect declines are a global issue with significant ecological and economic ramifications. Yet we have a poor understanding of the genomic impact these losses can have. Genome-wide data from historical specimens has the potential to provide baselines of population genetic measures to study population change, with natural history collections representing large repositories of such specimens. However, an initial challenge in conducting historical DNA data analyses, is to understand how molecular preservation varies between specimens. This talk highlights how Next Generation Sequencing methods developed for studying archaeological samples can be applied to determine DNA preservation from only a single leg taken from entomological museum specimens, some of which are more than a century old. The dataset includes 113 red-tailed bumblebee (Bombus lapidarius) specimens, from five British museum collections, to quantify DNA preservation over time. We find that the DNA from museum entomological specimens suggests a rapid and large-scale post-mortem reduction in DNA fragment size. However, after the initial decline, we find a relatively consistent rate of DNA decay in our dataset. This demonstrates that historical insects have significant potential to act as sources of DNA to create valuable genetic baselines. The relatively consistent rate of DNA degradation, both across collections and through time, mean that population level analyses - for conservation or evolutionary studies - are entirely feasible, as long as the degraded nature of DNA is accounted for.

ABSTRACT ODAP-001

Exploring class and time influence on the oral microbiome through ancient DNA analysis of Classical and post-Classical Italian populations

Speaker: **Martina Farese**
Sapienza University of Rome, Italy

Co-authors: Adrian Forsythe[1], Tom van der Valk[2,3], Laura Parducci[1,4], Mary Anne Tafuri[4], Katerina Guschanski[1,5,6]

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[2] Centre for Palaeogenetics, Sweden
[3] Swedish Museum of Natural History, Sweden
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[5] University of Edinburgh, UK
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Abstract:

This study investigates the similarities and differences among three Classical and post-Classical Italian cemeteries: Lucus Feroniae (I-III cent. CE), composed of locals, freemen and war veterans; Portus Romae (I-III cent. CE), composed of members of high and low social classes; Selvicciola (IV-VIII cent. CE) composed of members of lower social classes and, likely, Longobards. Previous palaeopathological and isotopic investigations performed on these populations showed similarities between Lucus Feroniae and Portus Romae, distinct from Selvicciola, which suffered an impoverishment in the diet and a worsening in living conditions. This study furthers our knowledge of these cemeteries through metagenomic analysis of dental calculus. Dental calculus is a calcified microbial deposit that accumulates on teeth. It undergoes periodic mineralisation, producing a fossil-like tissue protected from exogenous contamination. Ancient DNA (aDNA) extracted from dental calculus can be used to study the oral microbial community, the diet and the genomics of human remains. We collected and shotgun-sequenced 80 samples of dental calculus and soil, plus laboratory controls. Metagenomic analyses revealed a clear oral microbiome signature for the dental calculus samples, distinct from the soil. Differences in the oral microbial composition can be observed among the cemeteries, mainly between Selvicciola and the other two necropolises. However, Lucus Feroniae and Portus Romae also show near-significant differences from each other. Such differences may also be due to individual characteristics - e.g. pathologies, age and maternal lineage. Analyses of human reads preserved in dental calculus showed that most individuals were genetically similar to present-day Italians. These characteristics will be further explored by integrating various data types to provide a comprehensive picture of these individuals' lifestyles and health statuses and the changes prompted by the fall of the Roman Empire.

ABSTRACT ODAP-002

Proteomic analyses applied to consolidated prehistoric wooden artifacts: how to overcome perturbations by polyethylene glycol and acrylic resin ?

Speaker: **Ingrid Bertin**
Autonomous University of Barcelona, Spain

Co-authors: Deborah Roversi[1,2], Krista McGrath[3], Isabelle Théry-Parisot[2], André Carlo Colonese[3], Kirsty Penkman[1]

[1] University of York, UK
[2] University Côte d’Azur, France
[3] Autonomous University of Barcelona, Spain

Abstract:

Biomolecular analyses have mainly focused on organic residues found in inorganic material (ceramics, lithic tools) or animal remains (bone, teeth, leather, parchment, shell), but organic plant artefacts have been little studied. La Draga (Banyoles, Spain), dated to 5300-4900 cal BC, is one of the few Early Neolithic sites particularly rich in plant-based artefacts, with a great diversity of wooden objects (bowls, spoons, combs, sickles, handles, needles, agricultural tools, worked wooden sticks, arrows and weapons) and some elements made of plant fibres (basketry, rope). Many of these objects show various organic residues such as traces of hafting, food crusts, coatings or waterproofing, traces of use in the form of the presence of fibres (animal or vegetable) and black residues. Since their discovery between 1995 and 2012, restoration practices, consisting mainly of polyethylene glycol impregnation/imbibition and surface application of acrylic resin, have been applied to these artefacts, which has limited investigations of these external residues. Despite the application of several preservative removal tests prior to carbon-14 dating (Pinder, et al. Sci. Rep. 2017; Fedi, et al. Radiocarbon 2014; Brock, Radiocarbon et al. 2018), little is known about the survival of proteins after consolidate cleaning. Here we discuss the use of different consolidant removal methods on plant artefacts from La Draga. Consolidant removal was assessed using Fourier transform infrared spectroscopy (FT-IR), and amino acids racemisation analysis was carried out to assess amino acid preservation, while proteins were identified via shotgun proteomics. The results indicate that even with consolidation treatment and subsequent removal, amino acids are preserved within the plant material, potentially allowing for a better understanding of the substances applied, processed, stored within the plant artefacts, their manufacture and the resources management.

ABSTRACT ODAP-004

Combining biomolecular, osteological analysis and historical research for the characterization of a post-medieval monastic community in northern Italy

Speaker: **Sarah Sandron**
University of Turin, Italy

Co-authors: Cynthianne Spiteri[1], Alessandra Cinti[1], Emanuele Grotto Maffiotti[1], Alfredo Santovito[1], Dominique Scalarone[1], Meaghan Mackie[1,2,3], Alison Beach[4], Anita Radini[3], Beatrice Demarchi[1], Rosa Boano[1]

[1] University of Turin, Italy
[2] University of Copenhagen, Copenhagen, Denmark
[3] University College Dublin, Ireland
[4] University of St. Andrews, UK

Abstract:

In the framework of the project “From text to teeth: the case study of Santa Maria della Stella”, funded by the Royal Society of Edinburgh, we carried out micromorphological and biomolecular analysis of dental calculus from 13 ancient human skeletal remains in order to improve our knowledge of the daily lives of a post-medieval Cistercian community of nuns from Saluzzo (Piedmont, Italy). The presence of a wealth of archival documents related to this community make the S. Maria della Stella’s assemblage one of a kind: they provide a valuable record of the lifestyle of the nuns, who lived as a closed religious community, as well as of the food and beverages that were consumed in the 18th century. The micromorphological analysis of “micro-débris” of diverse origin (animal, plant, mineral) and lipid analysis of dental calculus, as well as the osteological assessment of the remains, yielded interesting information on the diet of the community, which was very poor (the nuns were required to fast very frequently) and yet contained a range of exotic products, from corn to chocolate. Furthermore, metaproteomics on dental calculus combined with a comprehensive palaeopathological assessment revealed the impact of cloistered life on women's health. From a methodological point of view, this study carried out on pre-modern human remains demonstrates that there is good correspondence between information obtained from archival sources and from bioarchaeological studies - therefore supporting the application of the latter to case studies where textual information is not available.

ABSTRACT ODAP-005

Biomolecular archaeology as a tool for reconstructing site biographies: the case of the 1980s rescue excavations at Chiomonte-La Maddalena, Western Alps

Speaker: **Alessia Monticone**
Università degli Studi Torino, Italy; Musei Reali di Torino, Italy

Co-authors: E. Panero[1], P. Petitti[1], R. Boano[2], C. Spiteri[2], A. Santovito[2], E. Cilli[3], D. Luiselli[3], I. Stefanini[2], E. Pessione[2], B. Demarchi[2]

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[3] Università di Bologna, Italy

Abstract:

Here we present the results of a multidisciplinary project from the site of Chiomonte-La Maddalena, a multi-period site in the Western Alps, near Turin, Italy. The area was excavated in the 1980s as a rescue excavation and the abundant anthropological, faunal and ceramic material has never been fully studied. Chiomonte-La Maddalena is the only Neolithic site which has been found in the Piedmontese Alps to date, and therefore represents a unique opportunity to investigate human-environment relationships in a marginal upland area. Research is currently ongoing to rescue the scant and scattered excavation documentation, and to reconstruct the complex stratigraphy. In the 2000s, a pilot morphological study was carried out on the more diagnostic macrofauna. We are complementing this with Zooarchaeology by Mass Spectrometry on the more fragmented faunal remains in the assemblage to identify resources utilised for subsistence. Results indicate that both wild and domesticated herbivores were being consumed and that fragmentary human remains were also present in the sample. The latter has been selected for radiocarbon dating. Targeted aDNA analyses will be carried out to clarify the phylogeny of some animal taxa. In parallel, lipid residues from Neolithic ceramic vessels are being extracted and characterised to identify subsistence patterns. Overall this study showcases the potential of biomolecular archaeology for reconstructing the biography of complex sites on the basis of data-poor legacy collections.

ABSTRACT ODAP-006

Human and language migration to the shores of the Gulf of Finland during the Iron Age - Finnic languages, tarand burial culture and climate anomalies.

Speaker: **Anne-Mai Ilumäe**
University of Tartu, Estonia

Co-authors: Jussi Moisio[1], Päivi Onkamo[1], Outi Vesakoski[1], Markku Oinonen[2]

[1] University of Turku, Finland
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Abstract:

The pre-Roman Iron Age brought a change in burial practises to the southern shores of the Gulf of Finland – the appearance of tarand (low fence) graves: burial sites surrounded by roughly rectangular stone fences built of boulders of varying sizes and re-deposited piles of bones suggesting some sort of ritual activities performed on site. Earliest tarand-graves belong to the coastal zones of northern and western Estonia, with later findings unearthed in central Estonia, northern Latvia, southwestern Finland, Ingria and the eastern part of Sweden. In Estonia and northern Latvia, tarand-type graves remained in use throughout the Roman Iron Age until ca 500 AD. Tarand-graves and specific types of archaeological items set apart territories north of the Väina River from the southern areas. The sharp cultural boundary could potentially manifest a linguistic and ethnic border that emerged during the Roman Iron Age between speakers of Finnic and Baltic languages (Lang 2007). In holistic and interdisciplinary study of human history, time is the invisible thread binding different scientific fields. Our research aims to examine the potential connection between tarand-graves and the arrival of Proto-Finnic to the northwestern Eurasia through a unified chronological enquiry. We produced a total of 9 new radiocarbon dates of bone collagen from Finnish and Ingrian tarand-graves and analysed them in conjunction with published radiocarbon dates from Estonian tarand-sites, time estimates of linguistic disintegration and climatic events. We formally test the chronological succession of events to explore the question whether the temporal period of early tarand-graves matches with the proposed diversification timeframe for western Uralic languages and with a timeline of climate anomalies of the late Holocene. References: Lang, V. (2007). Baltimaade pronksi- ja rauaaeg. Tartu: Tartu Ülikooli Kirjastus.

ABSTRACT ODAP-007

Assessing Biomolecular Degradation using a multi-omic approach

Speaker: **Jack Sharpen**
University of Manchester, UK

Co-authors: Byron Boggi[1], Konstantina Drosou[1]

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Abstract:

Biomolecule degradation has been a long-standing problem within ancient DNA (aDNA) and forensic science. Degradation accounts for fragmentation of the primary DNA, protein and lipid structure, which ultimately causes data loss in downstream processes. Although missing data is irreversible, understanding the mechanisms of degradation is key for authentication purposes but also the application of omics within forensic science. To address this, we developed a, multi-omic model to observe the process of degradation in real time and tested it on artificially degraded porcine skin and muscle tissues. These were subjected to varying post-mortem diagenetic conditions over a time point series, and key biomolecules were extracted over the course of thirty days, before identifying through mass spectrometry for metabolomes, lipidomes and proteomes, next generation sequencing for genomes and downstream bioinformatics. Taphonomic patterns were subsequently investigated by causal networks analysis and hypernetwork modelling. Omics data was successfully extracted and variations in degradation patterns corresponded with the time points. An increase in metabolites biomarkers is correlated with the degradation of larger organic compounds , including modified amino acid derivatives and nucleosides during earlier time points, whilst increased protein modifications within muscle tissue is linked with prolonged degradation. Genomic analysis and further hypernetwork building are in ongoing. The characterisation of biomolecular degradation between different biomolecules and their corresponding tissues provides the first comprehensive overview of the post-mortem multiome, and the techniques applied lays the foundations for novel forensic estimations in post-mortem intervals, assessing degradation rates within ancient artefacts and provides an open database platform of degraded biomolecules.

ABSTRACT ODAP-008

A Bayesian high-resolution osteo-biography of an unknown individual found in a Roman camp in Brno, Czech Republic

Speaker: **Carlo Cocozza**
Max Planck Institute of Geoanthropology, Germany; Università della Campania, Italy

Co-authors: Vera Klontza-Jaklova[1], Jan Jílek[1], Václav Kolařík[2], Christian Hamann[3], Ricardo Rodríguez-Varela[4], Anders Nils Götherström[4], Patrick Roberts[5], Carmine Lubritto[6], Ricardo Fernandes[1,5,7]

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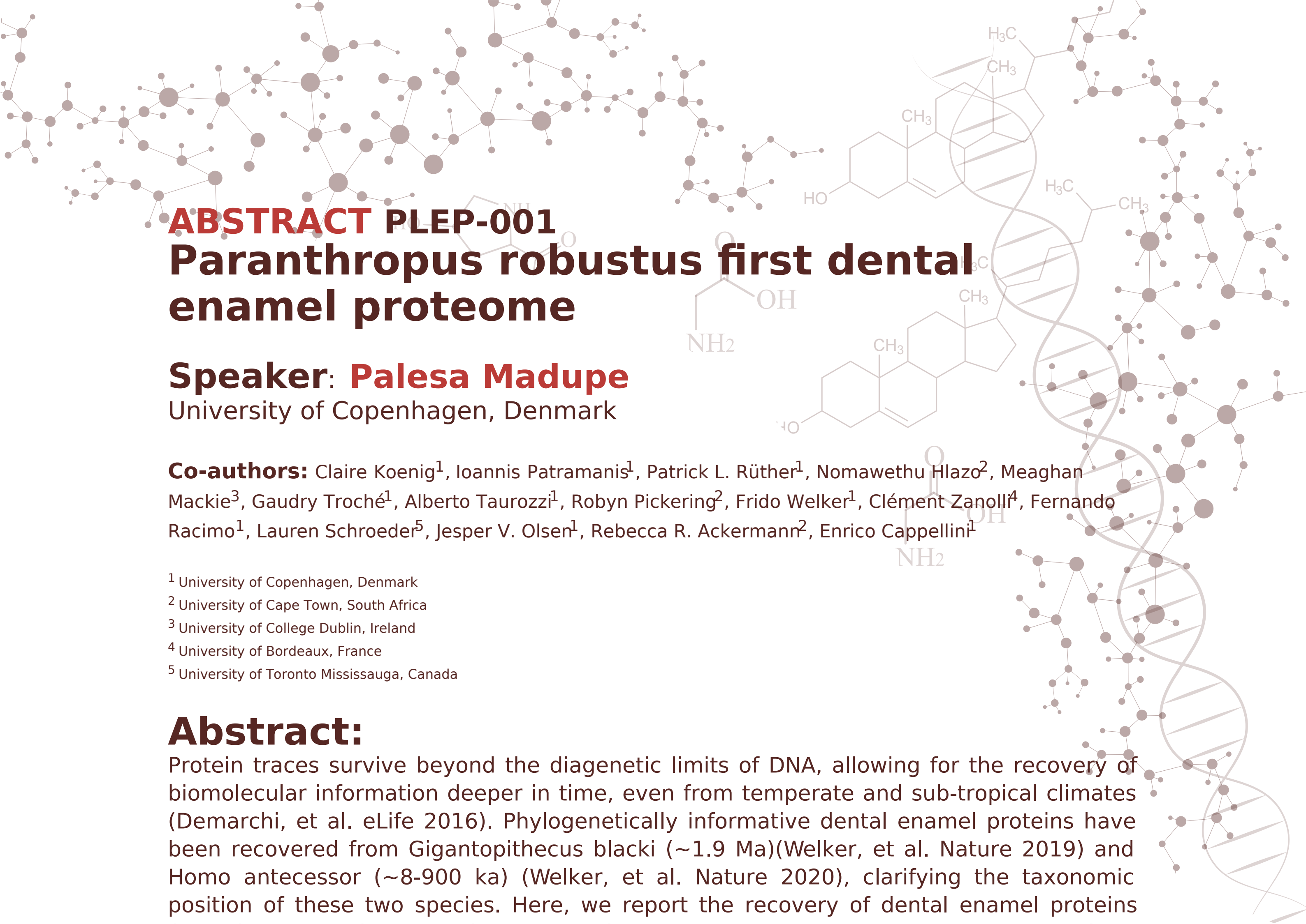
[4] Stockholm University, Sweden
[5] Max Planck Institute of Geoanthropology, Germany
[6] Università della Campania, Italy
[7] University of Princeton, USA

Abstract:

In our contribution we employ Bayesian modelling of multi-proxy data to reconstruct the osteo-biography of an individual buried in a Roman camp in Brno, Czech Republic. Skeletal material was subject to osteological analysis and sampled for stable isotope, radiocarbon dating, and aDNA measurements. Teeth were sectioned to reconstruct the diet and movements of the individual at a high temporal resolution. Osteological analysis indicates that the investigated individual was a circa 25 years old male and radiocarbon results date him to the late 2nd century CE. It is likely that he was somehow involved in the Marcomannic wars between Rome and Germanic tribes north of the Danube. According to aDNA results the individual had genomic affinity with modern-day populations from northern Greece and southern Balkans. Although oxygen stable isotope results are not consistent with an origin from these regions. Tooth isotopic data shows that the individual started the weaning process around six months of age and this was completed when he was approximately two. Overall, he had a diet that included a significant contribution from C4 protein throughout his life, although the predominant protein source was C3. Such a high consumption of C4 protein is typically observed for central European populations during the Migration Period. The obtained results illustrate the utility of generating high-resolution osteo-biographies in the study of past individuals.



ABSTRACT PLEP-001

Paranthropus robustus first dental enamel proteome

Speaker: **Palesa Madupe**
University of Copenhagen, Denmark

Co-authors: Claire Koenig[1], Ioannis Patramanis[1], Patrick L. Rüther[1], Nomawethu Hlazo[2], Meaghan Mackie[3], Gaudry Troché[1], Alberto Taurozzi[1], Robyn Pickering[2], Frido Welker[1], Clément Zanolli[4], Fernando Racimo[1], Lauren Schroeder[5], Jesper V. Olsen[1], Rebecca R. Ackermann[2], Enrico Cappellini[1]

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[3] University of College Dublin, Ireland
[4] University of Bordeaux, France
[5] University of Toronto Mississauga, Canada

Abstract:

Protein traces survive beyond the diagenetic limits of DNA, allowing for the recovery of biomolecular information deeper in time, even from temperate and sub-tropical climates (Demarchi, et al. eLife 2016). Phylogenetically informative dental enamel proteins have been recovered from Gigantopithecus blacki (~1.9 Ma)(Welker, et al. Nature 2019) and Homo antecessor (~8-900 ka) (Welker, et al. Nature 2020), clarifying the taxonomic position of these two species. Here, we report the recovery of dental enamel proteins from four Paranthropus robustus specimens (SK830, SK835, SK850, SK14132) from Swartkrans, South Africa, dated to 2.2-1.8 Ma. We employed a digestion-free extraction protocol and tandem mass spectrometry for peptide sequencing. We combined different data search strategies to reconstruct protein sequences from MS/MS spectra. Specimens SK835 and SK850 were identified as biological males through the confident identification of amelogenin Y (AMELY)-specific peptides. The ability to investigate biological sex opens the possibility of reassessing our understanding of sexual dimorphism in P. robustus and potentially in other early hominins. The reconstructed enamel protein sequences from P. robustus were compared to their orthologous ones from all extant and some extinct hominid taxa. The multi-sequence alignment enabled us to assess the variation within the hominid group and intra-species variation. Although the coverage breath of the ancient enamel proteome sequence recovered is limited, we identified potentially informative single amino acid polymorphisms, which enabled the tentative phylogenetic placement of P. robustus. Extending this work to other African hominin species will provide a better understanding of the variation within and between these taxa in Africa.

ABSTRACT PLEP-002

The high-coverage genome of a male Neandertal

Speaker: **Diyendo Massilani**
Yale University School of Medicine, USA

Co-authors: Stéphane Peyrégne[1], Cesare De Filippo[1], Leonardo N. M. Iasi[1], Alba Bossoms Mesa[1], Divyaratan Popli[1], Arev Pelin Sümer[1], Christian Heide[1], Yaniv Swiel[1], Maxim B. Kozlikin[2], Michael V. Shunkov[2], Anatoly P. Derevianko[2], Samantha Brown[3], Thomas Higham[4], Katerina Douka[4], Matthias Meyer[1], Hugo Zeberg[1], Benjamin M. Peter[1], Janet Kelso[1], Svante Pääbo[1]

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[3] University of Tübingen, Germany
[4] University of Vienna, Austria

Abstract:

To date only three high-coverage Neandertal genome sequences are available. Using collagen fingerprinting, we identified an undiagnostic bone fragment from Denisova Cave (Layer 12, East Chamber) in the Altai Mountains (Russia) as being of hominin origin. We named this individual Denisova 17. Sequencing of DNA libraries prepared from the specimen revealed that ~73% of the DNA fragments sequenced map to the human genome and that less than 1% of these fragments are present-day human DNA contamination. The exceptional ancient DNA preservation allowed the genome to be sequenced to 35-fold average genomic coverage. Analyses of the genome reveals that Denisova 17 belonged to a Neandertal male individual. This is the first male Neandertal from whom a genome has been sequenced to high coverage, providing the first insight into Neandertal Y chromosome structure. We estimated his age to be ~110,000 years before present based on the accumulation of nucleotide substitutions in his mitochondrial and nuclear genomes. This individual belonged to a population related to a ~120,000-year-old female individual from the same cave (Denisova 5 or Altai Neandertal) and is distinct from later Neandertals in the same region and in Western Eurasia. Similarly, to Denisova 5, the genome of Denisova 17 shows a high level of inbreeding, confirming that mating among close relatives was common among these early East Eurasian Neandertals. The availability of a fourth high-coverage Neandertal genome will allow genomic changes unique to Neandertals to be more reliably identified and allows us to describe additional haplotypes that were introgressed from Neandertals to present-day humans. Results of these analyses will be presented, including a haplotype unique to Denisova 17 that affects female reproductive physiology and was introgressed from Neandertals to present-day Asian populations.

ABSTRACT PLEP-003

New genetic and chronological data from the oldest Upper Paleolithic Burial in Poland

Speaker: **Elena Zavala**

Max Planck Institute for Evolutionary Anthropology, Germany; University of California,USA; San Francisco State University, USA

Co-authors: Helen Fewlass[1,2], Yoann Fagault[3], Thibaut Tuna[3], Edouard Bard[3], Jean-Jacques Hublin[1,4], Mateja Hajdinjak[1,2], Jarosław Wilczyński[5]

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Abstract:

Borsuka Cave is located in the Szklarka River valley in southern Poland. During the initial excavations between 2008 and 2010, six deciduous teeth were found along with 112 auroch and European Elk teeth pendants near the entrance of the cave. The human teeth were identified as belonging to a 12-18 month old child, but it was not possible to determine the child's sex. The layers above and below these pendants and teeth were archaeologically sterile and the only other artefact found within the layer was a distal fragment of a flint blade, precluding associating the assemblage to a specific culture. Two of the pendants were radiocarbon dated to 32,890 - 30,760 cal BP and 29,900–29,120 cal BP (95.4% probability) respectively1-3. While these dates indicate that this was an Upper Paleolithic burial, the exact date is still uncertain. In addition, as the human teeth and pendants were spread over several meters, there was still uncertainty as to their association. We attempted to clarify this association via new genetic and dating analysis. Ancient DNA was recovered from two of the child's teeth, indicating they were consistent with coming from the same individual and that the child was female. In addition, new radio carbon dates were generated from these teeth and six of the pendants. This new data allows us to discuss the potential cultural associations of the burial with other Upper Paleolithic humans from Central Europe. References: Wilczyński, et al. Eurasian Prehistory 2012a; Wilczyński, et al. International Journal of Osteoarchaeology 2016

ABSTRACT PLEP-004

Palaeogenomics of European hunter-gatherers across the LGM: insights from the Italian peninsula

Speaker: He Yu

Peking University, China

Co-authors: Cosimo Posth[1,2], Kathrin Nägele[2], Rita Radzeviciute[2,3], Martina Lari[4], Alessandra Modi[4], Stefania Vai[4], Tina Saupe[5], Christiana L. Scheib[5,6], Giulio Catalano[7], Luca Pagani[5,8], Sahra Talamo[1,9], Stefano Ricci[10,11], Annamaria Ronchitelli[10], Gregorio Oxilia[9], Eugenio Bortolini[12], Vitale Sparacello[13], Elisabetta Starnini[14], Luca Sineo[7], Francesco Boschin[10,11,15], Stefano Benazzi[9], Matteo Romandini[9,16,17], David Caramelli[4], Johannes Krause[1]

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[8] University of Padova, Italy
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[10] Università degli Studi di Siena, Italy
[11] Accademia dei Fisiocritici, Italy
[12] Institución Milá y Fontanals de Investigación en Humanidades, Spain
[13] Università Degli Studi di Cagliari, Italy
[14] Università di Pisa, Italy
[15] Centro Studi sul Quaternario ODV, Italy
[16] Pradis Cave Museum, Italy
[17] University of Ferrara, Italy

Abstract:

Modern humans populated the Italian peninsula for at least 45,000 years but our knowledge of the genetic relatedness and structure of Italian hunter-gatherers is still limited. During the Upper Paleolithic, the Italian peninsula was populated by hunter-gatherer populations associated with different archeological cultures such as the Gravettian (~33-26 ka) and the Epigravettian (~24-12 ka). In addition, this region has traditionally been considered a climatic refugium for human populations during the Last Glacial Maximum (LGM, ~25-19 ka), the coldest period of the last Ice Age. However, the level of genetic continuity between individuals before and after the LGM is not fully explored, nor is the population structure among Epigravettian-associated individuals. Here, we describe the genetic analyses of new genomic data from five hunter-gatherer individuals from present-day Italy - one associated with the Gravettian culture and four with the Epigravettian culture - and co-analyze them with other 351 European hunter-gatherer genomes. We reveal a genetic turnover from a Gravettian-associated ancestry, known as Věstonice, to an Epigravettian-associated ancestry, known as Villabruna, suggesting a local replacement of human groups across the LGM. Epigravettian-associated populations likely entered northeastern Italy from the Balkans. This was followed by a north-to-south expansion into the Italian peninsula alongside a population decline through sequential bottlenecks. Our findings challenge the role of the Italian peninsula as a climatic refugium for humans during the LGM, but also highlight the importance of further genomic studies on Upper Paleolithic individuals from still unsampled Italian regions.