8th INTERNATIONAL SYMPOSIUM ON BIOMOLECULAR ARCHAEOLOGY

18th–21st SEPTEMBER 2018

PROGRAMME

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Dear colleagues,

It is our pleasure to welcome you at the "8th International Symposium on Biomolecular Archaeology", which is taking place from 18th–21st September in Jena, Germany.

Jena is a lively city shaped by science. The University, founded in 1558, three Max Planck institutes, three Leibniz institutes, the Carl Zeiss Jena GmbH and many biotech companies with young and dynamic researchers provide an incredible impetus to the city.

The symposium brings together scientists from a multitude of disciplines in the field of Biomolecular Archaeology in order to have the opportunity to discuss their latest work on a multidisciplinary basis and to join their forces for applying state-of-the-art biomolecular techniques to archaeological research.

Various sessions cover diverse methodologies such as proteomics, genetics and analysis of other biomolecules or isotopes applied to a range of exciting topics covering for example human migrations and population genetics, diet and nutrition, domestication, adaptation and ecology or microbiomes and pathogens.

We look forward to sharing with you interesting, comprehensive and enjoyable days in Jena!

Sincerely yours,

Johannes Krause

Venue conference
Friedrich-Schiller-University of Jena
Auditorium maximum/lecture hall 24
Fürstengraben 1
07743 Jena, Germany

Conference website
www.isba8.de

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SCIENTIFIC PROGRAMME • TUESDAY, 18th SEPTEMBER

18:00–19:00	**Keynote lecture**
Room	Auditorium maximum (see p. 27)
18:00	Welcome to ISBA VIII and introduction of the keynote speaker Johannes Krause (Jena/DE)
18:10	Keynote lecture – What makes us human? Insights from Neandertal genomes Svante Pääbo (Leipzig/DE)
19:00–20:30	**Welcome reception**
Room	Auditorium maximum (see p. 27)

SCIENTIFIC PROGRAMME • WEDNESDAY, 19th SEPTEMBER

09:00–10:30	**Population structure and migration I**
Room	Auditorium maximum
Chair	Johannes Krause (Jena/DE)
09:00 O–PSM–01	The genetic history of the Iberian Peninsula over the last 8000 years Iñigo Olalde (Boston, MA/US)
09:15 O–PSM–02	Ancient DNA and the peopling of the British Isles – pattern and process of the Neolithic transition Selina Brace (London/GB)
09:30 O–PSM–03	Ancient genomes from the Lech Valley, Bavaria, suggest socially stratified households in the European Bronze Age Alissa Mittnik (Boston, MA/US)
09:45 O–PSM–04	Genomics of Middle Neolithic farmers at the fringe of Europe Federico Sanchez Quinto (Uppsala/SE)
10:00 O–PSM–05	Tracing the origin and expansion of the Turkic and Hunnic confederations Pavel Flegontov (Ostrava/CZ)
10:15 O–PSM–06	The Genomic Formation of South and Central Asia David Reich (Boston, MA/US)
11:00–12:30	**Paleoproteomics**
Room	Auditorium maximum
Chair	Jessica Hendy (Jena/DE)
11:00 O–PAL–01	Ancient proteins analysis of Pleistocene hyena fossils Huiyun Rao (Beijing/CN)
11:15 O–PAL–02	Palaeoproteomic analysis of early Pleistocene Gigantopithecus blacki Frido Welker (Copenhagen/DK)
11:30 O–PAL–03	Enamel proteome sequences from Dmanisi (Georgia) enable molecular phylogeny of fauna remains beyond the limits of ancient DNA preservation Enrico Cappellini (Copenhagen/DK)
11:45 O–PAL–04	Discovery of age related protein modifications Patrick Leopold Rüther (Copenhagen/DK)
12:00 O–PAL–05	The history of dairying in ancient Mongolia Shevan Wilkin (Jena/DE)

12:15 Direct proteomic evidence of early dairying at Çatalhöyük
O–PAL–06 Richard Hagan (Jena/DE)

14:00–15:30 Population structure and migration II
Room Auditorium maximum
Chair Choongwon Jeong (Jena/DE)

14:00 The first Epipaleolithic genome from Anatolia suggests a limited role of demic diffusion in the development
O–PSM–07 of farming in Anatolia
Michal Feldman (Jena/DE)

14:15 North African ancestry in Islamic Medieval Spain
O–PSM–08 Marina Silva (Huddersfield/GB)

14:30 The Neolithic transition in the Iberian Peninsula – reviewing an old question from new laboratory and
O–PSM–09 computational approaches
Gloria Gonzalez-Fortes (Ferrara/IT)

14:45 Genetic transition in the Swiss Late Neolithic and Early Bronze Age
O–PSM–10 Anja Furtwängler (Tübingen/DE)

15:00 Barbarian migration and social organisation in medieval Europe – a paleogenomic approach
O–PSM–11 C. Eduardo Guerra Amorim (Los Angeles, CA/US)

15:15 A 1400-year transect of ancient DNA reveals recent genetic changes in the Finnish population
O–PSM–12 Elina Salmela (Helsinki/FI)

14:00–15:30 Domestication I
Room Lecture hall 24
Chair Ludovic Orlando (Toulouse/FR)

14:00 Whole genome sequences in ancient bean seeds – new insights into the domestication history of common
O–DOM–01 bean (Phaseolus vulgaris) in South America
Martina Lari (Florence/IT)

14:15 The independent legacy of maize evolution in South America
O–DOM–02 Logan Kistler (Washington, D.C./US)

14:30 Modern and ancient DNA evidence for the origins and spread of broomcorn millet (Panicum miliaceum) from
O–DOM–03 China
Harriet Hunt (Cambridge/GB)

14:45 When chickens colonised Europe – dispersal routes, phenotypes and patterns of admixture based on ancient
O–DOM–04 and modern genomes
Ophélie Lebrasseur (Oxford/GB)

15:00 The arrival of domestic cats to the UK and Ireland – an ancient DNA study
O–DOM–05 Alex Jamieson (Oxford/GB)

15:15 Viking Age sheep in the North Atlantic
O–DOM–06 Albína Hulda Pálsdóttir (Reykjavik/IS)

16:00–17:30	**Population structure and migration III**
Room	Auditorium maximum
Chair	Stephan Schiffels (Jena/DE)
16:00 O–PSM–13	Demographic processes in the territory of Estonia from the earliest inhabitants to modern times Kristiina Tambets (Tartu/EE)
16:15 O–PSM–14	Gene geography of the Russian Far East populations – faces, genome-wide profiles, and Y-chromosomes Oleg Balanovsky (Moscow/RU)
16:30 O–PSM–15	Genomic insight into the Neolithic transition peopling of Northeast Asia Chao Ning (Jena/DE)
16:45 O–PSM–16	Genome wide ancient DNA from the enigmatic skeletons of Roopkund Lake reveal complex population history Eadaoin Harney (Boston, MA/US)
17:00 O–PSM–17	Ancient genomics reveals four prehistoric migration waves into Southeast Asia Hugh McColl (Copenhagen/DK)
17:15 O–PSM–18	Language continuity despite population replacement in Remote Oceania Kathrin Nägele (Jena/DE)
16:00–17:30	**Domestication II**
Room	Lecture hall 24
Chair	William Taylor (Jena/DE)
16:00 O–DOM–07	Ancient genomics and the evolutionary origins of dogs Greger Larson (Oxford/GB)
16:15 O–DOM–08	Friends in high places – an integrated examination of the long term relationship between humans and dogs in the Arctic Tatiana Feuerborn (Copenhagen/DK)
16:30 O–DOM–09	Cattle on the Western Atlantic edge of Europe – a time series of ancient cattle genomes through Ireland and Britain Victoria E. Mullin (London/GB)
16:45 O–DOM–10	Ancient genomics reveals patterns of gene flow and trait evolution in European domestic pigs Laurent Frantz (London/GB)
17:00 O–DOM–11	Tracking six millenia of horse selection, admixture and management with complete genome time series Ludovic Orlando (Toulouse/FR)
17:15 O–DOM–12	Selection trajectories of genetic variants underlying domestic animal traits Evan K. Irving-Pease (Oxford/GB)

09:00–10:30 **Plagues and pathogens**
Room Auditorium maximum
Chair Kirsten Bos (Jena/DE)

09:00
O–PAP–01 Epidemic decline in colonial Mesoamerica – molecular and computational approaches for identifying a possible pathogenic cause
Kirsten Bos (Jena/DE)

09:15
O–PAP–02 A 15th century louse-borne relapsing fever genome – virulence, immune evasion and evolution
Meriam Guellil (Oslo/NO)

09:30
O–PAP–03 3,800-year-old Yersinia pestis suggests Bronze Age origin for bubonic plague
Maria A. Spyrou (Jena/DE)

09:45
O–PAP–04 Public access to the population structure of bacterial pathogens in the genomics era
Mark Achtman (Coventry/GB)

10:00
O–PAP–05 Alternative scenarios for the origins of tuberculosis in the Pleistocene
David Minnikin (Birmingham/GB)

10:15
O–PAP–06 The significance of helminths in the UK over time
Hannah Ryan (Oxford/GB)

11:00–12:30 **Microbiomes**
Room Auditorium maximum
Chair Christina Warinner (Jena/DE)

11:00
O–MIB–01 The dental calculus metabolome in modern and historic samples
Irina Velsko (Central, SC/US)

11:15
O–MIB–02 Reconstruction of oral microbiomes from extinct and extant anthropoids through ancient DNA
James A. Fellows Yates (Jena/DE)

11:30
O–MIB–03 Exploring the microbial diversity of archaeological remains with high-throughput DNA sequencing
Clio Der Sarkissian (Toulouse/FR)

11:45
O–MIB–04 Profiles of microbial diversity and function within museum dental calculus samples extracted from wild great apes
Andrew Ozga (Tempe, AZ/US)

12:00
O–MIB–05 The individuality of disease – evidence from the oral metaproteome of medieval Danes
Liam Lanigan (Copenhagen/DK)

12:15
O–MIB–06 Consequences of European arrival on ancient Indigenous American microbiota
Laura Weyrich (Adelaide/AU)

14:00–15:30	**Microremains and residues**
Room	Auditorium maximum
Chair	Philipp Stockhammer (Jena/DE)
14:00 O–MAR–01	Identification of the residue in sphero-conical vessels reveals ancient explosives, oils, perfumes and medicines from Jerusalem Carney Matheson (Nathan/AU)
14:15 O–MAR–02	Molecular investigation of resin cargos found on two asian shipwrecks dated to the 12th century Julien Perthuison (Strasbourg/FR)
14:30 O–MAR–03	What's cooking? – investigating vessel-use and culinary practices in the Indus Civilisation through organic residue analysis Akshyeta Suryanarayan (Cambridge/GB)
14:45 O–MAR–04	Improving the analysis of liquid plant products absorbed in Mediterranean transport amphorae Léa Drieu (York/GB)
15:00 O–MAR–05	Investigating the nature and timing of the earliest human occupation of North America using a lipid biomarker approach Helen Whelton (Bristol/GB)
15:15 O–MAR–06	Multiple criteria for the detection of plant resources processed in hunter-gatherer pottery vessels from the Upper Volga, Russia Manon Bondetti (Groningen/NL)
14:00–15:30	**Advances in metagenomics**
Room	Lecture hall 24
Chair	Alexander Herbig (Jena/DE)
14:00 O–ADM–01	DNA from the Wine-Dark Sea – searching for DNA on ancient shipwrecks Lisa Briggs (Oxford/GB)
14:15 O–ADM–02	Revealing and understanding the marine palaeolandscape of the North Sea using sedaDNA Roselyn Ware (Coventry/GB)
14:30 O–ADM–03	Optimisation of efficient ancient DNA extraction from lake sediment Peter D. Heintzman (Tromsø/NO)
14:45 O–ADM–04	Deciphering ancient microbes with modern population genomic databases Nabil-Fareed Alikhan (Coventry/GB)
15:00 O–ADM–05	HOPS – a pipeline for screening archaeological remains for pathogen DNA Ron Huebler (Jena/DE)
15:15 O–ADM–06	Functional analysis of ancient metagenomic reads using genomic alignments Caner Bağcı (Tübingen/DE)

16:00–17:30	**Mobility**
Room	Auditorium maximum
Chair	Philipp Stockhammer (Jena/DE)
16:00 O–MOB–01	Estimating mobility using sparse data – application to human genetic variation Liisa Loog (Manchester/GB)
16:15 O–MOB–02	Early population history of the island of Crete in Greece – isotopic evidence for diet and mobility Argyro Nafplioti (Cambridge/GB)
16:30 O–MOB–03	Bronze Age population dynamics and the rise of dairy pastoralism on the eastern Eurasian Steppe Christina Warinner (Jena/DE)
16:45 O–MOB–04	The Steppe was sown – multi-isotopic research changes our understandings of Scythian diet and mobility Alicia R. Ventresca Miller (Jena/DE)
17:00 O–MOB–05	Isotope evidence of human migration and mobility at the Roman and Byzantine port city of Ephesus, Turkey Michael Richards (Vancouver/CA)
17:15 O–MOB–06	Testing the frequency of human colonisation of Rapa Nui (Easter Island) Kyriaki Anastasiadou (Oxford/GB)
16:00–17:30	**Pathogen genomics**
Room	Lecture hall 24
Chair	Alexander Herbig (Jena/DE)
16:00 O–PGE–01	Historic treponema pallidum genomes from Colonial Mexico Verena Schuenemann (Zurich/CH)
16:15 O–PGE–02	Neolithic and medieval virus genomes reveal the complex evolution of Hepatitis B Julian Susat (Kiel/DE)
16:30 O–PGE–03	A pathogen and a delicacy – the genomics of historic corn smut Nathan Wales (York/GB)
16:45 O–PGE–04	Zoonotic mycobacterium tuberculosis complex strains from geographically dispersed pre-contact South American human populations Åshild Vågene (Jena/DE)
17:00 O–PGE–05	Recovery of ancient oral pathogens by integrated analysis of serial dental calculus samples and modern genomes Sandra Bedarida (Coventry/GB)
17:15 O–PGE–06	Reconstruction of new ancient mycobacterium leprae genomes from Europe Saskia Pfrengle (Tübingen/DE)

09:00–10:30	**Genetic adaptation, evolution, ecology and extinction**
Room	Auditorium maximum
Chair	Choongwon Jeong (Jena/DE)
09:00 O–GAE–01	Gene diversity in archaic and present day humans David Reher (Leipzig/DE)
09:15 O–GAE–02	Using ancient genomes to explore the demography, behaviour and disappearance of the woolly mammoth Patrícia Pečnerová (Leipzig/DE)
09:30 O–GAE–03	Studying selection in “real-time” by genotyping HLA immune genes from ancient DNA Federica Pierini (Plön/DE)
09:45 O–GAE–04	Illuminating the role of selection in shaping human diversity Yassine Souilmi (Adelaide/AU)
10:00 O–GAE–05	Reconstructing the unique genetic history of the Japanese wolves Jonas Niemann (Copenhagen/DK)
10:15 O–GAE–06	Historical and modern rabbit populations reveal parallel adaptation to myxoma virus across two continents Joel Alves (Oxford/GB)
11:00–12:30	**Deep human population prehistory**
Room	Auditorium maximum
Chair	Cosimo Posth (Jena/DE)
11:00 O–DHP–01	Genome-wide data from a first-generation Neandertal/Denisovan offspring Viviane Slon (Leipzig/DE)
11:15 O–DHP–02	Modelling early human lineages in Africa Pontus Skoglund (London/GB)
11:30 O–DHP–03	Pleistocene North Africans show dual genetic ancestry from the ancient Near East and sub-Saharan Africa Marieke van de Loosdrecht (Jena/DE)
11:45 O–DHP–04	Genomic analysis of an early Homo sapiens from Europe increases complexity of early European demographic structure E. Andrew Bennett (Paris/FR)
12:00 O–DHP–05	The aboriginal heritage project and the modern human colonisation of Australia João Teixeira (Adelaide/AU)
12:15 O–DHP–06	Reconstructing the Deep Population History of Central and South America Cosimo Posth (Jena/DE)

14:00–15:30 **Diet and nutrition I**
Room Auditorium maximum
Chair Alicia R. Ventresca Miller (Jena/DE)

14:00 Reevaluating Neanderthal subsistence
O–DAN–01 Noreen Tuross (Cambridge, MA/US)

14:15 Isotopic evidence for high mammoth consumption by late Neandertals and early modern humans in Europe
O–DAN–02 and its possible ecological impact
Hervé Bocherens (Tübingen/DE)

14:30 Back to basics – introducing a model calculus system to test fundamental aspects of dental calculus research
O–DAN–03 Bjørn Peare Bartholdy (Leiden/NL)

14:45 Isotopic variation in Foxtail millet (Setaria Italica) with variety and watering regime
O–DAN–04 Emma Lightfoot (Cambridge/GB)

15:00 From birth to toddling – changes in diet revealed by the novel use of hydrogen isotopes (δ2H) in combination
O–DAN–05 with other stable isotopes (δ18O, δ13C, δ15N) of tooth dentin
Saskia E. Ryan (Cambridge, MA/US)

15:15 Food for thought – concentration dependent isotopic mixing models applied to data from early Neolithic
O–DAN–06 Turkey and Greece
Sidney Sebald (Martinsried/DE)

14:00–15:30 **Analytical methods in population genetics**
Room Lecture hall 24
Chair Wolfgang Haak (Jena/DE)

14:00 Joint estimates of heterozygosity and runs of homozygosity for modern and ancient samples
O–AMG–01 Gabriel Renaud (Copenhagen/DK)

14:15 The impact of reference bias on ancient DNA studies of prehistoric human populations
O–AMG–02 Torsten Günther (Uppsala/SE)

14:30 Estimation of ancient nuclear DNA contamination using breakdown of linkage disequilbrium
O–AMG–03 Nathan Nakatsuka (Boston, MA/US)

14:45 Inferring the selection history of Europe over the last 10,000 years using a novel statistical approach
O–AMG–04 Louise Ormond (London/GB)

15:00 MitoBench & MitoDB – novel interactive methods for population genetics of human mitochondrial DNA
O–AMG–05 Judith Neukamm (Zurich/CH)

15:15 DeamMeth, a full probabilistic model for reconstructing ancient methylomes
O–AMG–06 Kristian Hanghøj (Toulouse/FR)

16:00–17:30	**Diet and nutrition II**
Room	Auditorium maximum
Chair	Alicia R. Ventresca Miller (Jena/DE)
16:00 O–DAN–07	Investigation of Neolithic cattle diet and landscape by intra-tooth amino acid δ15N analysis Iain Kendall (Bristol/GB)
16:15 O–DAN–08	Farming vs. herding – subsistence economy during the late Neolithic evidenced by stable carbon and nitrogen isotopes in Northern Shaanxi Province, China Xianglong Chen (Beijing/CN)
16:30 O–DAN–09	The diversity in C4 crop consumption across Kazakhstan during the Bronze and Iron Ages based on stable isotope analysis of human and animal collagen Elina Ananyevskaya (Vilnius/LT)
16:45 O–DAN–10	A new approach to trace cereal agriculture based on absorbed lipid residues in archaeological pottery Simon Hammann (Bristol/GB)
17:00 O–DAN–11	Inverstigating Early Celtic consumption practices using organic residue analyses on local and imported pottery Cynthianne Spiteri (Tübingen/DE)
17:15 O–DAN–12	Gender-specific food consumption in conversion period inhumation cemetery at Kukruse, NE-Estonia Ester Oras (Tartu/EE)
16:00–17:30	**Archaeology of the invisible**
Room	Lecture hall 24
Chair	Christina Warinner (Jena/DE)
16:00 O–AOI–01	Ancient DNA in sediment – a micromorphology approach Diyendo Massilani (Leipzig/DE)
16:15 O–AOI–02	Exploring the genomic impact of colonization in North-Eastern Siberia Andaine Seguin-Orlando (Toulouse/FR)
16:30 O–AOI–03	Cracked it! – dati ng potsherds using compound-specifi c radiocarbon analysis of adsorbed lipids Emmanuelle Casanova (Bristol/GB)
16:45 O–GAE–07	Discovering the legacy of Atlantic cod exploitation using ancient DNA Giada Ferrari (Oslo/NO)
17:00 O–GAE–08	Ancient RNA – long-term survival and tissue specificity in permafrost tissues of Pleistocene animals Oliver Smith (Copenhagen/DK)
17:15 O–GAE–09	Characterisation of extinct bison methylomes using bisulphite sequencing Bastien Llamas (Adelaide/AU)
17:45–18:00	**Poster prizes and announcement of ISBA9**
Room	Auditorium maximum Johannes Krause (Jena/DE)
19:00–23:00	**Conference dinner**
Room	Ratszeise (see p. 27)

Population structure and migration

P–001 Migration and social organisation studies through ancient genomic analysis of multi-faith populations from medieval Sicily (ERC Project "Sicily in Transition", SICTRANSIT)
Aurore Monnereau (York/GB)

P–002 Kinship relationships and genomic origins of the peoples buried in an early medieval cemetery in central Europe
David Díez del Molino (Stockholm/SE)

P–003 Ancient genomes from Iceland reveal the making of a human population
Sigridur Sunna Ebenesersdottir (Reykjavik/IS)

P–004 Ancient genome-wide analysis of the early Neolithic mass grave individuals from Talheim, Germany
Lena Granehäll (Bolzano/IT)

P–005 The lady from Barfüsser Church – identity reconstruction of a mummy through the mtDNA of living relatives
Christina Wurst (Bolzano/IT)

P–006 Why were 17 people buried in a well in 12th century Norwich? – genome-wide analysis of medieval human remains from Chapelfield, Norwich, UK
Tom Booth (London/GB)

P–007 Ancient DNA from Misión Salesiana, Tierra del Fuego
Anne Stone (Tempe, AZ/US)

P–008 A new targeted enrichment method, "BAC-double capture," for ancient DNA analysis
Kae Koganebuchi (Nishihara, Okinawa/JP)

P–009 Reconstructing the demographic history of dingoes using ancient genomic data
Shing Yan Kwong (Adelaide/AU)

P–010 Maternal genetic origin of the Avar period (7th century) nomadic elite in the Carpathian Basin
Anna Szécsényi-Nagy (Budapest/HU)

P–011 First genetic data from the Holocene "Green Sahara" – new insights into the human mitochondrial phylogeny
Stefania Vai (Florence/IT)

P–012 Genetic continuity in the western Eurasian Steppe broken not due to Scythian dominance, but rather at the transition to the Chernyakhov culture (Ostrogoths)
Mari Järve (Tartu/EE)

P–013 Indian genetic heritage in Southeast Asian populations
Piya Changmai (Ostrava/CZ)

P–014 Genetic identity and relatedness of pre-Dogon and early Dogon populations (Mali)
Nonhlanhla Dlamini-Stoll (Geneva/CH)

P–015 How spread of agriculture and historic trade have affected the genetic diversity of emmer wheat landraces
Liisa Loog (Manchester/GB)

P–016 Population structure and population history of the ancient Chachapoya from northeast Peru
Evelyn Guevara (Helsinki/FI)

P–017 Genome-wide data describe Siberian ancestry in ancient Fennoscandia
Kerttu Majander (Jena/DE)

P–018 New chronology for Late Upper Palaeolithic sites in Belgium
Jennifer A. Tripp (London/GB)

Paleoproteomics

P–019 Proteomic evidence of dairy consumption in Neolithic Sudan
Madeleine Bleasdale (Jena/DE)

P–020 New insights into British Neolithic milk consumption
Sophy Charlton (London/GB)

P–021 Fossil Collagen – still not easy to get it pure – Is MIP the solution?
Hartwig Elster (Bremen/DE)

P–022 Using proteomics to understand the conservation history of a painting
Meaghan Mackie (Copenhagen/DK)

P–023 Bottom up and top down proteomics applied to tempera paints – focus on chemical modifications and crosslinking
Francesca Galluzzi (Villeneuve d'Ascq cedex/FR)

P–024 Understanding the craft of Parchment production using Proteomics
Carla Soto Quintana (Heslington, York/GB)

P–025 Components of human Palaeolithic diet identified using proteomic analysis of dental calculus from Southern Italy
Gabriele Scorrano (Copenhagen/DK)

Domestication

P–026 Early holocene dispersal of Near Eastern domesticates into high mountain Central Asia – Zooarchaeology by Mass Spectrometry (ZooMS) analysis of archaeofaunal remains from Obishir V, Kyrgyzstan
William Taylor (Jena/DE)

P–027 Bronze Age meat industry – ancient mitochondrial DNA analyses of pig (Sus scrofa) bones from the prehistoric salt mines of Hallstatt (Austria)
Sabine Hammer (Vienna/AT)

P–028 Ancient DNA and archaeology as tools for understanding the domestication of South American camelids
Paloma Fernández Díaz-Maroto (Copenhagen/DK)

P–029 Unveiling early horse domestication and mule production with ancient genome-scale data
Antoine Fages (Toulouse/FR)

Plagues and pathogens

P–030 Molecular screening for historical diseases in Mechelen, Belgium
Karen Giffin (Jena/DE)

P–031 Screen pathogens from ancient remains and reconstruct the Phylogenetic history of ancient pathogens
Xiyan Wu (Changchun/CN)

P–032 Molecular archaeoparasitology as a novel archaeological tool
Patrik Flammer (Oxford/GB)

P–033 Revisiting the evolutionary history of Yersinia pestis during the second pandemic
Amine Namouchi (Oslo/NO)

P–034 Search for *plasmodium spp*. in ancient Sardinian populations
Megan Michel (Cambridge, MA/US)

Microbiomes

P–035 Clinical metagenomics applied to the Iceman and other mummified human remains
Frank Maixner (Bolzano/IT)

P–036 A complete metagenomic analysis from a single mummy to assess microbiome differences in distinct body parts
Enrique Rayo (Zurich/CH)

P–037 The microbiome and isotopic fractionation
Noreen Tuross (Cambridge, MA/US)

P–038 The application of historic dental calculus for reconstructing killer whale ecotypes
Courtney Hofman (Norman, OK/US)

Microremains and residues

P–042 A multiomic approach to stone tool residues
Carney Matheson (Nathan/AU)

Advances in metagenomics

P–044 Using sedaDNA from North Sea sediment cores to reconstruct the early Holocene palaeoenvironment
Becky Cribdon (Coventry/GB)

Mobility

P–045 A new bioavailable strontium isoscape for Northwest Europe – using machine learning approaches
Jason Laffoon (Leiden/NL)

P–046 Analytical review of oxygen isotope analyses for sourcing human and animal skeletal remains
Maura Pellegrini (Pistoia/IT)

P–047 Ancient DNA and isotopic analysis of archaeological remains from Guam
M. George B. Foody (Huddersfield/GB)

Pathogen genomics

P–048 Investigating ancient syphilis – macroscopic suspicions and molecular detection of Treponema pallidum subspecies pallidum in 150-year-old foetal remains, Marseille, France
Avril Meffray (Aix-en-Provence/FR)

P–049 Analysis of a 17th century Mycobacterium tuberculosis genome from Lund, Sweden extracted from a lung nodule
Susanna Sabin (Jena/DE)

P–050 An automated pipeline for detection and characterisation of recombination patterns in bacterial genomes
Aditya Kumar Lankapalli (Jena/DE)

Genetic adaptation, evolution, ecology and extinction

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Jiao Ma (Beijing/CN)

P–052 An aukward tale of extinction – the demise of the great auk
Michael Knapp (Dunedin/NZ)

P–053 Time-dependent molecular evolution in ancient DNA
Audrey Lin (Oxford/GB)

P–054 Reconstructing local palaeoseasonality and palaeoclimate at Middle Palaeolithic sites in Western Europe: sampling, data handling, and temperature conversion in oxygen isotope seasonality models
Sarah Pederzani (Leipzig/DE)

P–055 An epistatic effect of Asian-specific nonsynonymous variants of ABCC11 and EDAR on the amount of facial bacteria
Ryosuke Kimura (Nishihara, Okinawa/JP)

P–056 Phenotypic inference based on ancient DNA of Iron Age individuals from Luistari in Southern Finland
Ambra D'Aurelio (Rome/IT)

P–057 Caving for ancient DNA – looking for human impact on the environment
Anna Linderholm (College Station, TX/US)

P–058 The genetic makeup of enslaved Africans from early Colonial Mexico City
Rodrigo Barquera (Jena/DE)

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Ainash Childebayeva (Ann Arbor, MI/US)

P–061 Giant deer (Megaloceros giganteus) phylogeography and population dynamics – insights from Late Quaternary mitogenomes from Eurasia
Alba Rey de la Iglesia (Copenhagen/DK)

P–062 Ancient genomics of the Baltic harp seal
Maiken Hemme Bro-Jørgensen (Stockholm/SE)

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Alan Rogers (Salt Lake City, UT/US)

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Mateja Hajdinjak (Leipzig/DE)

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Andrea Göhring (Munich/DE)

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Jack Dury (Stockholm/SE)

P–067 Diet and population mobility in the early medieval Alpine area (Italy)
Valentina Coia (Bolzano/IT)

P–068 Dental microwear analysis and diets of Yanghai ancient population in Xinjiang, China
Xuezhu Liao (Changchun/CN)

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Nicolas Bourgon (Leipzig/DE)

P–070 Tabula rasa – a new look at light stable isotopes in archaeological contexts
Linda M. Reynard (Cambridge, MA/US)

P–071 A compound specific isotope approach to breastfeeding and weaning in archaeological populations
Alison Harris (York/GB)

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Samantha Leggett (Cambridge/GB)

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Pablo Librado (Toulouse/FR)

P–074 A stainless-steel mortar, pestle and sleeve design for the efficient fragmentation of ancient bone
Bastiaan Star (Oslo/NO)

P–075 MUSIAL – MUlti Sample varIant AnaLysis
Kay Nieselt (Tübingen/DE)

Archaeology of the invisible

P–076 Crop δ15N values – A tool for reconstructing past soil fertility?
Amy Styring (Frankfurt a. M./DE)

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Zandra Fagernäs (Jena/DE)

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Christiana Scheib (Tartu/EE)

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Zdravka Hincak Daris (Zagreb/HR)

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Tibor Török (Szeged/HU)

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Sanni Översti (Helsinki/FI)

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Maria Lundström (Linköping/SE)

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Valentina Coia (Bolzano/IT)

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Ashleigh Simpson (Durham/GB)

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Natalia Przelomska (Washington, D.C./US)

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Frederik Seersholm (Bentley/AU)

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Ashot Margaryan (Copenhagen/DK)

P–141 Punctuated evolution of the genus homo – evidence from mtDNA pseudogenes
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Konstantin Khrapko (Newton, MA/US)

Deep human population prehistory

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Edvard Ehler (Prague/CZ)

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Archaeology of the invisible

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P–161 Exploring biomolecules of Lobor (Croatia)
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P–162 Improving radiocarbon dating by pedigree-based Bayesian modeling
Ronny Friedrich (Mannheim/DE)

P–163 The comparison of DNA preservation across multiple skeletal elements from individuals recovered from the abandonded medieval graveyard of Krakauer Berg, Germany
Cody Parker (Jena/DE)

GENERAL HINTS FOR AUTHORS AND PRESENTERS

Poster session
All poster sessions will take place on the ground and first floors of the conference venue. The poster session for the posters P–001 to P–082 is taking place on Wednesday, 19th September, 17:30–19:00. The poster session for the posters P–083 to P–163 is taking place on Thursday, 20th September, 17:30–19:00. Authors are requested to be present at their posters during the poster session.

The pinboards will be numbered and should be used only with the designated pins. You will find your poster number and presentation group in the programme book on page 15–25.

Please note that the posters of the first group should be hanging on Wednesday, 19th September, by 14:00 and be removed at the latest by Thursday, 20th September, 11:00. Posters of the second group should be hanging on Thursday, 20th September, 14:00 and be removed until Friday, 21th September, 14:00. Posters that have not been removed by that time will be considered as waste.

Poster prize
The two best posters will be awarded with 250 EUR each.

Publication of abstracts
All abstracts of oral presentations and posters are published in the online version of this programme book, which can be found under www.isba8.de.

Submission of a presentation/technical information
The presentation should be prepared as PDF, MS Office PowerPoint for Windows or Keynote for Macintosh DVD in format 4:3. A presentation notebook with a PDF reader and MS Office PowerPoint 2016 will be provided. The use of personal notebooks is possible upon prior arrangement. However, it may interrupt the flow of the programme in the lecture hall. The date projector works with a VGA input. Please provide an adapter if necessary.

Presentation upload
It is possible to upload your presentation directly in the lecture hall. For submission, please use a USB flash drive, CD or DVD disc that is not protected by any software. Professional staff and equipment will be available for you to arrange and preview your presentation.
To guarantee a smooth running programme please upload your presentation in advance, at least 2 hours before your presentation is due to start.

Time allocation
Please prepare your presentation for the allotted amount of time. Chairs and moderators may interrupt should you overrun your time limit. The allotted time for all single session and parallel session talks is set with twelve minutes of speaking and three minutes discussion time.

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PLOS GENETICS

State: August 2018

Keynote lecture and welcome reception

We kindly invite you to get in touch with your colleagues and enjoy a pleasant evening with a few snacks and drinks. This year's keynote lecture is all about being human. It is a great pleasure for us to win one of the leading thinkers and co-founders of paleogenetics for our event. Together with Svante Pääbo we will examine the topic in detail, before we end the day in a relaxed atmosphere.

Date	Tuesday, 18th September
Time	18:00
Venue	Friedrich-Schiller-University of Jena Auditorium maximum Fürstengraben 1 07743 Jena, Germany
Costs	included in the conference fee
Speaker	Svante Pääbo (Leipzig/DE)
Talk	What makes us human? – insights from Neandertal genomes

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Conference dinner

Located directly on the market square below the town hall, the "Ratszeise" combines Thuringian cordiality with the culinary delights of regional and international cuisine. Enjoy the last evening of the conference with your colleagues, the cozy ambience invites you to linger.

Date	Friday, 21st September
Time	19:00
Venue	Ratszeise Markt 1 07743 Jena, Germany
Costs	45 EUR per person*

* Limited places. Registration is required.

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Registration fees

Conference registration	215 EUR *
Conference dinner	45 EUR **

* incl. welcome reception and keynote lecture at the "Friedrich-Schiller-University", 18th September 2018

** Limited places. Registration is required

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Opening hours	**Tuesday**	**Wednesday**	**Thursday**	**Friday**
Check-in	17:00–19:30	08:30–17:30	08:45–17:30	08:45–17:30
Poster exhibition	not open	08:30–19:00	08:30–19:00	08:30–14:00

Internet/WIFI access

In addition to Eduroam, a special conference WIFI is available free of charge throughout the whole conference area. Please ask at the check-in desk for the login data.

Certificate of attendance

Certificates of attendance will be made available on the last day of the conference at the check-in desk.

Name badge

Please wear your name badge during all conference events, including the networking activities. Admission to scientific sessions and to the poster exhibition is restricted to participants wearing their badge. Participants will receive their name badge when collecting their conference documents at the check-in desk.

Cloakroom

The coat and luggage room at the conference is situated directly in the lecture hall and is provided free of charge. However, it is unattended and the conference organisation cannot accept any liability for damage or loss to personal items.

Smoking

Smoking is prohibited inside the entire conference venue.

Catering

Foods and drinks will be provided during the breaks at the foyer of the venue.

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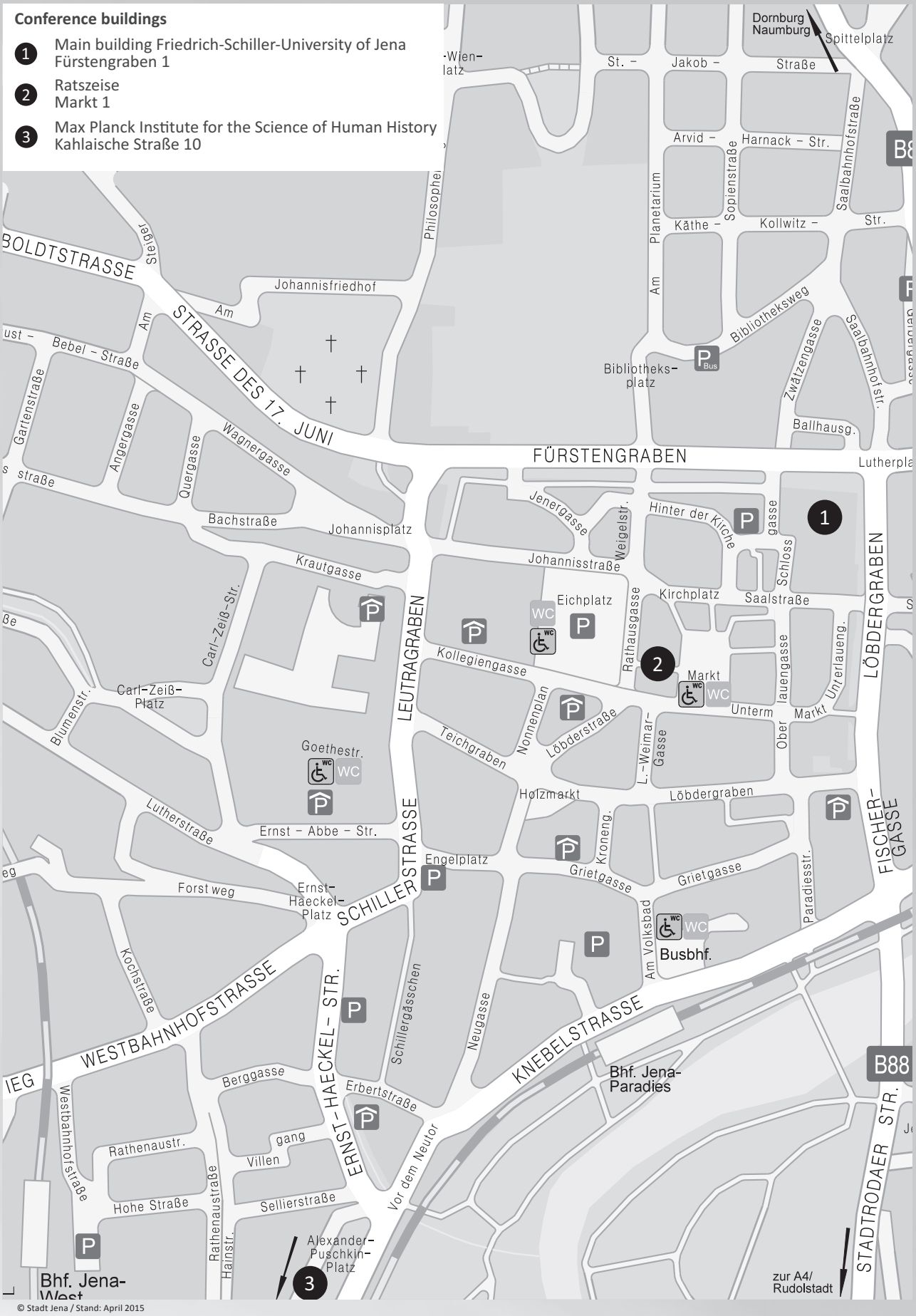
The location only offers very few parking spaces next to the main building at the "Schlossgasse". You can either use the car parks "Neue Mitte" (Leutragraben 1) or "Eichplatz" (Eichplatz square) both within walking distance of the conference venue.

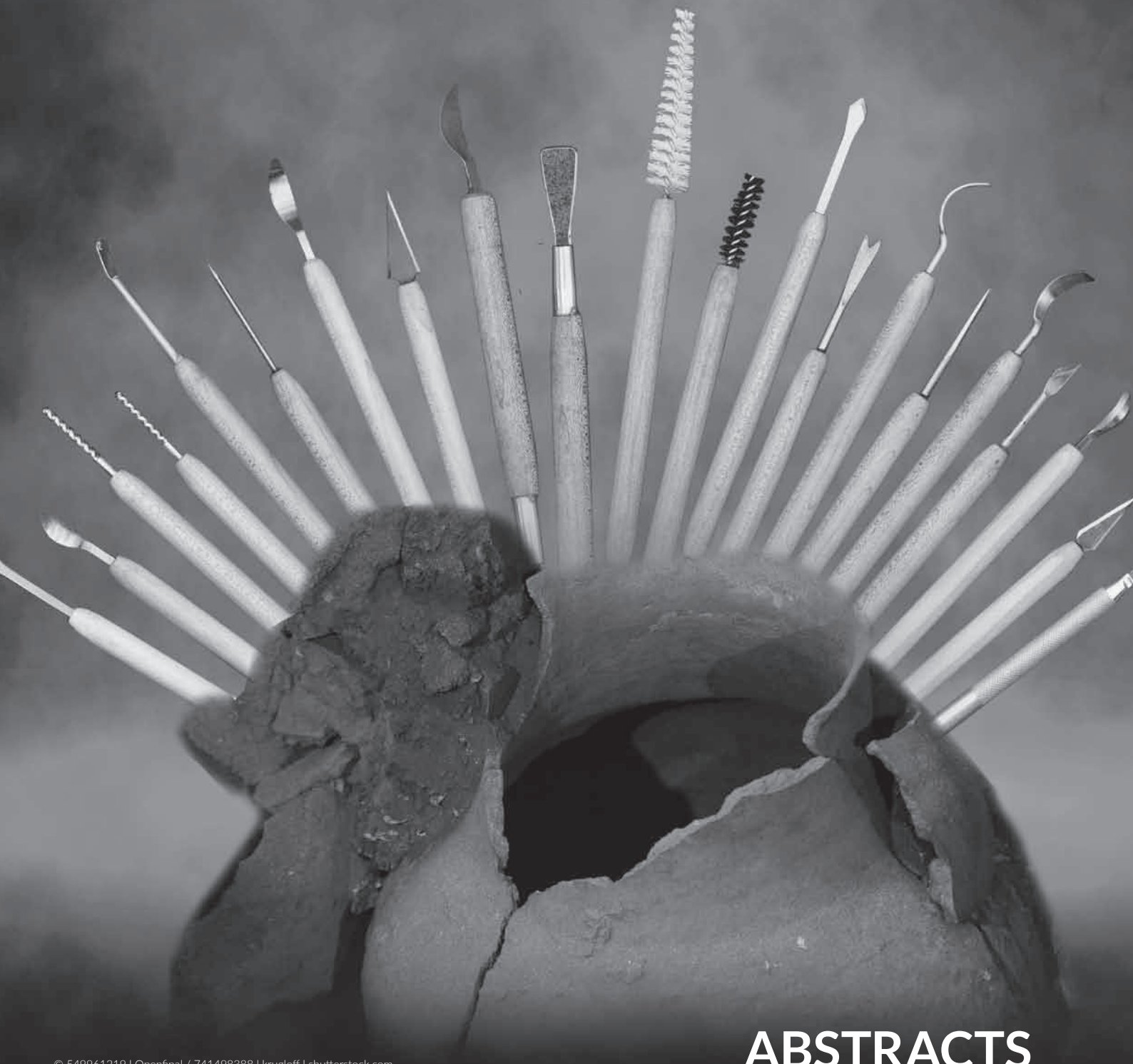
Conference buildings

1. Main building Friedrich-Schiller-University of Jena
   Fürstengraben 1
2. Ratszeise
   Markt 1
3. Max Planck Institute for the Science of Human History
   Kahlaische Straße 10



8th INTERNATIONAL SYMPOSIUM ON BIOMOLECULAR ARCHAEOLOGY

18th–21st SEPTEMBER 2018



ABSTRACTS

Session • Population structure and migration I

O–PSM–01
The genetic history of the Iberian Peninsula over the last 8000 years

I. Olalde[1], N. Rohland[1], S. Mallick[1,2,3], N. Patterson[2], M. Allentoft[4], K. Kristiansen[5], K. G. Sjögren[5], R. Pinhasi[6], C. Lalueza-Fox[7] D. Reich[1,2,3]

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The Iberian Peninsula, lying on the southwestern corner of Europe, provides an excellent opportunity to assess the final impact of population movements entering the continent from the east and to study prehistoric and historic connections with North Africa. Previous studies have addressed the population history of Iberia using ancient genomes, but the final steps leading to the formation of the modern Iberian gene pool during the last 4000 years remain largely unexplored. Here we report genome-wide data from 153 ancient individuals from Iberia, more than doubling the number of available genomes from this region and providing the most comprehensive genetic transect of any region in the world during the last 8000 years. We find that Mesolithic hunter-gatherers dated to the last centuries before the arrival of farmers showed an increased genetic affinity to central European hunter-gatherers, as compared to earlier individuals. During the third millennium BCE, Iberia received newcomers from south and north. The presence of one individual with a North African origin in central Iberia demonstrates early sporadic contacts across the strait of Gibraltar. Beginning ~2500 BCE, the arrival of individuals with steppe-related ancestry had a rapid and widespread genetic impact, with Bronze Age populations deriving ~40% of their autosomal ancestry and 100% of their Y-chromosomes from these migrants. During the later Iron Age, the first genome-wide data from ancient non-Indo-European speakers showed that they were similar to contemporaneous Indo-European speakers and derived most of their ancestry from the earlier Bronze Age substratum. With the exception of Basques, who remain broadly similar to Iron Age populations, during the last 2500 years Iberian populations were affected by additional gene-flow from the Central/Eastern Mediterranean region, probably associated to the Roman conquest, and from North Africa during the Moorish conquest but also in earlier periods, probably related to the Phoenician-Punic colonization of Southern Iberia.

O–PSM–02
Ancient DNA and the peopling of the British Isles – pattern and process of the Neolithic transition

S. Brace[1], Y. Diekmann[2], T. Booth[1], O. Craig[3], C. Stringer[1], D. Reich[4], M. Thomas[2], I. Barnes[1]

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Over recent years, DNA projects on ancient humans have flourished and large genomic-scale datasets have been generated from across the globe. Here, the focus will be on the British Isles and applying aDNA to address the relative roles of migration, admixture and acculturation, with a specific focus on the transition from a Mesolithic hunter-gatherer society to the Neolithic and farming. Neolithic cultures first appear in Britain ca. 6000 years ago (kBP), a millennium after they appear in adjacent areas of northwestern continental Europe. However, in Britain, at the margins of the expansion the pattern and process of the British Neolithic transition remains unclear. To examine this we present genome-wide data from British Mesolithic and Neolithic individuals spanning the Neolithic transition. These data indicate population continuity through the British Mesolithic but discontinuity after the Neolithic transition, c.6000 BP. These results provide overwhelming support for agriculture being introduced to Britain primarily by incoming continental farmers, with surprisingly little evidence for local admixture. We find genetic affinity between British and Iberian Neolithic populations indicating that British Neolithic people derived much of their ancestry from Anatolian farmers who originally followed the Mediterranean route of dispersal and likely entered Britain from northwestern mainland Europe.

Session • Population structure and migration I

O–PSM–03
Ancient genomes from the Lech Valley, Bavaria, suggest socially stratified households in the European Bronze Age

A. Mittnik[1,2], K. Massy[3], C. Knipper[4], R. Friedrich[4], W. Haak[2], S. Schiffels[2], P. W. Stockhammer[2,3], J. Krause[2]
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[2]Max Planck Institute for the Science of Human History, Department of Archaeogenetics, Jena, Germany
[3]LMU, Munich, Germany
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Archaeogenetic research has so far focused on supra-regional and long-term genetic developments in Central Europe, especially during the third millennium BC. However, detailed high-resolution studies of population dynamics in a micro-regional context can provide valuable insights into the social structure of prehistoric societies and the modes of cultural transition.
Here, we present the genomic analysis of 102 individuals from the Lech valley in southern Bavaria, Germany, which offers ideal conditions for such a study. Several burial sites containing rich archaeological material were directly dated to the second half of the 3rd and first half of the 2nd millennium BCE and were associated with the Final Neolithic Bell Beaker Complex and the Early and Middle Bronze Age. Strontium isotope data show that the inhabitants followed a strictly patrilocal residential system. We demonstrate the impact of the population movement that originated in the Pontic-Caspian steppe in the 3rd millennium BCE and subsequent local developments. Utilising relatedness inference methods developed for low-coverage modern DNA we reconstruct farmstead related pedigrees and find a strong association between relatedness and grave goods suggesting that social status is passed down within families. The co-presence of biologically related and unrelated individuals in every farmstead implies a socially stratified complex household in the Central European Bronze Age.

O–PSM–04
Genomics of Middle Neolithic farmers at the fringe of Europe

F. Sanchez Quinto[1], M. Fraser[1,2], H. Malmström[1], L. Girdland-Flink[3], E. M. Svensson[1], J. Storå[4], A. Götherström[5], M. Jakobsson[1]
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Agriculture emerged in the Fertile Crescent around 11,000 years before present (BP) and then spread, reaching central Europe some 7,500 years ago (ya.) and eventually Scandinavia by 6,000 ya. Recent paleogenomic studies have shown that the spread of agriculture from the Fertile Crescent into Europe was due mainly to a demic process. Such event reshaped the genetic makeup of European populations since incoming farmers displaced and admixed with local hunter-gatherers. The Middle Neolithic period in Europe is characterized by such interaction, and this is a time where a resurgence of hunter-gatherer ancestry has been documented. While most research has been focused on the genetic origin and admixture dynamics with hunter-gatherers of farmers from Central Europe, the Iberian Peninsula, and Anatolia, data from farmers at the North-Western edges of Europe remains scarce. Here, we investigate genetic data from the Middle Neolithic from Ireland, Scotland, and Scandinavia and compare it to genomic data from hunter-gatherers, Early and Middle Neolithic farmers across Europe. We note affinities between the British Isles and Iberia, confirming previous reports. However, we add on to this subject by suggesting a regional origin for the Iberian farmers that putatively migrated to the British Isles. Moreover, we note some indications of particular interactions between Middle Neolithic Farmers of the British Isles and Scandinavia. Finally, our data together with that of previous publications allow us to achieve a better understanding of the interactions between farmers and hunter-gatherers at the northwestern fringe of Europe.

Session • Population structure and migration I

O–PSM–05

Tracing the origin and expansion of the Turkic and Hunnic confederations

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Turkic-speaking populations, now spread over a vast area in Asia, are highly heterogeneous genetically. The first confederation unequivocally attributed to them was established by the Göktürks in the 6th c. CE. Notwithstanding written resources from neighboring sedentary societies such as Chinese, Persian, Indian and Eastern Roman, earlier history of the Turkic speakers remains debatable, including their potential connections to the Xiongnu and Huns, which dominated the Eurasian steppe in the first half of the 1st millennium CE. To answer these questions, we co-analyzed newly generated human genome-wide data from Central Asia (the 1240K panel), spanning the period from ca. 3000 to 500 YBP, and the data published by de Barros Damgaard *et al*. (137 ancient human genomes from across the Eurasian steppes, *Nature*, 2018). Firstly, we generated a PCA projection to understand genetic affinities of ancient individuals with respect to present-day Tungstic, Mongolic, Turkic, Uralic, and Yeniseian-speaking groups. Secondly, we modeled hundreds of present-day and few ancient Turkic individuals using the *qpAdm* tool, testing various modern/ancient Siberian and ancient West Eurasian proxies for ancestry sources. A majority of Turkic speakers in Central Asia, Siberia and further to the west share the same ancestry profile, being a mixture of Tungusic or Mongolic speakers and genetically West Eurasian populations of Central Asia in the early 1st millennium CE. The latter are themselves modelled as a mixture of Iron Age nomads (western Scythians or Sarmatians) and ancient Caucasians or Iranian farmers. For some Turkic groups in the Urals and the Altai regions and in the Volga basin, a different admixture model fits the data: the same West Eurasian source + Uralic- or Yeniseian-speaking Siberians. Thus, we have revealed an admixture cline between Scythians and the Iranian farmer genetic cluster, and two further clines connecting the former cline to distinct ancestry sources in Siberia. Interestingly, few Wusun-period individuals harbor substantial Uralic/Yeniseian-related Siberian ancestry, in contrast to preceding Scythians and later Turkic groups characterized by the Tungusic/Mongolic-related ancestry. It remains to be elucidated whether this genetic influx reflects contacts with the Xiongnu confederacy. We are currently assembling a collection of samples across the Eurasian steppe for a detailed genetic investigation of the Hunnic confederacies.

Session • Population structure and migration II

O–PSM–07

The first Epipaleolithic genome from Anatolia suggests a limited role of demic diffusion in the development of farming in Anatolia

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Anatolia was home to some of the earliest farming communities, which in the following millennia expanded into Europe and largely replaced local hunter-gatherers. The lack of genetic data from pre-farming Anatolians has so far limited demographic investigations of the Anatolian Neolithisation process. In particular, it has been unclear whether and to what extent the development of farming in central Anatolia involved the migration of farmers from earlier farming centres. Here we present the first genome-wide data from an Anatolian Epipaleolithic hunter-gatherer excavated at the site of Pınarbaşı, Turkey who lived ca 15,000 years ago, as well as from early farmers from Anatolia and the Levant. We find a high degree of genetic continuity between the hunter-gatherer and early farmers of Anatolia and detect two distinct ancestry waves entering central Anatolia during the Neolithic transition. Our results support models of cultural diffusion for the development of agriculture in Anatolia with only a limited role of population movement.

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O–PSM–08
North African ancestry in Islamic Medieval Spain

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We sequenced the genome of an individual buried in a medieval Islamic necropolis (10th–13th century AD), in Plaza del Almudin, Segorbe (province of Castellon, Spain), whose burial stands out from all the others in the cemetery. This was a ~20 year-old male, considerably taller than all the other individuals buried in the same site (184–190 cm). It was the best preserved skeleton found in the cemetery, which allowed a thorough anthropological study that concluded that the individual suffered from various non-lethal pathologies and impoverished nutrition during childhood. We sampled a molar tooth for ancient DNA and stable isotope analysis. We performed sample processing, DNA extraction and library preparation in a dedicated ancient DNA facility. Whole-genome shotgun sequencing yielded an average coverage of 0.06x. Genomic analysis confirms that the individual is a male and genome-wide comparisons show affinity to North African populations. His mtDNA lineage is U6a1a1 (mean mtDNA coverage: 16x). Haplogroup U6 reaches a peak in Northwest African modern populations, and U6a1a is found at very low frequencies (<1%) in present-day Spain. We complemented the analysis with published ancient North African and Iberian genomes, and with a newly-sequenced large modern mtDNA Spanish dataset (*n*>1000).

Session • Population structure and migration II

O–PSM–09

The Neolithic transition in the Iberian Peninsula – reviewing an old question from new laboratory and computational approaches

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In this study we investigated the demographic impact of the Neolithic transition in the Iberian Peninsula by combining cutting edge technologies in ancient DNA studies and statistical inference methods. The Neolithic was a major revolution in human prehistory, as human populations moved from a nomadic hunter-gatherer (HG) way of life to sedentary communities living on farming and agriculture. It was a global process that spread fast from the Near East into Europe by a combination of cultural and demographic events. As a general picture, recent studies have shown that in south and central Europe the Neolithic transition was mainly mediated by migration and admixture between pioneering farmers and local HG, while in the north and northeastern latitudes, cultural diffusion seems to have played a major role. In our study we investigated the dynamics and demographic effects of the Neolithic transition at a local scale. We sampled ancient human remains in the north and south of the Iberian Peninsula, and based on whole genome data and 14C dates, we have investigated the times, modes and demographic sources of the Neolithic diffusion at the two westernmost shores of Europe: the Atlantic and Mediterranean areas in Iberia. Our results show a different genomic background in samples from the North and South of the Iberian Peninsula, which could be explained by a combination of: 1) a different rate of admixture with the pioneering farmers; and 2) the pre-existence of some genetic structure in the Iberian populations before the Neolithic transition.

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O–PSM–10

Genetic transition in the Swiss Late Neolithic and Early Bronze Age

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Major genetic turnovers in European populations marked the beginning as well as final stages of the Neolithic period as shown by recent studies. The transition from hunter-gatherers to agriculturalists and farmers in the 6th millennium BCE coincided with a human migration from the Near East. A second migration into Central Europe occurred originating from the Pontic steppe in the 3rd millennium BCE and was linked to the spread of the Corded Ware Culture which ranged as far southwest as modern day Western Switzerland. These genetic processes are well studied, for example for the Middle-Elbe-Saale region in Eastern Germany, however, little is known from the regions that connect Central and Southern Europe.

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In this study, we investigate genome-wide data from 97 individuals from the Swiss Plateau, Southern Germany and the Alsace Region in France that span the transition from the Neolithic to the Bronze Age (5500 to 4000 BP). Our results show a similar genetic process as reported for the Middle-Elbe-Saale region suggesting that the migration from the Pontic steppe reached all the way into the Swiss Plateau. However, our evidence suggests that the onset of that transition may have started even earlier in Switzerland compared to the Middle-Elbe-Saale region.
The existence of core families within multiple burials, the determination and quantification of different ancestry components and the evaluation of a migration route taken by the ancestors of the Late Neolithic populations in this region were analysed. Our data represent the first comprehensive genome wide dataset from Neolithic individuals from the Swiss Plateau and provide the first insights into the genetic history of this region.

O–PSM–11
Barbarian migration and social organization in Medieval Europe – a paleogenomic approach

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Few topics in European history are as controversial as the barbarian migrations that took place in the Middle Ages. The extent to which these involved mass invasions and how barbarian groups were organized and interacted are topics of vigorous debates. To better understand this key era that marks the dawn of modern European societies, we obtained ancient genomic DNA from 63 samples from two cemeteries (Szólád in Hungary and Collegno in Northern Italy) that have been previously associated with the *Longobards*, a barbarian group noted for ruling large parts of Italy for over 200 years after invading from the Roman province of Pannonia (central/east Europe) in 568 CE. Our approach is unique in that we attempt to characterize all of the interred individuals, rather than sampling specific ones based on material culture markers. Our interdisciplinary approach, including a dense cemetery-based sampling, detailed isotopic analysis and archeological characterization, revealed that each cemetery was primarily organized around one large pedigree, suggesting that biological relationships played an important role in these early Medieval societies. The major families in each cemetery contained militarized, high-status individuals that may have formed the core of what Medieval texts denominate "fara" – a term whose meaning remains elusive. Curiously, we found no adult woman belonging to the largest family in the Hungarian cemetery, suggesting these may have not always migrated together with their male partners. Furthermore, we identified a population genetic structure in each of these cemeteries involving at least two ancestry groups (northern and southern European) that were very distinct in terms of their material culture and dietary isotope diversity, and thus potentially also different in what regards their social roles and status. These groups coexisted but at most only rarely admixed, as pointed out by the fact that there were no inter-group marriages. Finally, the combination of genomic and strontium isotope data was consistent with the hotly debated long-distance migration of barbarian peoples from northern Europe to the South – one of the hallmarks of what is known in popular culture as "The Barbarian Invasions". Beyond this specific application, our study provides a starting point for assessing the dynamics of allele frequency changes in the Middle Ages, an era in which population size in Europe is thought to have dramatically changed.

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O–PSM–12

A 1400-year transect of ancient DNA reveals recent genetic changes in the Finnish population

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Introduction: In the last few years, studies of ancient DNA (aDNA) have proven powerful in illuminating the geographic origin and migrations of past populations. Those studies have, however, so far focused disproportionately on Central and Western Europe, often due to the lack of access to suitable samples from elsewhere. Northeastern Europe, including Finland, remains one of the understudied regions, possibly because the acidic soils of the coniferous forest zone radically reduce the preservation of organic remains and aDNA. In contrast, the modern population of Finland has been extensively studied, largely for medical genetic interest. The contemporary Finnish gene pool is known to differ markedly from most other European populations and to harbor substantial substructure between the eastern and western parts of the country. Little is known, however, of the temporal origin of these remarkable features.

Objectives: Our objective was to use aDNA to study the population history of Finland. For this aim, we sampled and sequenced 35 individuals from ten archaeological sites across southern Finland, representing a time transect from 5th to 18th century.

Methods: Following genomic DNA extraction and preparation of indexed libraries, the samples were enriched for 1,2 million genome-wide SNPs using in-solution capture and sequenced on an Illumina HighSeq 4000 instrument. The sequence data were then compared to other ancient populations as well as modern Finns, their geographical neighbors and worldwide populations. Authenticity testing of the data as well as population history inference were based on standard computational methods for aDNA, such as principal component analysis and F statistics.

Results: Despite the relatively limited temporal depth of our sample set, we are able to see major genetic changes in the area, from the earliest sampled individuals - who closely resemble the present-day Saami population residing markedly further north - to the more recent ancient individuals who show increased affinity to the neighboring Circum-Baltic populations. Furthermore, the transition to the present-day population seems to involve yet another perturbation of the gene pool.

Conclusion: Our aDNA data suggest that the population of Finland has been subject to relatively recent genetic changes, which may partly relate to the late arrival of agriculture in the area, and do correlate with known archaeological influence from neighboring regions.

Session • Population structure and migration III

O–PSM–13
Demographic processes in the territory of Estonia from the earliest inhabitants to modern times

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This interdisciplinary project deals with the studies of temporal population dynamics of the eastern coast of the Baltic Sea, in the territory of present-day Estonia. We use the skeletal material from Estonian archaeological collections to characterize the genetic structure of the population in time series starting from the earliest layers of lithic cultures to the contemporary population. The sample consisted of 72 individuals – 24 from the Bronze Age stone-cist graves, 13 from the Iron Age *tarand*-graves and 35 from the Medieval rural and town cemeteries. We produced low-coverage Illumina whole-genome sequencing data. The resulting data was analyzed in a context of modern Estonian and European genetic variation.

Hgs N3 and R1a are the two most common chrY hgs among modern Estonians. While we have previously found that hg R1a appears in Estonia together with farmers of Neolithic Corded Ware culture (CWC) people, the arrival of hg N, which has been proposed to be connected with the arrival of Uralic languages to Europe, is yet to be studied. We found that the Iron Age individuals do in fact carry chrY hg N3 while all 18 Bronze Age males belong to R1a. Furthermore, based on their autosomal data, all of the studied individuals appear closer to hunter-gatherers and modern Estonians than Estonian CWC individuals do.

The Medieval period started in the eastern Baltic region much later than in Central Europe and in Scandinavia. The crusades and conquest in 13th century AD brought along vast social, economical and cultural changes, which presumably changed the structure of the local population. While the Medieval individuals buried in rural cemeteries are considered as the representatives of the local Estonian population, those of big towns can often be associated with the new wave of people who arrived, mostly from Western Europe, together with Christianity via the economical, cultural and political networks. We find that there is a clear difference between the genome-wide data of individuals belonging to Medieval urban and rural communities. The urban elite clusters genetically with modern Germans but the rural local class with modern Estonians. We did find a few individuals of mixed genetic ancestry, but the overall admixture between the two classes was limited.

Our results reveal several population shifts during the prehistory of the region and show a clear continuity of the population starting at least from the Iron Age.

O–PSM–14
Gene geography of the Russian Far East populations – faces, genome-wide profiles, and Y-chromosomes

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Russian Far East is not only a remote area of Eurasia but also a link of the chain of Pacific coast regions, spanning from East Asia to Americas, and many prehistoric migrations are known along this chain. The Russian Far East is populated by numerous indigenous groups, speaking Tungusic, Turkic, Chukotko-Kamchatka, Eskimo-Aleut, and isolated languages. This linguistic and geographic variation opens question about the patterns of genetic variation in the region, which was significantly undersampled and received minor attention in the genetic literature to date. To fill in this gap we sampled Aleuts, Evenks, Evens, Itelmens, Kamchadals, Koryaks, Nanais, Negidals, Nivkhs, Orochi, Udegeis, Ulchi, and Yakuts. We also collected the demographic information of local populations, took physical anthropological photos, and measured the skin color. The photos resulted in the "synthetic portraits" of many studied groups, visualizing the main features of their faces.

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We genotyped 150 samples using the Illumina genome-wide SNP panels: 730k OmniExpress chip and the largest commercially available 4M Omni5Exome-4 chip. This dataset revealed the contrast between gene pools of populations from Amur basin, Chukotka-Kamchatka speakers, and Evenks/Evens. The Chukotka-Kamchatka populations are genetically very specific comparing with all other Eurasian groups. They demonstrated weak signals of similarity with Amerinds and might carry a portion of the Upper Paleolithic Beringian ancestry. The other Russian Far East groups carry mainly the Amur basin/Central Asian genetic component, traced back till the Neolithic aDNA samples from the Amur region, but also East Asian and North Siberian components.
We also analyzed ~1,000 Y-chromosomes from the same indigenous groups. The subset was sequenced, resulting in the detailed phylogenetic tree with many newly revealed branches. The remained samples were genotyped by Y-SNPs, including those defining the new branches. The Y-chromosomal data confirmed the genetic peculiarity of the Asian north-easternmost populations. We also demonstrated that gene pool structure corresponds with the clan structure, and clans within the same group might have different origin.
To conclude, we performed the molecular anthropological and physical anthropological study of the Russian Far East revealing the complex and ancient gene pools which are structured not only by geography, but also by language and clans.

O–PSM–15
Genomic insight into the Neolithic transition peopling of Northeast Asia

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East Asian representing a large geographic region where around one fifth of the world populations live, has been an interesting place for population genetic studies. In contrast to Western Eurasia, East Asia has so far received little attention despite agriculture here evolved differently from elsewhere around the globe. To date, only very limited genomic studies from East Asia had been published, the genetic history of East Asia is still largely unknown. In this study, we shotgun sequenced six hunter-gatherer individuals from Houtaomuga site in Jilin, Northeast China, dated from 12000 to 2300 BP and, 3 farming individuals from Banlashan site in Liaoning, Northeast China, dated around 5300 BP. We find a high level of genetic continuity within northeast Asia Amur River Basin as far back to 12000 BP, a region where populations are speaking Tungusic languages. We also find our Compared with Houtaomuga hunter-gatherers, the Neolithic farming population harbors a larger proportion of ancestry from Houtaomuga related hunter-gathers as well as genetic ancestry from central or perhaps southern China. Our finding further suggests that the introduction of farming technology into Northeast Asia was probably introduced through demic diffusion.

O–PSM–16
Genome wide ancient DNA from the enigmatic skeletons of Roopkund Lake reveal complex population history

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Situated at over 5,000 meters above sea level in the Himalayan Mountains in India, the site of Roopkund Lake is considered one of the region"s most enigmatic sites. The lake is home to the scattered skeletons of several hundred individuals dating to the 9th century. Little is known about the identity of these individuals, or their reason for traveling to Roopkund Lake, although both have been the subject of a great deal of speculation. We present genome-wide ancient DNA from 37 individuals from Roopkund Lake. We find that they cluster genetically into two distinct groups—consistent with observed morphological variation. Using population genetic analyses, we determine that one group is composed of individuals with broadly South-Asian-related ancestry, consistent with being composed of individuals from multiple locations throughout the region. The second group is comprised of individuals with West Eurasian-related ancestry, most closely related to present-day Greek populations, with additional affinities to ancient Near Eastern groups.

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O–PSM–17
Ancient genomics reveals four prehistoric migration waves into Southeast Asia

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Two distinct population models have been put forward to explain present-day human diversity in Southeast Asia. The first model proposes long-term continuity (Regional Continuity model) while the other suggests two waves of dispersal (Two Layer model). Here, we use whole-genome capture in combination with shotgun sequencing to generate 25 ancient human genome sequences from mainland and island Southeast Asia, and directly test the two competing hypotheses. We find that early genomes from Hoabinhian hunter-gatherer contexts in Laos and Malaysia have genetic affinities with the Onge hunter-gatherers from the Andaman Islands, while Southeast Asian Neolithic farmers have a distinct East Asian genomic ancestry related to present-day Austroasiatic-speaking populations. We also identify two further migratory events, consistent with the expansion of speakers of Austronesian languages into Island Southeast Asia ca. 4 kya, and the expansion by East Asians into northern Vietnam ca. 2 kya. These findings support the Two Layer model for the early peopling of Southeast Asia and highlight the complexities of dispersal patterns from East Asia.

O–PSM–18
Language continuity despite population replacement in Remote Oceania

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Recent genomic analyses show that the earliest peoples reaching Remote Oceania—associated with Austronesian-speaking Lapita culture—were almost completely East Asian, without detectable Papuan ancestry (Skoglund et al. 2016). However, Papuan-related genetic ancestry is found across present-day Pacific populations, suggesting that peoples from Near Oceania have played a significant, but largely unknown, ancestral role. A co-analysis of recently published genome-wide data from 33 ancient South Pacific individuals and 212 present-day ni-Vanuatu individuals (Posth et al. 2018 and Lipson et al. 2018) provide direct evidence of a so-far undescribed Papuan expansion into Remote Oceania starting ~2,500 yr bp. This date is far earlier than previously estimated and supports a model from historical linguistics and coincides with changes in morphological features (Valentin et al 2016). Genome-wide data from contemporary ni-Vanuatu demonstrate a subsequent and almost complete replacement of Lapita-Austronesian by Near Oceanian ancestry. Despite this massive demographic change, incoming Papuan languages did not replace Austronesian languages. Population replacement with language continuity is extremely rare—if not unprecedented—in human history. Our analyses show that rather than one large-scale event, the process was incremental and complex, with repeated migrations and sex-biased admixture with peoples from the Bismarck Archipelago.

Session • Paleoproteomics

O–PAL–01
Ancient proteins analysis of Pleistocene hyena fossils

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Today spotted hyenas (*Crocuta crocuta*) are only found in Africa, but during the geological period they almost occupied the entire Eurasian continent. There is little consensus in the literature regarding their taxonomic and systematic analysis, and it is still not clear whether they originated in Africa or Asia and how they spread throughout Africa, Europe and Asia. Both morphology-based analyses and ancient DNA approaches have been applied to the hyena fossils, but cannot resolve these questions completely. Thus it is rather important to try new methods and obtain more phylogenetic information. Here we apply proteomic analysis to the hyena fossils (skeletons and teeth) at two sites (Lingxian Cave and Shanyangzhai Site) from Qinhuangdao City, Hebei Province, Northern China. For each specimen, multi-enzyme digestion, homology database analysis and de novo sequencing have been used to obtain high sequence coverage of type I collagen a1- and a2-chains. Phylogenetic analysis was then performed based on the molecular data of fossilized and extant spotted hyena. The variations in collagen sequences have been used to explore evolutionary relationships and divergence time. The interior nodes have also been calibrated against the fossil records. With developments of instrumentation and analytical methods, proteomics holds promising potential for the phylogenetic reconstruction of ancient fauna and probably could reach much further back in time.

O–PAL–02
Palaeoproteomic analysis of Early Pleistocene *Gigantopithecus blacki*

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Gigantopithecus blacki is a giant hominid known from a few subtropical or tropical localities between 2.0 and 0.3 Ma in southern China and northern Vietnam. The first remains of the species were discovered and identified by von Koenigswald in a Hong Kong drugstore where they were sold as "dragon teeth". Knowledge on the species remains limited despite the availability of relatively large amounts of teeth, but only four mandibles and no other cranial or postcranial material. Nevertheless, it is one of the few, if not the only, extinct non-hominin hominid for which Pleistocene fossil specimens are available. The species is currently considered a diverging side branch of *Pongo*, although initial phylogenetic assessments proposed *Gigantopithecus* to represent an ancestral hominin. Its relationships with *Pongo* and other extinct pongines (such as *Sivapithecus*) remains tentative due to the paucity of postcranial *Gigantopithecus* remains, and the primitive status of most shared dental characteristics between *Gigantopithecus blacki, Indopithecus giganteus* (a presumed late Miocene ancestor) and *Sivapithecus*.
To clarify the phylogenetic status of *Gigantopithecus blacki*, we sampled a *Gigantopithecus* molar from Chuifeng Cave, China, for palaeoproteomic analysis. The site is dated by ESR, U-series and paleomagnetic methods to approximately 1.38-1.92 Ma. The *Gigantopithecus* molars are associated with a typical Early Pleistocene fauna that does not include any *Pongo* specimen. We attempted proteomic analysis of both dentine and enamel samples and obtained a variety of protein identifications. We explore this proteome in terms of endogenous and contaminating proteins, and utilize any endogenous proteins to describe the phylogenetic relationship of *Gigantopithecus* in relation to extant hominids from a molecular point of view.

Session • Paleoproteomics

O–PAL–03

Enamel proteome sequences from Dmanisi (Georgia) enable molecular phylogeny of fauna remains beyond the limits of ancient DNA preservation

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We ignore how species who faced extinction earlier than one million years (Ma) ago are genetically related to the living ones because ancient DNA degrades after ~0.5-1 Ma. Here we show that this limit can be overcome by using proteomics. Dental enamel is the hardest tissue in vertebrates, frequently recovered and identified at palaeontological sites. We present a novel analytical approach using high-resolution, high-sensitivity tandem mass spectrometry (MS) that retrieves a population of peptides that are "mapped" to extant enamel protein reference sequences. The reconstructed sequences are then aligned and compared with homolog sequences from extant species using conventional phylogeny procedures.

From most of the fauna specimens analysed, limited peptide fragments of collagen type 1-alpha 1 and 2, as well as collagen type 3-alpha 1, were identified from bone and dentine, while extended stretches of amelogenin, enamelin, and ameloblastin were identified in enamel samples. To our knowledge, such an extended coverage, from samples of similar age and geographic origin, has never been achieved before. Glutamine deamidation, a spontaneous modification extensively observed in ancient samples, was surprisingly high. This observation is a strong indicator of the authentic ancient endogenous origin of the sequences retrieved. Another element supporting authenticity is the tissue-specificity of the proteins identified. Enamel proteins are not expressed in other tissues, they never appear among regular random laboratory contaminants, and they are not detected in ordinary saliva proteomes. Finally, they were absent in any extraction and injection blanks involved in the study.

Enamel protein sequencing also provides valuable information for paleontological reconstructions. As the amelogenin gene is located on the non-recombining regions of the X and Y chromosomes, identification of amelogenin X and Y isoform-specific peptides provides a tool to determine the biological sex of ancient animal remains. We demonstrate palaeoproteomics provides access to genetic evidence older than 1 Ma, enabling molecular investigation of major, so far intractable, evolutionary processes.

O–PAL–04

Discovery of age-related protein modifications

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Over the past 18 years, Palaeoproteomics has rapidly developed to a stage, at which species identification in reasonably well conserved samples is a relatively simple task. Just like in biomedical proteomics, ancient proteins can provide a lot more information than the origin of a specimen. Therefore, our group and many others have started to focus more and more on post-translational modifications (PTMs). These have the potential of giving us insight into the degradation, conservation, and processing history of proteins in cultural heritage material.

We developed an analysis workflow for LC-MS/MS data, which overcomes the limit of about five measurable PTMs per search and allows us to assess the relative degree of modification in ancient samples. Our strategy is based on a two-step database search starting with the "dependent peptides" feature in MaxQuant, which facilitates unbiased search of modifications by mass-shifts, and finishing with a conventional database search for validation and quantification.

The first successful application of this method was recently published (Mackie et al., Angew. Chem., 2018). With our approach, we were able to detect photo-modifications and glycations, which we would not have discovered with conventional methods. We believe that this contribution to the field of Palaeoproteomics will lead to the discovery of new aging-linked PTMs telling us a more detailed story about the history of ancient proteins.

Session • Paleoproteomics

O–PAL–05
The History of Dairying in ancient Mongolia

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The use of mass spectrometry based proteomics presents a novel method for investigating human dietary intake and subsistence strategies from archaeological materials. Studies of ancient proteins extracted from dental calculus, as well as other archaeological material, have robustly identified both animal and plant-based dietary components. Here we present a recent case study using shotgun proteomics to explore the range and diversity of dairying in the ancient eastern Eurasian steppe. Contemporary and prehistoric Mongolian populations are highly mobile and the ephemerality of temporarily occupied sites, combined with the severe wind deflation common across the steppes, means detecting evidence of subsistence can be challenging. To examine the time depth and geographic range of dairy use in Mongolia, proteins were extracted from ancient dental calculus from 32 individuals spanning burial sites across the country between the Neolithic and Mongol Empire. Our results provide direct evidence of early ruminant milk consumption across multiple time periods, as well as a dramatic increase in the consumption of horse milk in the late Bronze Age. These data provide evidence that dairy foods from multiple species were a key part of subsistence strategies in prehistoric Mongolia and add to our understanding of the importance of early pastoralism across the steppe.

O–PAL–06
Direct proteomic evidence of early dairying at Çatalhöyük

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Çatalhöyük is a key site in understanding early animal domestication in Neolithic Anatolia. Bovine and caprovine faunal remains at Çatalhöyük suggest an increasingly intense exploitation of these animals. It has been argued that bovine remains from the site represent both wild aurochs (*Bos primigenius)* and domesticated cattle and that sheep formed the primary source of meat, but whether or not these animals were also exploited for dairying is still debated. Mortality profiling suggests that dairying may have been practiced at the site, but direct evidence is lacking. Recent advances in the recovery and identification of ancient dietary proteins from human dental calculus have shown that proteins specific to dairy milk can persist through archaeological time. In this study, we investigate direct evidence for the consumption of dairy products at Çatalhöyük by performing LC-MS/MS analysis of dental calculus belonging to individuals excavated from the East Mound. Identification of several milk proteins in dental calculus — including beta-lactoglobulin and alpha-S1-casein—indicates the consumption of both whey and curd proteins from the genera *Bos* and *Ovis*. These results suggest dairy products were produced and consumed at Çatalhöyük in the Neolithic.

Session • Domestication I

O–DOM–01

Whole-genome sequences in ancient bean seeds –new insights into the domestication history of common bean (*Phaseolus vulgaris*) in South-America

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Investigating the domestication history of cultivated plants in different geographic areas is relevant to understanding human history, human-induced changes in plant genomes, and local adaptations to new environments. Genomic analyses on modern common bean (*P. vulgaris*) accessions indicate that two major genetic pools can be associated to Mesoamerica and the Andes, supporting the hypothesis of two independent domestication events that occurred approximately 8,000 years ago. To investigate genomic change following domestication in the Andes, we collected ancient bean seeds from seven pre-Columbian archeological sites in Northern Argentina spanning at least 1800 years. Preliminary analysis showed that DNA was extremely well preserved in most of the seeds and we sequenced 19 genomes with coverage between 1 and 18X. All the seeds showed a domestication-associated phenotype. Comparing the genomes of these ancient seeds to a panel of modern genomes with wild and domesticated samples from Central and South America, we find that ancient seeds don"t have their closest relatives among the modern varieties cultivated in the same region today. On the contrary, they show higher genetic similarity to modern accessions commonly found in Chile, possibly as a consequence of ancient trades or ancestral traits sharing. Ancient seeds cluster in one genetic group indicating that these varieties were likely the product of a single domestication event and were cultivated in that area without major transitions at least until the Spanish colonization of South America. By investigating the different levels of similarity and dissimilarity between modern (wild and domestic) and ancient seeds at different genes, we aim to study the genetic basis of the phenotypic changes that occurred following domestication.

Session • Domestication I

O–DOM–02
The independent legacy of maize evolution in South America

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Maize was domesticated from wild teosinte in Mexico beginning around 9,000 BP, and it traversed Central America to spread into South America by ~6,500 BP. However, recent genomes from archaeological maize dating to ~5,300 BP in the Tehuacan Valley reveal partial domestication—a mix of maize-like and teosinte-like alleles at loci involved in domestication. This creates a paradox: maize was still only partially domesticated near its site of domestication long after it became established as a crop species in South America, so it is unclear how the full complement of domestication syndrome genes came to fixation in South American lineages. We sequenced forty landraces from traditional cultivation contexts in Peru, Chile, Argentina, the Brazilian Amazon, and the Brazilian Savanna, as well as nine complete archaeological maize genomes from the Andes and eastern Brazil. Using these and published datasets, we suggest that South American maize left the source region in Mexico and the primary domestication gene pool as a partial domesticate, and deeply structured, locally adapted lineages evolved *in situ* after arriving in South America. Thus while domestication began in a large single gene pool in Mexico, the linkage and fixation of domestication traits likely occurred in multiple regions and cultural contexts independently. Our results highlight the complexity of maize domestication, and suggest revisions to our broader understanding of the maize domestication process are in order.

O–DOM–03
Modern and ancient DNA evidence for the origins and spread of broomcorn millet (*Panicum miliaceum*) from China

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Broomcorn millet (*Panicum miliaceum*) has been a staple cereal in semi-arid regions of Eurasia, particularly northern China, for at least eight thousand years. It is generally accepted to have been domesticated in the north China centre of agricultural origins, but questions have remained over where in this vast region it originated, and whether there is credible evidence for additional domestication events further west in Eurasia. These questions have implications for the development and interaction of Neolithic farming cultures in China, and the cross-Eurasian translocation of crops. To address these questions, we analysed genetic diversity in over 340 broomcorn millet landraces from across Eurasia using microsatellite markers and the *GBSSI* locus. Statistical analyses support a single broad origin of cultivated broomcorn millet in China, more specifically in the western Loess Plateau. Westward translocation of broomcorn millet occurred via Xinjiang and the Inner Asian Mountain Corridor from the Bronze Age, with a possible later second wave of expansion via the steppe to the north. Genotyping of the *GBSSI* locus in thirteen archaeological grain samples from Xinjiang, dated between 1700 BC and 900 AD, support this scenario. The *GBSSI* genotypes in modern and ancient samples provide the first biomolecular archaeological evidence for the geographical boundary between deep-seated eastern and western culinary traditions of cereal processing and consumption. We will discuss how the genetic inferences relate to recent archaeobotany and palaeodietary studies on the spread and consumption of millet.

Session • Domestication I

O–DOM–04

When chickens colonised Europe – dispersal routes, phenotypes and patterns of admixture based on ancient and modern genomes

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Introduction: Domestic chickens (*Gallus gallus*) have played crucial roles in the development of modern human societies, not only as a food source, but also in religion, entertainment and medicine. Originally native to Southeast Asia, chickens have been transported to Europe solely via human-mediated means but little is known of their timing or dispersal route. Neither has any research been done on the physical appearance(s) preferred by various human societies through time. Furthermore, published studies revealed chickens interbred with other *Gallus* subspecies including *Gallus sonneratii* which led to domestic chickens possessing yellow legs. Despite the fact that this trait has been highly selected for in the last few centuries, the admixture between *G. gallus* and *G. sonneratii* is not believed to have been involved in the domestication process.
Question: We here seek to investigate the spatial and temporal introduction(s) of chickens in Europe, their phenotypes and assess their admixture levels with other subspecies through time.

Methods: We undertake this through the analysis of ancient mitochondrial and nuclear data from a comprehensive archaeological European chicken dataset of over 150 individuals. Particular attention was given to the role chickens played during specific time periods and geographical regions given this may have influenced selection and subsequent population pressures.

Results: Our results show that almost all our chickens belong to haplogroup E, the most common and widespread haplogroup, with the exception of a few individuals, most likely introduced through trade. We are currently undertaking the phenotypic and admixture analyses through bait capture.

Concusion: Our current results show a lack of haplogroup diversity in ancient chickens, though more 'exotic' individuals (non-E) were brought in Europe as part of specific cultural practices. The findings of this research are important to better understand today"s genetic make-up of chickens and the implications for the future both in terms of the chickens" well-being and food security.

O–DOM–05

The arrival of domestic cats to the UK and Ireland – an ancient DNA study

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Cats are one of the most popular pets, yet we seem to know very little about their arrival to Britain and Ireland. Research on their arrival to mainland Europe has only been recently conducted by Ottoni et al. (2017). While extensive, this study however contained no samples from Britain or Ireland. The only evidence thus far for domestic cats in the British Isles is from archaeological evidence. However, it is very difficult to morphologically distinguish between wild cats (*F.s.sylverstris*) and domestic cats (*F.s.lybica*). Wildcats were present when domestic cats were introduced which makes it hard to determine which cat species was found on a site, wild or domestic. The earliest evidence for possible domestic cats comes from the Iron Age site of Gussage-All-Saints, Dorset (Harcourt, 1979). The classification of the cats as *F.s.lybica* and not *F.s.sylvestris* was based on kittens being found on the site suggesting a commensal relationship. This puts the earliest arrival of domestic cats to Britain to the Iron Age according to archaeological evidence. Their arrival in Ireland is even less well understood and was likely in the Roman period. The present study uses an ancient DNA approach to further our understanding of the commensal relationship between cats and people. Recent research has made a start to furthering our understanding of cats in Europe and my work builds upon this research by studying cats from a range of sites and time periods throughout the British Isles.

Session • Domestication I

O–DOM–06
Viking Age Sheep in the North Atlantic

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Sheep played a central role in subsistence for the 9th and 10th century settlers of Iceland, Greenland and the Faroe Islands. They provided milk, meat, horns and wool and were very well suited to the wet and cold climate of the North Atlantic. Sheep bones are common in Viking Age excavations in the region, but little is known about the genomic composition of these sheep or their genetic contributions to modern breeds.
Using whole genome sequences of ancient and modern sheep we determine the origin of the Icelandic and Faroese sheep breeds and examine functional traits of Viking Age sheep in the North Atlantic. For this study we have selected over 80 sheep bones from archaeological excavations in Iceland, Greenland, the Faroe Islands, Norway and the UK. We compare these ancient genomes to those of modern sheep in the North Atlantic.
Our analyses will deepen the understanding of how the rapid settlement of the North Atlantic shaped population structure and genetic diversity of sheep in the region and how they have changed in the past thousand years. Furthermore, we will shed light on environmental adaptation of these animals as well as human selection of traits relating to the products produced by sheep. With the refinement of ancient DNA methodologies, it is now possible to answer questions like these which are largely outside the realm of traditional zooarchaeological analysis.

Session • Domestication II

O–DOM–07
Ancient genomics and the evolutionary origins of dogs

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Despite numerous investigations leveraging both genetic and archaeological evidence, the geographic origins of dogs remain unknown. On the basis of an ancient Irish dog genome and an assessment of the spatiotemporal appearance of dogs in the archaeological record, a recent paper suggested that dogs may have been domesticated independently in Eastern and Western Eurasia from distinct wolf populations. A subsequent study of two additional Neolithic dog remains showed genomic continuity from the Neolithic to the present day, but left open the possibility of a unique pre-Neolithic population in Europe. More recent mitochondrial assessments are suggesting multiple waves of dogs into Europe coincident with the movement of people, but the question of whether dogs were derived from independent lineages of wolves remains open. To test this hypothesis, we have generated nuclear genomes of ~10 ancient dogs and mitochondrial genomes from ~400 dogs spanning the last 15,000 years across Eurasia. The results of this analysis will reveal the phylogenetic affinities of dogs that were present across the Old World prior to the introduction of dogs associated with farming communities. This study will also allow us to pinpoint the timing of the European mitochondrial turnover and to assess whether there was a commensurate turnover at the nuclear level, thus directly addressing whether dogs were domesticated from more than one population.

O–DOM–08
Friends in high places – an integrated examination of the long-term relationship between humans and dogs in the Arctic

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Dogs, Canis lupus familiaris, have expanded to all corners of the Earth alongside humankind, including harsh environments such as the Arctic and Antarctic. The earliest Arctic communities known to possess dogs have been uncovered in the Siberian Arctic, dating to as early as 9,500 years before present. Archaeological and genetic evidence indicates that the populations and cultures which migrated across Beringia, into the Americas, in a separate wave from the initial peopling of the Americas, originated from the Russian Arctic. The archaeological record in Alaska, the point of arrival in the Americas, shows that various cultures occupied the region through time, who then continued to expand east across the Arctic. Ancient DNA studies have confirmed that multiple human migration waves spread across the North American Arctic. It remains unknown whether the various cultures arrived with their own commensal dogs from Eurasia, they adopted the dogs they encountered in the Americas brought with the initial migrations, or whether both are true and the dogs were admixed in the process. The final cultural complex, the Thule Culture, spread rapidly across the entire North American Arctic, reaching Greenland at around 800 years before present. Their speed and successful expansion was enabled by their well adapted toolkit including their dogs and sledges. This population is known to be the ancestors of the First Nations peoples of Arctic Canada as well as the Greenland Inuit, with their dogs also likely being directly descended from the Thule dogs. The nature of the relationship between the dogs of the various waves of cultural migrations to and across the North American Arctic and ancient Siberian Arctic dogs is explored in this project through a combination of mitochondrial and geometric morphometric analyses.

Session • Domestication II

O–DOM–09
Cattle on the Western Atlantic edge of Europe – a time series of ancient cattle genomes through Ireland and Britain

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The domestication of cattle marks a significant period of time in human prehistory. Cattle were domesticated in the Near East from their wild progenitor *Bos primigenius* (auorchs) approximately 10,000 years ago. During the Neolithic, human mediated migration of domestic cattle into Europe occurred. This initial movement of cattle across Western Europe concluded with the movement of animals to the Western Atlantic Edge; the islands of Ireland and Britain. A common approach to understanding this past has been the study of variation in modern cattle genomes to model past demography, admixture and selection. However, ancient genomes provide a snapshot of the genetic diversity present in the past, allowing for the exploration of the timing of population events such as an admixture, migration and turnover. We have sequenced a time series of ~50 ancient Irish and British cattle nuclear genomes, with genome coverage ranging from 0.1× to 16×, sampled from the Neolithic (3500BC) to the Middle Ages (1200AD). The application of population genomics techniques to these data provide new insights into the population structure, migration, admixture and demography of the prehistoric livestock of these islands.

O–DOM–10
Ancient genomics reveals patterns of gene flow and trait evolution in European domestic pigs

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The Neolithic expansion was characterized by the human-mediated dispersal of a suite of domesticated plants and animals that were derived from wild species indigenous to the Near East. Some of the introduced domestic animals that arrived from the Near East were exposed to genetically differentiated wild populations of the same species in Europe, with which they could potentially interbreed. Ancient mitochondrial DNA data indicated that pigs began acquiring an indigenous European wild boar mitochondrial signature soon after they arrived from the Near East. This suggested that extensive gene-flow between wild and domestic pigs took place. What remains unknown is the extent of this gene flow and how pigs would have maintained their domestic integrity despite introgression from the wild. One possibility is that modern European domestic pigs retained a sufficient fraction of Near Eastern domestic ancestry that underlies domestic traits. To test this hypothesis we sequenced mitochondrial and nuclear genomes of >400 archaeological pig remains in order to assess the speed and extent to which Near Eastern pigs acquired European wild boar ancestry, and the likelihood that modern pigs retain a Near Eastern component necessary to maintain their domestic integrity. Overall, our results suggest that the original population of pigs domesticated ~9,500 years ago in Anatolia was rapidly replaced and has not left any significant genetic legacy (<4% of the genome) in modern European domestic pigs. This is surprising since both modern and ancient domestic pigs possess phenotypes necessary to live and reproduce within a human niche. Instead, we find that domestic pigs introduced alongside incoming Near Eastern farmers admixed with European wild boar thus resulting in the rapid adoption of a novel genomic ancestry that, at least initially, would have eroded the phenotypic differences between wild and domestic pigs. To explain this surprising result, we propose that, at least in pigs, it is possible to select for domestic traits in highly differentiated wild populations so long as human-mediated selection is maintained.

Session • Domestication II

O–DOM–11
Tracking six millenia of horse selection, admixture and management with complete genome time-series

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The domestication of the Horse and its impact on warfare, transportation and agriculture, have revolutionized human history. Even though most modern breeds have been engendered within the last couple of centuries, humans have managed horse livestock for over five millenia. Recent selective and management strategies have tremendously impacted the genetic structure of horse populations. As a result, modern patterns of genetic diversity can only partly help reconstruct the horse domestication process prior to the modern era. Recent research in our laboratory, carried out in the framework of the ERC PEGASUS programme, has endeavoured to sequence complete horse genomes from accross their whole temporal and geographical domestication range in order to identify how the many past human cultures progressively forged the horse genome by means of selection, drift and admixture. This work revealed two different dynamics at play within early and late domestication stages, involving the selection for different functional pathways, different management strategies for the genetic resource available, including stallion diversity, and a recent increase in the genomic deleterious load. Our new genome dataset now allows us to document such changes at unprecedented scales and reveals unexpected features of the whole population dynamic underlying horse domestication.

O–DOM–12
Selection trajectories of genetic variants underlying domestic animal traits

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The study of animal domestication is an important model system for understanding adaptive responses to changes in environmental conditions, demography and selective pressures over time. Despite speculation surrounding the existence of "domestication genes", the underlying genetic basis of traits differentiating domestic animals them from their wild counterparts remains poorly understood. Using genome-wide modern DNA, previous studies have contrasted populations of wild and domestic animals to scan for segregating signatures of selection in their respective genomes. Due to the intensive nature of modern breeding practices, it is unclear which candidate genes identified by these methods were under selection during the initial process of domestication, and which represent more recent improvement traits. Time series data, obtained from ancient DNA, can resolve these questions by directly observing changes in allele frequencies over time. Here, we reconstruct the allelic trajectory of hundreds of variants associated with quantitative trait loci (QTLs) in four key domestic species (cattle, pigs, horses and goats). Using a novel dataset of >300 ancient nuclear genomes, spanning ~12,000 years of evolutionary history, we are able to quantify the temporal origins and strength of selection for genetic variants associated with health, reproductive, performance, production, aesthetic and behavioural traits in domestic animal populations. The resulting timelines allow direct correlation between changes in ecological conditions within the domestic niche and selection for specific adaptive traits. Our results demonstrate the critical importance of time series data in resolving the underlying evolutionary process of animal domestication.

Session • Plagues and pathogens

O–PAP–01

Epidemic decline in colonial Mesoamerica – molecular and computational approaches for identifying a possible pathogenic cause

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Indigenous populations of the Americas experienced high mortality during the early contact period as a result of infectious diseases. While many are assumed to be of Old World origin, intense debate persists regarding their aetiology. Here we demonstrate the applicability of a metagenomic analysis tool (MALT) for pathogen screening in victims of one such New World colonial epidemic, the 16th century "cocoliztli" of southern Mexico. We detected *Salmonella enterica* in individuals buried in an early contact era epidemic cemetery at Teposcolula Yucundaa, Oaxaca, a cemetery linked to the 1545–1550 CE epidemic that contributed to catastrophic demographic collapse in large parts of Mesoamerica. From a subsequent enrichment via hybridization capture, we present genome-wide data from ten individuals for *Salmonella enterica subsp. enterica* serovar Paratyphi C, a bacterial cause of enteric fever that has a low global prevalence today. The cause of the cocolizti has been debated for over a century, and we propose here that S. Paratyphi C be considered a strong candidate for the epidemic population decline during the 1545 outbreak at Teposcolula Yucundaa.

O–PAP–02

A 15th century louse-borne relapsing fever genome – virulence, immune evasion and evolution

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Louse-borne relapsing fever (LBRF), once a global killer, has disappeared from the Western world since the beginning of the 20th century. Very much a disease of poverty and famine, having a history of appearing during times of war and crisis, it is known for its involvement in devastating historical epidemics, such as the Irish Potato Famine. Its etiological agent, *Borrelia recurrentis*, is a human specialist and shares its only vector, the human body louse, with major epidemic pathogens, such as *Rickettsia prowazekii* and *Yersinia pestis*.

We shotgun sequenced double-stranded libraries of DNA extracted from an individual, which was recovered from a 15th century skeleton from St. Nicolay"s Church graveyard in Oslo, Norway. We screened the data for the presence of pathogens and identified reads for the human pathogen *B. recurrentis*. Using 14 HiSeq datasets, we assembled a full draft genome of the pathogen, reconstructed its phylogeny, and analysed its genome.

Our genome is the first available European and historical genome of *B. recurrentis*. Our distinct European lineage has a discrete genomic makeup and has no available modern representatives. The *B. recurrentis* strain differs from the modern African strains available to date by showcasing additional gene loss in antigenic variation sites and an ancestral *oppA-1* gene, potentially resulting in significant ecological and clinical changes, such as a reduction in the number of febrile relapses.

We provide first molecular evidence for the presence of Louse borne relapsing fever prior to its identification in 1868. The results of this study suggest that LBRF has been circulating within European populations since Medieval times. Our results also give further insights into the genomic evolution of immune evasion systems in a human pathogen over centuries and highlight the importance of lice to human transmission during major epidemics in European history.

Our results come on the heels of a LBRF resurgence in Europe, which prompted the ECDC to issue two rapid risk assessments in 2015, and after reports of undetected outbreaks of the disease amongst homeless people in Marseille. In the wake of these reports, our results could provide the first opportunity to determine the geographic origin of future outbreaks and to improve the surveillance of industrialised populations still affected by lice-infestation.

Session • Plagues and pathogens

O–PAP–03

3,800-year-old *Yersinia pestis* suggests Bronze Age origin for bubonic plague

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Yersinia pestis is a highly virulent bacterium that causes bubonic, pneumonic and septicaemic plague and is infamous for its three documented pandemic eruptions throughout human history. Its transmission is facilitated via the flea vector, through a mechanism that is considered a necessary prerequisite for manifestation of the, most typical, bubonic form. Ancient DNA analysis has provided key insights regarding the early stages of *Y. pestis* evolution, with the oldest strains thus far isolated stemming from the Late Neolithic and Early Bronze Age periods (LNBA- 5,000-3,500y BP). Although these strains were evidently causing human infections, they seem to lack key genetic components required for efficient flea transmission, thus making their disease presentation in humans unclear.

Here, we use a metagenomic approach to detect *Y. pestis* in Late Bronze Age (~3,800 yBP) remains from the Samara region of modern-day Russia and subsequently employ a hybridization capture method to enrich for the *Y. pestis* genome from putatively positive individuals. Our reconstructed strains show clear distinctions to the previously described LNBA strains, suggesting that flea-adapted *Y. pestis* was present already during the Bronze Age. Through phylogenetic and molecular dating analysis we propose that several *Y. pestis* lineages were established during that time, some of which persist to the present day (i.e. 0.PE4, 0.PE2, 0.PE7).

Taken together, our results suggest that the ability for flea-mediated transmission causing bubonic plague in *Y. pestis* was present at least 4,000 years ago.

Session • Plagues and pathogens

O–PAP–04

Public access to the population structure of bacterial pathogens in the genomics era

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The recent advent of next generation sequencing has facilitated the reconstruction of the genomes of bacterial pathogens that infected humans up to 5,000 years ago (*1-3*). Such analyses can help to reconstruct the history of bacterial pathogens, especially if they are interpreted within the context of extensive population genomics of global samples of extant bacterial isolates. However, most genomic sequences of extant bacteria are not published as assembled contigs, but rather are simply deposited in the form of short read archives (*4*). We have therefore developed a web resource, EnteroBase (http://enterobase.warwick.ac.uk), which automatically scours all short-read archives for sets of Illumina short reads and supports uploading short reads by registered users. EnteroBase assembles and polishes genomic contigs from the short reads within 2 hours, calls Multilocus Sequence (MLST) genotypes from each assembly, and can perform SNP-based mapping to a closely related reference genome for up to 1,000 bacterial genomes.

EnteroBase currently supports public access to genomic assemblies from *Salmonella* (>139,000 genomes), *Escherichia* (>68,000), *Yersinia* (>1,800), *Moraxella* (>130), and *Clostridiodes* (>6,900). Currently private databases have also been established for *Klebsiella*, *Helicobacter*, and *Vibrio*, and new databases for additional genera can be created and filled with publicly available data within days if needed. An initial description of the population genomics of *Salmonella* has now been published (*4*), and overviews of the other genera are under preparation.

EnteroBase also supports genetic analyses based on defined SNP matrices. SNP matrices facilitate the integration of SNPs defined by ancient bacterial genomes into SNP trees of extant bacteria, which can then be examined together with metadata with the help of via our new visualisation tool, GrapeTree (*5*).

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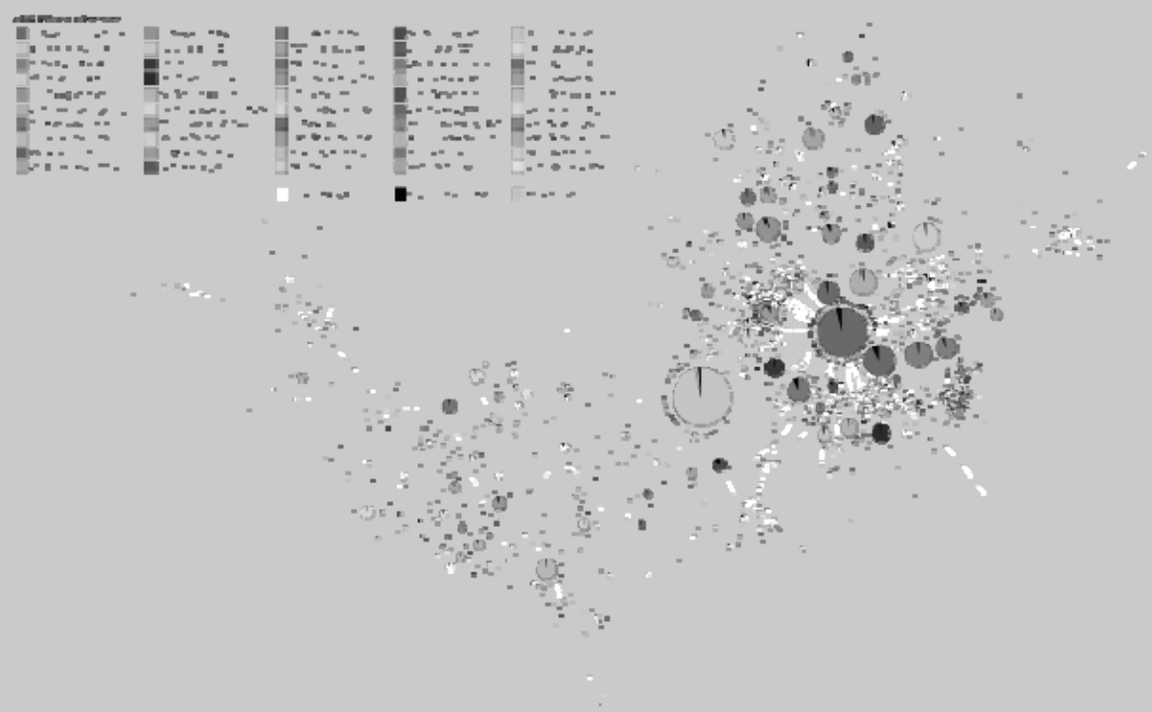
Fig 1



Session • Plagues and pathogens

O–PAP–05
Alternative scenarios for the origins of tuberculosis in the Pleistocene

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Introduction: Various data provide evidence for tuberculosis (TB) in archaeological specimens. Human and animal bone morphology pinpoint TB infection, backed up by biomarkers, such as full genomes, DNA fragment amplification and lipid biomarkers [1]. Combinations of DNA fragments and lipid biomarkers confirmed the oldest human TB cases from 9ka Atlit Yam, Israel and 10.5ka Dja"de el Mughara, Syria, along with a 17ka bison specimen from Natural Trap Cave, Wyoming [1]. The challenge is to detect TB in older Pleistocene mammals, elucidating true disease origins.

Objectives: To examine megafaunal Pleistocene bones for external and internal lesions, diagnostic of TB, by micro-CT scanning backed up by DNA and lipid biomarkers.

Methods: Micro-CT scanning was performed on metacarpals from *Bison priscus* ~35ka North Sea, Rotterdam; ~40ka Kent"s Cavern, Torquay; ~120ka Shropham, Norfolk and *Bison antiquus* ~20ka Natural Trap Cave, Wyoming; ~30ka Wasden, Idaho. DNA and lipid biomarkers were analysed as described previously [1].

Results: Micro-CT scanning revealed the presence of networks of internal cavities, related to external lesions. Particular metacarpals of *B. priscus* from ~120ka Shropham and ~35ka North Sea and *B. antiquus* ~30ka Idaho had distinct spherical internal cavities, remarkably similar in different bison species with very different ages and geographical origins. Control Shropham metacarpals and metatarsals had neither external nor internal lesions. Internal cavities were confirmed by bone dissection and the removed samples analysed for aDNA amplification and lipid biomarkers. In the sole significant ~40ka *B. priscus* case from Kent"s Cavern, mycocerosate TB markers were recorded but no TB aDNA was found.

Conclusions: Objective evidence is needed to determine the origins of TB in the Pleistocene. Currently, there is no direct evidence for the co-evolution of TB and *Homo sapiens* emerging "Out of Africa" or anywhere. The evolution of TB would have required a critical host population level, not available in African humans. Hordes of Northern Hemisphere megafauna would have provided ideal hosts for TB evolution from environmental mycobacteria, as indicated by the present results. A dramatic Late Pleistocene upsurge in TB pathogenicity correlates with mammalian extinctions and the rise of the modern TB complex in newly established human settlements at the start of the Holocene [1]. 1. Donoghue et al. Diversity 2017,9:46.

O–PAP–06
The significance of helminths in the UK over time

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Gastrointestinal helminths are a global problem, affecting about a sixth of the world's population. In 2001, delegates at the World Health Assembly unanimously endorsed a resolution (WHA54.19) urging endemic countries to start seriously tackling worms. Currently these helminths are treated using anthelmintics however there are issues of reinfection in communities that have been treated. Eradication of these organisms is therefore the most reliable means to limit their morbidity effects. The eradication of these infections is usually attributed to interruption of the fecal-oral route of infection by improved sanitation, better waste disposal systems and transportation of safe water. Unfortunately, in modern studies assessing the effectiveness of different sanitary elements in tackling helminth infections is difficult. A country which no longer supports the transmission cycles of these helminths, such as the UK, can provide a historical case example of the significance, and the subsequent eradication, of these organisms without anthelmintic intervention. Whilst helminths are reported from a range of archaeological sites within the UK, a systematic analysis of their epidemiological significance over time has not been undertaken. For this study, over 300 skeletal pelvic soil samples from 5 different time periods (Pre-historic, Roman, Anglo-Saxon, later Medieval and Industrial) were examined using microscopy and genetic techniques. The parasite load of historical England is comparable to modern day prevalence rates in rural developing countries, and the change from an endemic to a non-endemic country occurred rapidly, in relatively recent history. This study has also provided a temporal overview of changes in prevalence, risk factors (such as age and gender) and the stability of the helminth population in relation to an evolving human environment.

Session • Microbiomes

O–MIB–01
The dental calculus metabolome in modern and historic samples

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Introduction: Dental calculus is a mineralized microbial dental plaque biofilm that forms throughout life by precipitation of salivary calcium salts. Successive cycles of dental plaque growth and calcification make it an unusually well-preserved, long-term record of host-microbial interaction in the archaeological record. Recent studies have confirmed the survival of authentic ancient DNA and proteins within historic and prehistoric dental calculus, making it a promising substrate for investigating oral microbiome evolution via direct measurement and comparison of modern and ancient specimens.

Objective*:* We present the first comprehensive characterization of the human dental calculus metabolome using a multi-platform approach.

Methods*:* Ultra performance liquid chromatography-tandem mass spectrometry (UPLC–MS/MS) quantified 285 metabolites in modern and historic (200 years old) dental calculus, including metabolites of drug and dietary origin. A subset of historic samples was additionally analyzed by high-resolution gas chromatography–MS (GC–MS) and UPLC–MS/MS for further characterization of metabolites and lipids. Metabolite profiles of modern and historic calculus were compared to identify patterns of persistence and loss.

Results*:* Dipeptides, free amino acids, free nucleotides, and carbohydrates substantially decrease in abundance and ubiquity in archaeological samples, with some exceptions. Lipids generally persist, and saturated and mono-unsaturated medium and long chain fatty acids appear to be well-preserved, while metabolic derivatives related to oxidation and chemical degradation are found at higher levels in archaeological dental calculus than fresh samples.

Conclusions*:* The results of this study indicate that certain metabolite classes have higher potential for recovery over long time scales and may serve as appropriate targets for oral microbiome evolutionary studies.

Session • Microbiomes

O–MIB–02
Reconstruction of Oral Microbiomes from Extinct and Extant Anthropoids through ancient DNA

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While modern microbiome research has shown the importance of our microbial communities in health and disease, research has tended to focus on the gut microbiome of either Western industrialised societies or captive animals. Recent discoveries in the field of archaeogenetics have revealed dental calculus from skeletal remains as a rich source of well-preserved bacterial DNA. In contrast to sampling from live individuals, dental calculus from archaeological remains presents an opportunity to less-invasively study the oral microbiome from a wider diversity of species and populations.
We present results of a total over 3.5 billion shotgun DNA sequencing reads from ancient and modern dental calculus from over 90 hominids, including gorillas (29), chimps (20) and humans (45), as well as 14 Neanderthals from the Late Pleistocene and 5 New World monkeys. We show initial metagenomic and genomic analysis of similarities and differences in the oral plaque microbiome at different stages of anthropoid evolution. While preservation is variable in archaeological samples, dental calculus from the Late Pleistocene can still yield authentic ancient DNA attributable to known microbial taxa found in the modern human oral cavity. Expanding our knowledge of the diversity of the human microbiome through time and space will be important in understanding the deep relationship between hosts and their microbial communities.

O–MIB–03
Exploring the microbial diversity of archaeological remains with high-throughput DNA sequencing

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Microbes are essential to a number of key biogeochemical and ecological processes, with pathogens unleashing devastating epidemics, and commensals participating in metabolic, immune, and cognitive functions of their host. The large taxonomic and functional diversity of microbes constitutes a rich subject for ecological, evolutionary, medical, and archaeological research. In recent years, advances in ancient DNA research, especially methodologies harnessing the power of high-throughput DNA sequencing, have opened access to past microbial communities, leveraging the DNA fragments preserved in bones, teeth, dental calculus, coprolites, shells, and tissue collections. However, the degraded nature of ancient DNA molecules, as well as the co-extraction of DNA from hosts and ubiquitous environmental microbes, heavily challenge the accurate taxonomic identification and sequence reconstruction of ancient microbes. We will present a complete methodological framework for profiling microbial communities, and will apply this framework to high-throughput DNA sequencing datasets generated from ancient human, horse, and mollusc specimens. We will explore conditions and parameters influencing the sensitivity and accuracy of microbial reconstructions, as well as drivers for preservation. The microbial information gathered will finally be confronted to cultural, ecological, genomic, and epigenomic data within fully integrative evolutionary models for fine-grained investigation of processes as diverse as shifts in human lifestyle, horse domestication and epidemics onsets.

Session • Microbiomes

O–MIB–04

Profiles of microbial diversity and function within museum dental calculus samples extracted from wild great apes

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An understanding of the great ape microbiome is imperative to assessing the distribution of commensal and pathogenic oral bacteria across all primates. As access to saliva or plaque samples from living wild chimpanzees and gorillas is not feasible, an abundant alternative resource is calcified dental plaque removed from skeletons housed within museums. We obtained permission to remove dental calculus from 191 great apes (*Gorilla* n=76, *Pan* n=90, *Pongo* n=25) from four museums across the United States: Academy of Natural Sciences (Philadelphia, PA), Cleveland Museum of Natural History (Cleveland, OH), Field Museum of Natural History (Chicago, IL), and National Museum of Natural History (Washington D.C.). Twenty-four of those samples that yielded the highest abundance of DNA (yields range from 0.1 ng/µl to 70.3 ng/µl) have been selected to represent the oral microbial environment of wild apes. Each calculus sample was thoroughly decontaminated and extracted in a dedicated ancient lab at Arizona State University and shotgun prepped and sequenced using Illumina next generation sequencing. These samples will be quality filtered and examined using MEGAN and Humann2, with additional comparisons to *Pan troglodytes schweinfurthii* calculus from Gombe National Park in Tanzania and previously published metagenomic data from ancient and historic human calculus. Wild *P. t. schweinfurthii* oral microbiomes show an abundance of bacteria belonging to the "Red Complex", particularly *Porphyromonas gingivalis*, but the extent of this abundance across species and geography is not well known. We will discuss the implications of these commensal and pathogenic microbes along with their functional profiles on our understanding of the evolution of the human and non-human primate oral ecosystem and assess future directions of research utilizing museum collections.

O–MIB–05

The individuality of disease – evidence from the oral metaproteome of Medieval Danes

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The diversity and makeup of the ancient oral microbiome has recently become possible to investigate using advanced biomolecular methods such as metagenomics and metaproteomics. Many clinical studies have examined the structures of healthy and diseased microbiomes, but few have assessed this on the individual scale. This study presents an analysis of the individuality of the human metaproteome from the archaeological dental calculus of 21 Medieval Danish individuals with evidence of periodontal disease. We identify 3672 proteins across all samples of which 3454 are of bacterial origin, 206 are human, and the rest are dairy proteins, or belonging to the archaea domain. The bacterial profiles from individuals cluster into two distinct groups. The oral proteomes from these two groups also display more homogeneity than comparative modern samples. Furthermore, we applied high pH fractionation on a subset of samples, in combination with TMT labelling, which resulted in approximately 30% more protein identifications.

Session • Microbiomes

O–MIB–06
Consequences of European arrival on ancient Indigenous American microbiota

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European arrival in the New World brought many changes to Indigenous people, critically including the introduction of devastating diseases such as small pox, measles, and cholera. However, the chronic and long-term impacts of European arrival on health have not yet been explored. The ability to reconstruct the trillions of commensal microorganisms (microbiota) that lived within ancient people now provides a new opportunity to explore these changes in real time. Here, we reconstruct ancient oral microbiota by sequencing bacterial DNA preserved within calcified dental plaque (calculus) from 172 ancient North and South Americans, as well as nine post-Columbian individuals, to explore the long-term health impacts of European arrival in the New World. The oral microbiota of North and South Americans prior to European arrival was remarkably more diverse than that of their contemporaneous European counterparts and fell outside of known ancient and modern European variation. Discrete variation within the Americans was also present and is likely linked to their unique lifestyles and environments. The oral microbiota also remained similar over time in several single locations, despite cultural or regime changes. After European contact, historic oral microbiota diversity fell within ancient American diversity, suggesting that the immediate arrival and disease spread by Europeans in the Americas had few, rapid effects on the overall structure of oral microbiota. This research also suggests that the assimilation of modern oral microbiota throughout the Americas likely occurred due to Industrialisation and modernization after 1850. Ancient dental calculus provides a wealth of information to better understand how past events may have contributed to modern human health.

Session • Microremains and residues

O–MAR–01

Identification of the residue in sphero-conical vessels reveals ancient explosives, oils, perfumes and medicines from Jerusalem

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Small stoneware Sphero-conical vessels have been found on archaeological sites throughout the Middle East between the 9th and 15th century. Researchers have proposed many uses for these sphero-conical vessels, which include; smoking pipes, grenades and small containers holding medicines, mercury, oil, beer or perfume. Experimental archaeology maintains the plausibility of all these hypotheses. The unusual nature of the ceramic, being the only highly fired stoneware produced in the Middle East, together with the very thick walls of at least 1 cm on a typical 10 cm diameter vessel, would indicate the manufacture for highly specific and unusually dedicated functions that may have only existed at this time. The residues adhering to sherds from four small, thick-walled, sphero-conical, stoneware vessels, from 11-12th century Jerusalem, have been analysed using microscopy, biochemical characterisation and spectroscopy. These results indicate that the aperture of one of these vessels could have been sealed with resin. The variation between residue samples indicates different uses for these four ceramic vessels including containers for oils, scented materials and medicines while residues on one sherd are consistent with that vessel''s use as an explosive weapon.

Session • Microremains and residues

O–MAR–02
Molecular investigation of resin cargos found on two asian shipwrecks dated to the XIIth century

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Introduction : Two Southeast Asian shipwrecks, the « Flying Fish » and the « Lingga », dated to the early XIIth century, were discovered off Sabah, East Malaysia, and northwest of Lingga Island, Indonesia, respectively. Their main cargo consisted of Chinese ceramics and wrought and cast iron together with resins of unknown origin. The Flying Fish Wreck probably loaded in Quanzhou, China, while the Lingga Wreck most likely loaded in Guangzhou.

Objectives : Molecular investigations of a resin sample from each wreck were carried out in order to determine their molecular composition, as well as their botanical/geographical origin.

Methods : Fractions from the derivatized organic extracts of the resins were separated by column chromatography and investigated by GC-MS.

Results : Molecular analysis of the organic extracts revealed the occurrence of two main series of constituents corresponding to triterpenoids and sesquiterpenoids typical of resins from Dipterocarpaceae. Sesquiterpenoids are characterized by the occurrence of α-copaene, β-elemene and caryophyllene which are characteristic of resins from the genus *Shorea*. Remarkably for Dipterocarpaceae resins, the sequiterpenoids are accompanied by complex mixtures of dimeric and trimeric homologues possibly related to a polymeric component of the resins. They may correspond to native constituents or to diagenetic transformation products, a point to be clarified by further molecular investigation of fresh resins.
Globally, the molecular assemblage of triterpenoids is similar and is constituted by compounds from the oleanane, ursane, dammarane and lupane series characteristic of resins from Dipterpocarpaceae. Contrary to the resin from the « Lingga » wreck , the triterpenoids from the « Flying Fish » additionally comprise shoreic acid, a molecular marker also typical of resins from *Shorea*. This could indicate that both resins are related to the genus *Shorea*, but have been produced by trees from distinct species possibly in relation with their production site. Several alteration products of triterpenoids were also detected and are formed by diagenetic processes.

Conclusion : The two resins were identified as resins from *Shorea*. Taking into account the range of trees from the genus *Shorea*, they do not originate from China and have most likely been loaded locally.

O–MAR–03
What's cooking? – investigating vessel-use and culinary practices in the Indus Civilisation through organic residue analysis

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The Indus Civilisation, South Asia"s first urban civilisation, is known for its well-planned cities, elaborate crafts, enigmatic script, and sudden transformation from the urban (*c.* 2500-1900 B.C) to the post-urban (*c.* 1900-1500 B.C) period that correlates with abrupt climatic instability. Knowledge about agricultural strategies and animal exploitation at different Indus settlements has greatly increased our knowledge of the diversity of subsistence practices and their resilience in the post-urban period, however how this evidence relates to Indus culinary practices has been under-explored.
This paper presents lipid analyses of cooking jars, storage jars and perforated vessels from urban and rural settlements of the Indus Civilisation, dating to both the urban and post-urban period, relating it to the present known archaeobotanical, zooarchaeological, and ceramic evidence. As the first large-scale study on Indus ceramic lipids, the study reveals direct evidence for how vessels were being used and what foods were being cooked in the Indus Civilisation, and aims to reconstruct a holistic picture of the domestic culinary choices of Indus populations. The limitations and interpretational challenges of working within environments with low lipid preservation and minimal access to modern references are also presented.

Session • Microremains and residues

O–MAR–04
Improving the analysis of liquid plant products absorbed in Mediterranean transport amphorae

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Amphorae found across the Mediterranean in antiquity are thought to have been used to transport high value liquid plant commodities, such as olive oil and wine. Determining their exact contents using chemical analysis is needed to help characterise these important maritime economies and to understand how they changed through time. While the identification of animal fats (dairy products, adipose fats, marine and freshwater products) is now well established using organic residue analysis (ORA), plant products are rarely detected and are difficult to characterise at high taxonomic resolution. Indeed, the main molecular compounds are widespread in the plant kingdom and are highly susceptible to degradation. Wine appears to be an exception but there is little consensus concerning its detection. Despite some undeniable methodological improvements, no widely accepted analytical protocol has been set up and even the specificity of wine-biomarkers has been questioned.
Here we applied new analytical protocols to one hundred transport amphora sherds (5th-13th century) from Mediterranean contexts, which are believed to have contained predominantly olive oil or wine. A four-step protocol was applied to analyse a wide range of organic compounds. Samples were screened for lipids and phenolic and small acids with GC/MS after solvent extraction, followed by alkaline treatment on the remaining sherd powder. When enough lipids were preserved, acid extraction was performed to deeply investigate the unsaturated fatty acids and perform carbon stable isotope measurements. For samples containing phenolic and small acids, a soft acid extraction was tested to tentatively extract and analyse polyphenols with LC/MS/MS.
First screening steps yielded medium quantities of organics in most of the sherds, generally displaying unspecific distributions of lipids. However, the deep analysis of samples containing unsaturated fats reveals some trends in their distribution, suggesting various commodities (different plant oils, possible fish sauce, or mixing of products). Conifer exudates were also identified. Tartaric acid, usually reported to be a wine biomarker, was detected only in very few samples, but numerous other small and phenolic acids were also identified. The diversity of molecular distributions revealed by this study highlights the potential of ORA for identifying plant products absorbed in pottery and the interpretations will be deepened by comparison with modern samples.

O–MAR–05
Investigating the nature and timing of the earliest human occupation of North America using a lipid biomarker approach

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The question of how, when and why people first settled the Americas has been a subject of intense debate which continues to the present. There are two schools of thought, the "Clovis First" and "Pre-Clovis" theories, with the former asserting that the Clovis culture was the earliest human presence in North America arriving ca.13,500 cal BP. Evidence of "Pre-Clovis" human occupation in North America obtained through DNA analysis of coprolites from the Paisley Caves, south-central Oregon, has dated the earliest occupation to 14,300 B.P., one thousand years earlier than previous evidence suggests. Coprolites (fossil faeces) contain a suite of lipid biomolecules and are an invaluable source of palaeobiological and palaeoecological information. The identification of faecal matter through the presence of highly-specific lipid biomarkers (5β-stanols and bile acids) has been used to identify and characterise faecal input from a range of different sources.
Differentiation of these faecal markers is enabled through the diet, digestion and metabolism of the source animal. Lipid analysis of coprolites has also been used to identify dietary biomarkers, providing information regarding available plant resources. Here, a lipid biomarker approach has been applied to coprolite and associated sediment samples from the Paisley Caves with the aim of identifying the timing of the earliest occupation of North America by firstly characterising the origin of coprolites found in well-stratified archaeological deposits and then by using compound-specific 14C dating of 5β-stanols to precisely date the human presence in the cave. Biomarker analysis has also been applied to investigate the nature of the earliest occupation human of North America through dietary reconstruction which will enhance our understanding of the relationship between early humans and their environment.

Session • Microremains and residues

O–MAR–06

Multiple criteria for the detection of plant resources processed in hunter-gatherer pottery vessels from the Upper Volga, Russia

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In Northern Eurasia, the Neolithic is marked by the adoption of pottery by hunter-gatherer communities. The degree to which this is related to wider social and lifestyle changes is subject to ongoing debate and the focus of a new research programme. The use and function of early pottery by pre-agricultural societies during the 7th-5th millennia BC is of central interest to this debate. Organic residue analysis provides important information about pottery use. This approach relies on the identification and isotopic characteristics of lipid biomarkers, absorbed into the pores of the ceramic or charred deposits adhering to pottery vessel surfaces, using a combined methodology, namely GC-MS, GC-*c*-IRMS and EA-IRMS. However, while animal products (e.g., marine, freshwater, ruminant, porcine) have the benefit of being lipid-rich and well-characterised at the molecular and isotopic level[1], the identification of plant resources still suffers from a lack of specific criteria for identification. In hunter-gatherer contexts this problem is exacerbated by the wide range of wild, foraged plant resources that may have been potentially exploited. Here we evaluate approaches for the characterisation of terrestrial plant food in pottery through the study of pottery assemblages from Zamostje 2 and Sakhtysh 2a, two hunter-gatherer settlements located in the Upper Volga region of Russia.

GC-MS analysis of the lipids, extracted from the ceramics and charred residues by acidified methanol, suggests that pottery use was primarily oriented towards terrestrial and aquatic animal products. However, while many of the Early Neolithic vessels contain lipids distinctive of freshwater resources, triterpenoids are also present in high abundance suggesting mixing with plant products. When considering the isotopic criteria, we suggest that plants were a major commodity processed in pottery at this time. This is supported by the microscopic identification of Viburnum (*Viburnum Opulus L.*) berries in the charred deposits on several vessels from Zamostje 2.

The study of Upper Volga pottery demonstrated the importance of using a multidisciplinary approach to determine the presence of plant resources in vessels. Furthermore, this informs the selection of samples, often subject to freshwater reservoir effects, for ^{14}C dating[2].

References:

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Session • Advances in metagenomics

O–ADM–01
DNA from the Wine-Dark Sea – searching for DNA on ancient shipwrecks

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Finding a way to accurately characterise the contents of amphorae recovered from Mediterranean shipwrecks would provide invaluable insight into cargo compositions and trade dynamics. Is DNA the answer? There is tremendous potential for DNA studies to resolve long-standing questions in both terrestrial and underwater archaeology. Great optimism for the recovery of ancient DNA (aDNA) from maritime sites has spurred a series of studies claiming to have successfully extracted aDNA from a variety of artefacts recovered from underwater sites including plant remains (Elbaum et al 2005; Manen 2003), human skeletons (Hershkovitz 2008) and shipwreck amphorae (Hansson and Foley 2008, Foley et al. 2012). However, these studies have not adequately addressed the source of the DNA recovered: does it derive from taxa present in the underwater deposition environment or the artefact itself? My research eliminates this ambiguity by examining the efficacy of extracting aDNA from the ceramic matrix of vessels recovered from six ancient Mediterranean shipwrecks and establishing, through metagenomic analysis and bioinformatics, what DNA is present in the water column and seafloor sediments that surround these sites. The methods used in this research suggest new standards for the recovery of ancient DNA from underwater archaeological sites.

O–ADM–02
Revealing and understanding the marine palaeolandscape of the North Sea using sedaDNA

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Whilst ancient DNA studies have typically relied on valuable archaeological plant and animal macroremains, increasingly ancient sediments have been exploited as an abundant and widely available source of DNA (sedaDNA). sedaDNA has been used as a tool to explore hominin-environment interactions, for the development of palaeoenvionmental reconstructions, and to study floral and faunal extinction events.
Here we will use the work we are currently undertaking on sediment cores from Doggerland to reveal the early Holocene landscape before inundation led to the isolation of Britain, and discuss not only the limitations and challenges involved when working with sedaDNA, but also the power and relative merits of the approaches we can use. We will also demonstrate the benefits of using a variety of complimentary methods, in addition to sedaDNA approaches. These should be used in order to guide study design and, crucially, in the contextualisation and validation of findings.
sedaDNA analysis can be confounded by contamination from modern DNA sources, which can arise from leaching between the sediment strata, or during sampling and processing. Characteristic DNA breakdown patterns, including cytosine deamination, are used to authenticate the age of the ancient DNA. However, the extent of deamination expected under various environmental conditions is currently limited by a narrow training set of sample types that are unrepresentative of marine environments. We have demonstrated that, *in vitro,* rates of cytosine deamination are significantly reduced for free DNA in saline environments; a result has implications for the use of DNA damage patterns as a tool for the authentication of ancient DNA where samples are derived from a marine context.
The exploitation of sedaDNA has tremendous scope not just for expanding our understanding of human-environment interactions as in this study, but as a tool that can, potentially, be applied worldwide.

Session • Advances in metagenomics

O–ADM–03
Optimization of efficient ancient DNA extraction from lake sediment

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Insights derived from ancient DNA preserved in hard tissues, such as bone, are revolutionizing our knowledge of biotic dispersals and population histories. Although powerful, these data generally do not provide high temporal resolution for these events, in part due to the paucity of, and biases within, the hard tissue record. Ancient DNA from lake sediments (*sed*aDNA) has been shown to provide fine temporal resolution, and so has great potential to refine insights into the speed and dynamics of biotic changes, such as the appearance of a particular agricultural tradition or the immigration of key taxa to a region. However, unlike the mature methodology of ancient DNA extraction from hard tissues, the extraction of *sed*aDNA can be problematic, due to the complex and variable geo- and biochemical composition of sediments, which currently constrain the temporal and spatial availability of sediments amenable to ancient DNA analysis. In this study, we compared nine *sed*aDNA extraction protocols across a variety of sediment types. Although protocol chemistry impacted metabarcoding-inferred plant taxonomic diversity, sediment types with high organic content often yielded near-unusable results regardless of the protocol used. However, slight modification of an existing protocol greatly improved the results for some of these problematic sediment types. Together with other *sed*aDNA methodologies currently in development, this work brings us closer to unlocking the full potential of this underexploited ancient DNA source.

O–ADM–04
Deciphering ancient microbes with modern population genomic databases

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Metagenomics reveals the unprecedented genetic variation of microbial communities, including those from ancient human remains. The analysis of metagenomic data begins with taxonomic prediction of all microbes in the sample. Recent evaluation studies (*1*) demonstrate that current methods for taxonomic predictions either lack of sufficient sensitivity for species-level assignments or suffer from false positives, overestimating the number of species in the metagenome. Both are especially problematic for the identification of endogenous pathogens in low-abundance, common in ancient metagenomic samples. In addition, the reference genomes used in the predictions are limited and biased towards pathogens over environmental species. Reads from unknown sources, e.g. unknown environmental strains, can accidentally map onto distantly related pathogens.

We designed a new method, SPARSE, which improves the taxonomic predictions of metagenomic data. SPARSE normalizes existing biased databases by grouping reference genomes into similarity-based hierarchical clusters (Fig. 1). SPARSE also filters out reads from unknown sources using a probabilistic model, hence avoiding over-enthusiastic matches to known pathogens. Our evaluation using both simulations and real ancient samples demonstrated SPARSE"s improved precision in comparison to other methods.

We have also integrated SPARSE as part of EnteroBase. Enterobase is a centralized database that allows free access for the users to the genomes and molecular typing of ≥200K bacterial strains from several important pathogens through a graphical web interface. Enterobase includes automatic pipelines to characterize bacterial strains based on short reads from public databases or uploaded by registered users.

Here we demonstrate the utility of SPARSE in Enterobase using 22 previously published ancient plague samples (2-7). The Yersinia pestis specific reads were extracted by SPARSE and compared with 714 modern relatives in the EnteroBase Yersinia database (Fig. 2). The combination of SPARSE and EnteroBase allows reliable placements of aDNA within the entire evolutionary history of Y. pestis.

Session • Advances in metagenomics

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Fig 1

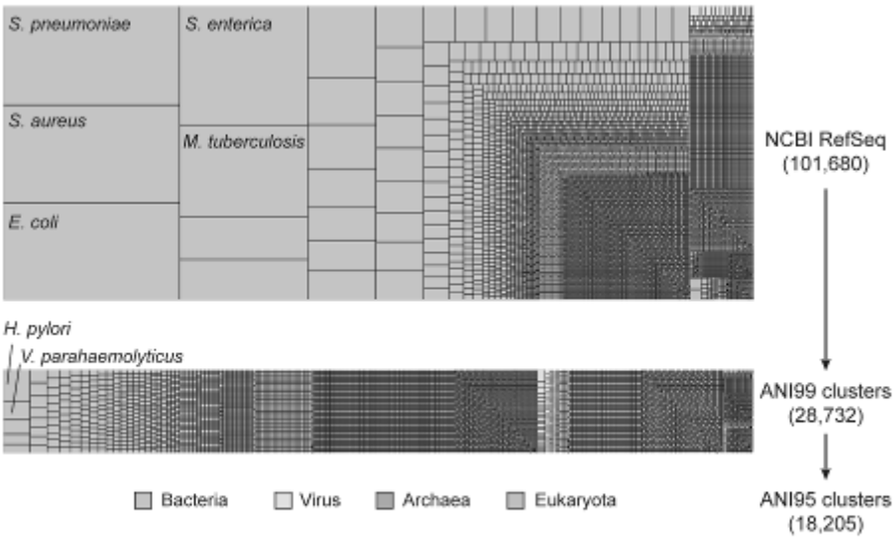

Fig. 1. Hierarchical clustering of 101,680 genomes in NCBI RefSeq database (Aug. 2017) into 18,205 ANI 95% clusters using SPARSE. Each rectangle represents such a cluster at ANI 95% level, with its area relative to the total number of genomes (top) or clusters at ANI 99% (bottom).

Fig 2

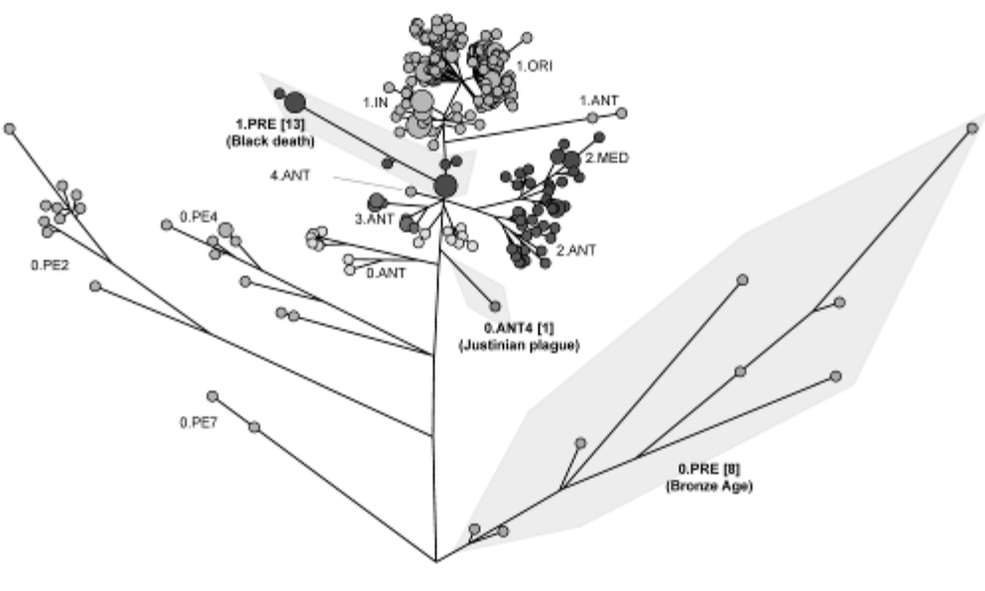

Fig 2. A maximum-likelihood phylogeny of 6,811 SNPs in the core genomic regions of 714 modern Yersinia pestis genomes and 22 ancient strains from 6 aDNA projects (2-7). The circles present tip nodes in the tree, and are connected by branches as in the phylogeny. These nodes are scaled by the numbers of genomes assigned to them and color-coded by the corresponding lineages. The names of the lineages are also shown nearby the nodes. The numbers of ancient strains in each of the three lineages (pink polygon) are indicated in brackets after the names of lineages (bold).

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O–ADM–05
HOPS – A pipeline for screening archaeological remains for pathogen DNA

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Insights into the relationship between hosts and pathogens throughout human history can be gained by leveraging large scale metagenomic datasets obtained from archaeological remains. However, technical challenges due to database biases and ancient DNA authentication make manual detection of microbes both difficult and time consuming.
Here we present HOPS (Heuristic Operations for Pathogen Screening), an automated pathogen screening pipeline for ancient DNA sequence data that provides a combined architecture for reproducible information on species identification and authentication in ancient metagenomic datasets. HOPS consists of a customized version of (1) MALT (Megan ALignment Tool), (2) MaltExtract, a Java tool that evaluates a series of authenticity criteria for a list of target species, and (3) customizable post-processing scripts to identify, filter, and visualize candidate hits from the MaltExtract output.
We evaluate the overall performance of HOPS in terms of specificity and sensitivity through analyses of both archaeological and *in silico* test datasets. We further demonstrate the suitability of HOPS through comparison against two other common approaches for metagenomic assessment, namely Kraken (k-mer matching) and MIDAS (marker gene-based). In addition, we assess and compensate for biases resulting from the reference database contents and structure.
HOPS successfully confirmed all experimental samples and correctly identified all simulated target pathogens that were present with at least 50 reads in the metagenomic library. Especially for low amounts of endogenous DNA (50 reads) HOPS was more sensitive than the other methodologies.
With HOPS we provide a versatile and fast pipeline for high-throughput microbial pathogen screening of archaeological material that aids in the identification of candidate samples for further analysis.

Session • Advances in metagenomics

O–ADM–06
Functional analysis of ancient metagenomic reads using genomic alignments

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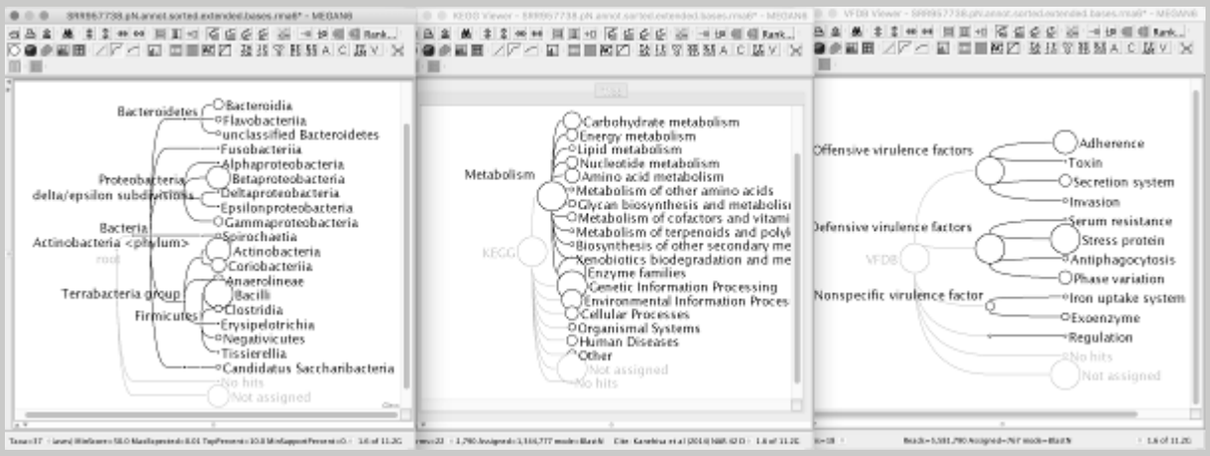
In the study of ancient human microbiomes and pathogens, functional information is of interest, for example, which genes or virulence factors were found (e.g. Weyrich et al, 2017 or Vågene et al, 2017). However, current methods of obtaining functional information rely on nucleotide-to-protein alignments (e.g. BLASTx), which struggle to classify the short DNA reads typical of ancient samples.

Here we present a computational pipeline that addresses this problem. In this approach, after quality control and ancient DNA processing, we propose to align the reads to all RefSeq microbial genomes (we use all archaeal and bacterial genome sequences of at least scaffold quality, from ftp://ftp.ncbi.nlm.nih.gov/refseq/) using a DNA aligner such as minimap (Li 2016) or MALT (Vågene et al, 2017).

A new program called AAdd is then used to process the resulting files, which adds protein accessions to them based on GFF files associated with the reference genomes. These augmented alignments are then imported into the microbiome analysis program MEGAN (Huson et al, 2016) to bin all reads to taxonomic and functional classes. For applications to ancient pathogens, we also discuss a new extension to MEGAN that bins reads to virulence factors as represented in VFDB (Virulence Factors of Pathogenic Bacteria database, Chen et al, 2005).

To illustrate the pipeline we used ancient dental calculus data from (Warinner et. al. 2014). In terms of taxonomic composition, our pipeline produced results similar to the original study. In addition, we produced functional annotation of these datasets for the InterPro2GO, COG, SEED, KEGG, PFAM and VFDB. Our pipeline found at least one alignment for 42% reads in one of the ancient samples (BG61), and 84% of the alignments received a protein accession. We could assign 24% of the aligned reads to a class in the KEGG classification, 35% in InterPro2GO, 14% in SEED, and 767 in VFDB. This method will enhance our ability to classify functional information from ancient metagenomic samples, allowing for new and refined insights into the functional repertoire of past microbiomes and pathogens.

Fig 1



Session • Mobility

O–MOB–01
Estimating mobility using sparse data – application to human genetic variation

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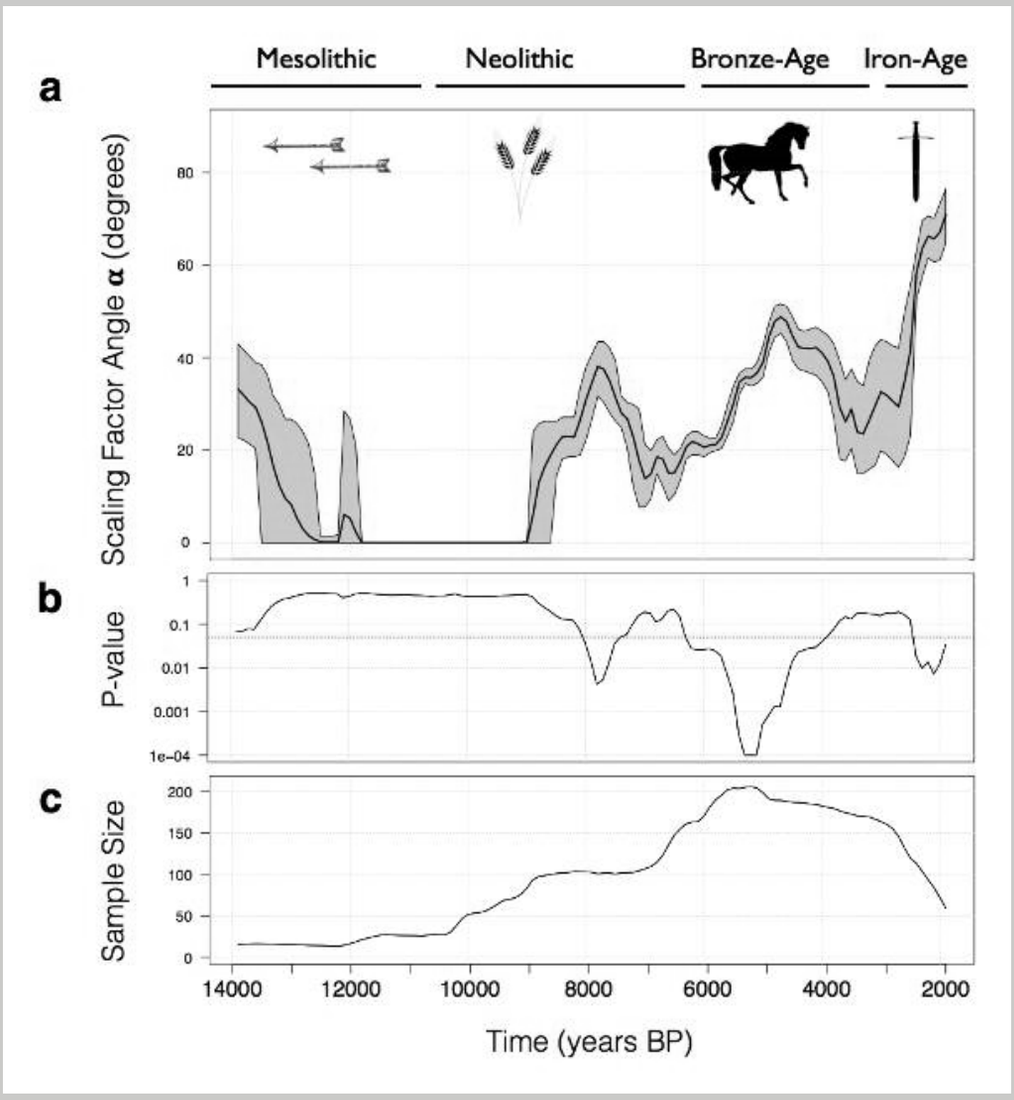
Mobility is one of the most important processes shaping spatiotemporal patterns of variation in genetic, morphological, and cultural traits. However, current approaches for inferring past migration episodes in the fields of archaeology and population genetics lack either temporal resolution or formal quantification of the underlying mobility, are poorly suited to spatially and temporally sparsely sampled data, and permit only limited systematic comparison between different time periods or geographic regions. Here we present an estimator of past mobility that addresses these issues by explicitly linking trait differentiation in space and time. We demonstrate the efficacy of this estimator using spatiotemporally explicit simulations and apply it to a large set of ancient genomic data from Western Eurasia. We identify a sequence of changes in human mobility from the Late Pleistocene to the Iron Age. We find that mobility among European Holocene farmers was significantly higher than among European hunter–gatherers both pre- and postdating the Last Glacial Maximum. We also infer that this Holocene rise in mobility occurred in at least three distinct stages: the first centering on the well-known population expansion at the beginning of the Neolithic, and the second and third centering on the beginning of the Bronze Age and the late Iron Age, respectively. These findings suggest a strong link between technological change and human mobility in Holocene Western Eurasia and demonstrate the utility of this frame- work for exploring changes in mobility through space and time.

Fig 1



Session • Mobility

O–MOB–02
Early population history of the island of Crete in Greece – isotopic evidence for diet and mobility

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Despite accumulating evidence for visitation of the island of Crete by Mesolithic and Palaeolithic foragers, there is a general consensus over a purposive Neolithic colonization by newcomers from Anatolia. Probably arriving in more than a single episode over several centuries, these newcomers are considered the first settlers. Dating back to the beginning of the seventh millennium BC, Knossos is one of the earliest farming sites in Europe.
In the above context, this paper presents and discusses results from a Marie Skłodowska-Curie project. This research used human skeletal remains from Crete, which date to the period between 5500 and 2000 BC, including the earliest known human collection from the island, and analysis of five complementary isotope systems to investigate geographical origins and diet as proxies for distinguishing between different groups, reconstruct mobility and gain insights into the lifeways and social organization of the respective communities. AMS radiocarbon dates, which were also generated as part of this project provided a clear chronological framework for this research.

O–MOB–03
Bronze Age population dynamics and the rise of dairy pastoralism on the eastern Eurasian steppe

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Recent paleogenomic studies have shown that migrations of Western steppe herders (WSH), beginning in the Eneolithic (ca. 3300-2700 BCE), profoundly transformed the genes and cultures of Europe and Central Asia. Compared to Europe, the eastern extent of this WSH expansion is not well defined. Here we present genomic and proteomic data from 22 directly dated Bronze Age khirigsuur burials from Khövsgöl, Mongolia (ca. 1380-975 BCE). Only one individual showed evidence of WSH ancestry, despite the presence of WSH populations in the nearby Altai-Sayan region for more than a millennium. At the same time, LC-MS/MS analysis of dental calculus provides direct protein evidence of milk consumption from Western domesticated livestock in 7 of 9 individuals. Our results show that dairy pastoralism was adopted by Bronze Age Mongolians despite minimal genetic exchange with Western steppe herders.

Session • Mobility

O–MOB–04
The Steppe was Sown – multi-isotopic research changes our understandings of Scythian diet and mobility

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Nomadic pastoralists conventionally known as the Scythians occupied the Pontic steppe during the Iron Age, c. 700-200 BC, a period of unprecedented pan-regional interaction. Popular science accounts of the Scythians promote narratives of roving bands of nomadic warriors traversing the steppe from the Altai Mountains to the Black Sea coastline. The quantity and scale of mobility in the region is usually emphasized based on the wide distribution of material culture and the characterization of Iron Age subsistence economies in the Pontic steppe and forest-steppe as mobile pastoralism. Yet, there remains a lack of systematic, direct analysis of the mobility of individuals and their animals. Here, we present a multi-isotopic analysis of humans from Iron Age Scythian sites in Ukraine. Mobility and dietary intake were documented through strontium, carbon and oxygen isotope analyses of tooth enamel. Our results provide direct evidence for mobility among populations in the steppe and forest-steppe zones, demonstrating a range of localized mobility strategies. However, we found that very few individuals came from outside of the broader vicinity of each site, often staying within a 90 km radius. Dietary intake varied at the intra-site level and was based in agro-pastoralism.
While terrestrial protein did form a portion of the diet for some individuals, there were also high levels of a 13C-enriched food source among many individuals, which has been interpreted as millet consumption. Individuals exhibiting 87Sr/86Sr ratios that fell outside the local range were more likely to have lower rates of millet consumption than those that fell within the local range. This suggests that individuals moving to the site later in life had different economic pursuits and consumed less millet. There is also strong evidence that children and infants moved at the pan-regional scale. Contrary to the popular narrative, the majority of Scythians engaged in localized mobility as part of agricultural lifeways while pan-regional movements included family groups.

O–MOB–05
Isotope evidence of human migration and mobility at the Roman and Byzantine port city of Ephesus, Turkey

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There is widespread mobility and migration around the Mediterranean in the Roman and late Byzantine periods. A key site in both of these times was the major port city of Ephesus, located in modern-day Turkey. Here we present the results of a large-scale strontium isotope study of human mobility, which included mapping the bioavailable strontium in the region surrounding the site. Our study was designed to integrate with the long-established Austrian Archaeological Institutes excavations at Ephesus, to combine the many lines of archaeological evidence with the new isotope data to see the level of movement of people into the site in the Roman period, and particularly in the Byzantine period when it was a major Christian pilgrimage site. In addition, we have measured the sulphur isotope values of human bone collagen, which gives us an insight into mobility in later life (in contrast to strontium in enamel, which mostly records childhood location).

Session • Mobility

O–MOB–06
Testing the frequency of human colonisation of Rapa Nui (Easter Island)

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The colonisation of Rapa Nui (Easter Island) by Polynesians was a rapid and relatively recent event, which took place around 1200 AD. The Pacific Rat (*Rattus exulans*) is a commensal species that was introduced to Remote Oceania by humans and was transported from island to island, following human colonisation pathways. Therefore, its mitochondrial genome can be a valuable source of information regarding the timing and route of the Polynesian dispersal in Remote Oceania. Previous ancient DNA studies have shown limited variation among Easter Island rat samples, indicating a limited introduction followed by isolation.
In this study, we aim to characterise the evolution of the mitochondrial genome in *Rattus exulans* through time by analyzing the complete mitochondrial genome of 60 individuals excavated from different stratigraphic layers from Anakena Beach, Easter Island. The DNA extracted from *Rattus exulans* bones was enriched for mtDNA through hybridization capture prior to sequencing. The analysis, which is currently underway, is expected to show if and when novel haplotypes were introduced to the Island. The presence of a specific genetic structure through time might indicate a unique colonization event whereas variation can suggest multiple introductions or contact with other islands. Our results, combined with previously published genetic data and other lines of evidence from the archaeological record, will contribute to reconstructing the journey humans undertook to reach one of the most remote places on earth.

Session • Pathogen genomics

O–PGE–01
Historic *Treponema pallidum* genomes from Colonial Mexico

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Among the worldwide prevalent treponemal diseases syphilis appears as a global threat that is currently re-emerging. However, the origins of syphilis and other treponemal diseases are so far unresolved and are subject to an intensive scholarly debate. Until now, assumptions on its origins and evolutionary history could only be drawn from osteological analyses of past cases and genetic analysis of contemporary *T. pallidum* genomes; contributions from ancient DNA are very rare and have, until now, failed to provide genome-level data.
Here we present three historic *T. pallidum* genomes (two from *T. pallidum* ssp. *pallidum* and one from *T. pallidum* ssp. *pertenue*) that have been reconstructed from skeletons recovered from the Convent of Santa Isabel in Mexico City, operational between the 17th and 19th century. Our analyses indicate that different *T. pallidum* subspecies caused similar diagnostic presentations that are normally associated with syphilis in infants, and potential evidence of a congenital infection of *T. pallidum* ssp. *pertenue,* the causative agent of yaws. This first reconstruction of *T. pallidum* genomes from archaeological material opens the possibility of studying its evolutionary history at a resolution previously assumed to be out of reach and thereby establishes a new method that could greatly contribute to uncover the mystery regarding the origins of treponemal diseases.

O–PGE–02
Neolithic and Medieval virus genomes reveal the complex evolution of Hepatitis B

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Introduction: The hepatitis B virus (HBV) is one of the most widespread human pathogens, with one third of the world population being infected, and an annual death toll of about 1 million globally. Despite being widespread and well-studied, the origin and evolutionary history of HBV is still unclear and controversial. Here, we report the analysis of three HBV positive human skeletal remains from the prehistoric Neolithic (Karsdorf and Sorsum) and Medieval Periods (Petersberg) in Central Europe.
Objectives: The main objective was the reconstruction of complete ancient HBV genomes and the assignment of their phylogenetic positions within the diversity of nowadays hominid HBV strains.
Methods: From each sample, double-stranded DNA sequencing libraries (UDGhalf) were prepared and sequencing was carried out. Post processed reads were mapped against a multi fasta reference containing eight different HBV genotypes and eight monkey strains. Mapped reads were de-novo assembled resulting in three full length ancient HBV genomes. Phylogenetic analysis was conducted resulting in a network consistent of 495 HBV genomes to mimic nowadays diversity.
Results: We present three full length HBV genomes from 1000-7000 year old skeletal remains in Central Europe. Phylogenetic network analysis revealed that two of our ancient genomes, namely Karsdorf and Sorsum, are most closely related to today's African non-human primates (NHP). Although the two Neolithic strains were recovered from humans who had lived about two thousand years apart, they show higher genomic similarity to each other than to any other human or NHP genotype. The genome from the 1000-year-old Petersberg individual clusters with modern D4 genotypes.
Conclusion: Our results demonstrate that HBV already existed in Europeans 7000 years ago and that its genomic structure closely resembled that of modern hepatitis B viruses. Both Neolithic viruses fall between the present-day human and the known NHP diversity. Therefore, it can be hypothesized that although the two Neolithic HBV strains are no longer observed today and thus may reflect two distinct clades that went extinct, they could still be closely related to the remote ancestors of the present-day genotypes, which is supported by signs of ancient recombination events. To disentangle the complex evolution of HBV more ancient precursors, intermediates and modern strains of both humans and NHPs need to be sequenced.

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O–PGE–03
A pathogen and a delicacy – the genomics of historic corn smut

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Domestication had a tremendous effect on crop species, leading to the appearance of new phenotypes, causing a decrease in effective population sizes, and reducing genetic diversity. In addition to transforming the species under selection, it is increasingly appreciated that domestication also impacted crop pathogens. Understanding how pathogen diversity and virulence changed through time can reveal how past farmers dealt with crop diseases as well as provide perspectives on how modern agricultural programs can sustainably manage various pathogens.
Ustilago maydis, the fungus that causes corn smut disease, has a paradoxical history as a scourge to farmers and a delicacy in Mexican cuisine. Despite coevolving with its host teosinte for millions of years, research suggests that all living populations of *U. maydis* descend from the time of the domestication of maize; however, these interpretations are based on a limited number of genetic markers and an imprecise molecular clock. To investigate whether recent maize breeding or propagation of the fungus for food may obscure the pathogen's evolutionary history, we characterized low to medium depth (1–25×) genomes from 28 historic teliospore specimens curated in herbaria. In addition, we established the first reference panel of high-coverage whole genomes from *U. maydis* collected throughout the Americas.
This foray into the genomic history of *U. maydis* provides new information on DNA preservation in fungal teliospores and evidence for coinfection of historic maize by diverse pathogen communities. After exploring computational strategies for merging diploid *U. maydis* individuals with a reference panel of haploid strains we determined phylogeographic structure was maintained in different locations across the Americas from the late 19th century to today, with little evidence for replacement of lineages even with our globally connected agricultural system. In addition, timing of the divergence of lineages and signatures of selective sweeps on key genes provide important details on how this pathogen tracked the movement of maize in the Americas over the past five millennia. Taken together, our results highlight the potential of using herbaria specimens to document co-evolutionary relationships between crops and pathogens.

O–PGE–04
Zoonotic *Mycobacterium tuberculosis* complex strains from geographically dispersed pre-contact South American human populations

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Members of the *Mycobacterium tuberculosis* complex (MTBC) evolved from soil dwelling mycobacteria to become a major human pathogen. In addition to several human adapted lineages, the MTBC also includes strains adapted to a broad range of animal hosts. Today, zoonotic transmissions of animal-adapted MTBC strains pose an increasing threat to human and animal health.
Recently, MTBC strains (*M. pinnipedii*) commonly found in modern seals and sea lions (pinnipeds) were isolated from coastal Peruvian human remains pre-dating European arrival in the New World. This was interpreted to result from an ancient zoonotic event where the bacterium was transferred from pinnipeds to humans as a consequence of frequent human contact with infected living pinnipeds or their tissues.
Human skeletal remains pre-dating European arrival from across the New World have been found to exhibit lesions consistent with prolonged MTBC infection, however many individuals hail from inland sites that are geographically incompatible with zoonotic transmission via direct contact with infected pinnipeds.
Here we present three additional pre-contact *M. pinnipedii* genomes, two from inland Colombia and one from coastal Peru. While zoonotic pinniped transmission remains possible for the Peruvian case, it does not comfortably account for its existence in inland Colombia – over 300km from the nearest coastline. Our new genomes expand the phylogenetic diversity of the *M. pinnipedii* clade by contributing two new branches, both of which diverge before the split between the previously published ancient Peruvian and modern genomes. Our data also highlight the difficulties of analyzing ancient MTBC DNA in the presence of a complex background of contaminant environmental DNA, where a notable proportion belongs to genetically related soil-dwelling mycobacteria.

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We discuss multiple scenarios that may account for *M. pinnipedii*"s transmission to inland Colombia, including the potential of human adaptation and/or animal-mediated dissemination. Together these data demonstrate the ability of ancient *M. pinnipedii* strains to cause human infection in the past and indicate a more complex transmission route than simple pinniped to human transfer.

O–PGE–05
Recovery of ancient oral pathogens by integrated analysis of serial dental calculus samples and modern genomes

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The dental calculus is a complex biofilm of hundreds of oral bacteria species, commensal and pathogenic, trapped in a mineralized matrix on the tooth surface. Metagenomic sequencing of the ancient calculus samples have been used to investigate the diet and health of past human populations as well as the evolution and interaction of the symbiotic relationship of these bacteria with their human hosts (*1-3*). However, state-of-the-art studies are restricted to species-level decompositions of the bacteria, rarely describing strain-level micro-evolution. The difficulties of such detailed evolutionary reconstructions come from not only the high DNA damages in ancient samples, but also a lack of knowledge in the population genetics of the modern oral bacterial species.
Recently, we reconstructed a nearly complete genome of an endogenous oral bacteria (*Eubacterium*) from a 1200 CE calculus sample (*4*). This inspired us to work on a larger project, which consists of metagenomic sequencing of 51 ancient Italian calculus samples dated from Bronze Age to Middle Age and previously published modern oral samples. We found good preservation of endogenous oral bacterial DNA in most of samples. Interestingly, low frequency of *Yersinia pestis* DNA were identified from a calculus sample of a 17th century plague victim. This suggests a preserve of pathogens causing systemic infections in the dental calculus or a low-level contamination from the teeth. Other than that, many of calculus samples, including those dating to the Bronze Age, contained pathogens related to chronic oral infection as periodontitis or systemic disease in modern patients. Deeper sequencing of the samples will allow us to *de novo* assemble some of these oral pathogens. For each reconstructed ancient genome, we will construct a database in EnteroBase of the same species, which consists of all genomes in public domain as well as additional genomes reconstructed from modern microbiomes. These databases enable us to compare ancient genomes with modern relatives and investigate the population dynamics of oral pathogens in the last 1,000"s of years.

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O–PGE–06
Reconstruction of new ancient *Mycobacterium leprae* genomes from Europe

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Leprosy is one of the oldest known diseases in human history with the so far oldest recorded osteoarchaeological possible cases around 3650 BC. Molecular biological approaches, such as ancient DNA research focussing on the causative agent, *Mycobacterium leprae*, can greatly contribute towards understanding the evolutionary history of the disease. Previous genetic studies of ancient *M. leprae* genomes and their comparison with modern ones has identified genomic continuity over the last 1000 years and the existence of at least two lineages in Medieval Europe. However, the ancient genomes published so far are restricted to the region of North-Western Europe. Current data may not reflect the diversity potentially present in other parts of Medieval Europe. In this study, we address this bias through the genetic examination of several Medieval and post Medieval samples from regions that have not yet been studied. Up to now three new ancient *M. leprae* genomes from these regions have been reconstructed: two Medieval genomes from Portugal (1340 ± 48 AD) and Norway (1328 ± 60 AD) and a genome from Russia dated to the 19th-20th centuries. The phylogenetic analysis of these genomes, including previously published modern and ancient genomes, reveals that the genomes from Portugal and Norway are falling on branch 3. The genome from Russia falls on branch 2F and clustering with modern Ethiopian strains. Overall, our results contribute to a better understanding of the past diversity of leprosy in Europe by adding genomic data from so far unstudied regions.

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O–GAE–01
Gene diversity in archaic and present-day humans

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The Neandertal and Denisovan genomes have provided unforeseen insights into human evolution. Genome-wide analyses of two Neandertals and a Denisovan have shown that these archaic humans had substantially reduced heterozygosity compared to anatomically modern humans, likely due to their small long-term effective population sizes (N_e). Genetic variation matters most in functional loci, and previous analyses of the exome sequences of three Neandertals showed that protein-coding genes as a group show a similar reduction in diversity. The availability of high-quality whole genome sequences for two Neandertals and a Denisovan now enable us to explore the levels of gene diversity in Neandertals and in Denisovans, and to compare this diversity at different time points on the Neandertal lineage. With this data, we can also evaluate whether any functional groups of genes show particularly extreme differences in diversity among these groups. In particular, we investigated in detail the levels of diversity in genes of the Major Histocompatibility Cluster (MHC) and in other genes involved in innate immunity, which are known to serve as a first line of defence against pathogens.
Genome-wide we find similar gene diversity in the Neandertals and Denisovan, with all three individuals having significantly lower diversity than individuals from any present-day human population. Nevertheless, there is no observable decrease in diversity over time, and no support for a specific reduction in diversity in any particular functional group of genes in the archaic individuals based on gene ontology analyses. As expected, in both archaic and present-day humans the genes with the highest levels of diversity are enriched for MHC-related functions. Interestingly, MHC genes in archaic humans show evidence of having retained more diversity than other genes of the innate immune system, while non-MHC innate immune genes show a reduction in diversity in line with what is observed in other genes. This suggest that genetic diversity in innate immune genes did not decline in archaic populations at a higher rate than in the rest of the genome, and in fact MHC diversity was retained at levels similar to those observed in modern humans.

O–GAE–02
Using ancient genomes to explore the demography, behaviour and disappearance of the woolly mammoth

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The woolly mammoth is one of the best understood extinct prehistoric species. Many aspects of mammoth biology and evolutionary history have been studied thanks to the remarkably preserved remains found in permafrost and fossil assemblages, depictions in cave art, ancient DNA and isotopes, and insights from closely related, living elephantids. However, the causes of the woolly mammoth"s extinction remain an open question because of the complexity of processes that likely contributed to its final demise. Here we used low-coverage genomic data from 98 woolly mammoths and six genomes sequenced to medium-high coverage to provide insights into the ecology and extinction of the woolly mammoth in the turbulent period of the Late Quaternary. The six complete genomes span the last 40-thousand years of mammoth existence and include three mammoths from the terminal refugium on Wrangel Island, including the last mammoth known to science. Genome-wide estimates of heterozygosity indicate a drastic decrease of diversity at the Pleistocene/Holocene boundary. Moreover, compared to the Pleistocene mainland mammoths, Wrangel Island mammoths had a considerably higher proportion of their genome allocated in runs of homozygosity. These results suggest that genetic drift and inbreeding triggered genomic deterioration in the last woolly mammoth population.

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O–GAE–03
Studying selection in real-time by genotyping HLA immune genes from ancient DNA

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The highly polymorphic genes of the human leukocyte antigen (HLA) system play a key role in adaptive immunity. Past and ongoing pathogen-mediated selection is proposed to be one of the major factors affecting the genetic variability at those genes. Selection at the HLA genes is a dynamic process that involves parallel mechanisms acting at different time scales and creating an intriguing combination of shared polymorphism but distinct allele pools among populations and possibly even species.

The recent development of genomic tools for the analysis of ancient DNA (aDNA) provides a unique opportunity to unravel the selection processes shaping the human genome. In this light, the investigation of ancient HLA genes in historical populations could shed light on mechanisms of pathogen-mediated selection in humans. However, HLA genes exhibit exceptional genetic variability that defies standard sequencing and assembly approaches. To overcome this obstacle, a novel DNA capture approach, optimized for short aDNA fragments, in combination with an aDNA-optimized pipeline is here being applied to analyze HLA polymorphism in historical human populations.

We show the importance of a reliable HLA genotyping pipeline for ancient DNA. The pipeline has already been applied successfully to a dataset of ancient samples, linking HLA variability with susceptibility to leprosy, and can be further applied to explore HLA allele frequency changes through time when temporal sample series are available. Using this approach we are currently analyzing HLA polymorphism in ancient and contemporary residents of the town of Xaltocan in central Mexico, to investigate potential HLA allele frequency shifts from pre- to post-European contact population.

O–GAE–04
Illuminating the role of selection in shaping human diversity

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Ancient human DNA studies have primarily focused on the questions surrounding ancestral migrations, phylogeography, demography, and to a degree the role of adaptation in shaping modern human diversity. With the number of publicly available ancient human genomic datasets reaching the 1000 milestone, it is now possible to utilise a range of modern population genetic approaches to elucidate the genetic history of multiple human phenotypes.

Using a comprehensive aDNA database, the Online Ancient Genome Repository (OAGR; oagr.org.au), we utilised >1000 ancient Eurasian genomes to explore human phenotypic evolution from the late Pleistocene to the present, a period covering the major socio-cultural transitions in human history. We scan each population group for selective signals, as well as predict 40+ putatively fitness-associated traits, including many common diseases, using a novel method that accounts for population structure to produce unbiased estimates of SNP effects. By assessing differences among groups and along spatiotemporal clines against a null model of drift, we were able to infer the specific times and places that selection has shaped modern Eurasian phenotypic diversity. Further, by performing joint trait analyses, our method allowed us to examine the extent to which modern Eurasian phenotypes have co-evolved; i.e., whether a correlated selection has simultaneously affected multiple phenotypes.

This analysis represents the first step in building a comprehensive spatiotemporal map of human adaptation over periods covering the major socio-cultural transitions in human history, providing a window into the factors that have shaped modern human diversity and pathology.

Session • Genetic adaptation and evolution ecology and extinction

O–GAE–05
Reconstructing the unique genetic history of the Japanese wolves

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Japanese wolves have been isolated from the Eurasian wolves due to the geography of Japan, being separated from the mainland by the Korean strait. This is reflected in their unique morphology and genetics, as they are among the smallest wolves and are distinct from the Eurasian wolves in mitochondrial lineages. The two distinct subspecies of Japanese wolves, Honshu and Hokkaido, are estimated to have colonized Japan about 50,000 and 10,000 years ago respectively and went extinct in the last century.
In this study, we use museum skin specimens from London"s Natural History museum, one each from Honshu and Hokkaido wolves, both dating back to 1886. These samples were whole genome sequenced using short read sequencing to a genome coverage of 0.4x for Hokkaido and 3.7x for Honshu. Combined with whole genome sequences from about 60 modern and ancient Eurasian wolf genomes, we address questions pertaining to the origin of the Japanese wolves and their placement in the context of Eurasian wolves.
Modern Eurasian wolves represent only a narrow subset of a formerly highly diverse clade of wolves. Preliminary results show that the Honshu wolf was an ice age relict that derives a large fraction of its genetic ancestry from a basal Siberian wolf lineage that went extinct in the late Pleistocene. However, the Hokkaido wolf is closest genetically to modern Eurasian wolves. Our study highlights the unique genetic history of the Japanese wolves using a combination of modern and historical samples.

O–GAE–06
Historical and modern rabbit populations reveal parallel adaptation to myxoma virus across two continents

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In the 1950s the myxoma virus was used as a biological weapon to control the invasive wild European rabbit populations in Australia and Europe. The subsequent pandemic decimated populations and resulted in a remarkable natural experiment, where rabbits in both continents rapidly evolved resistance to the virus. To investigate the genetic basis of this resistance, we compared the exomes of modern rabbits with the exomes of historical specimens collected before the virus release. By replicating our analyses in Australia, France and the United Kingdom we found a strong pattern of parallel selection across the three countries, with the same genetic variants changing in frequency over the last 60 years. Notably, these occurred in genes involved in antiviral immunity and viral replication. We experimentally validated the functional role of these genes as viral modulators and showed that selection acting on three amino acids in an interferon protein increased its antiviral effect. These results support a polygenic basis of resistance to myxomatosis with selection acting on variation that was present in the ancestral rabbit populations in continental Europe.

Session • Genetic adaptation and evolution ecology and extinction

O–GAE–07
Discovering the legacy of Atlantic cod exploitation using ancient DNA

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Atlantic cod (*Gadus morhua*) is of great cultural and economic importance for North Atlantic coastal regions and Norway in particular. The history of exploitation of this species dates back millennia, and is rich in chronicles of highly successful enterprises and of relentless economic downfall due to fisheries" collapse. This long exploitation history makes it difficult to quantify the extent of human impact since prehistoric times. Here, we analyse whole genome sequencing data of Atlantic cod bones up to 9000 years BP. We have two main goals: first, we aim to reconstruct the chronology of the Viking Age and subsequent Medieval long-distance fish trade by determining the biological origin of specimens from multiple archaeological sites in western Europe. We specifically compare sites of differing archaeological character: i.e. sites presumed to have been fishing settlements for the procurement of local catches and those presumed to have been centres of trade. Second, we build towards an extensive spatiotemporal genome-wide dataset to assess demographic and selective impacts on Atlantic cod. We are particularly interested in comparing samples that pre-date extensive human influence to those from later periods, including a whole genome sequencing reference dataset of over 850 modern Atlantic specimens. With this project, we aim to characterize the genomic diversity of this species over a large part of its distributional range, covering a period during which humans moved from a hunter-gatherer existence to complex societies that continue to impact marine ecosystems on a global scale.

O–GAE–08
Ancient RNA – long-term survival and tissue specificity in permafrost tissues of Pleistocene animals

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The long-term survival of RNA has generally been considered to be lower than that of DNA, especially in animal tissues, where post-mortem autolytic processes are thought to accelerate nuclease activity on RNA. While transcriptomes of archaeological plant material have been sequenced using NGS in the past decade, these have been limited to desiccated seed endosperm which have evolved for extended biomolecular storage. More recent targeted qPCR-based approaches have identified tissue specificity in permafrost ~5,300 yBP human tissues, from a preselected set of microRNAs. Here we show that shotgun sequencing of ancient RNA from permafrost soft tissues has the power to resolve tissue specificity well beyond this range, with greater target breadth and sequencing depth, in remains of (so far) up to 14,000 yBP.
We successfully extracted aRNA from various tissues of wolves (*Canis lupus*) and mammoths (*Mammuthus primigenius*), using a combination of short RNA enrichment techniques, pH-based RNA / DNA separation, and ssDNA nuclease treatment. We then compared datasets to others of the same individual, and existing comparable data from modern material, using separate bioinformatics and statistical methods to ensure validity of our interpretations. We found that tissue specificity can be confidently assigned, especially in deep tissues, from aRNA of up to 14,000 years of age. Superficial tissues such as skin and cartilage are generally less clear, displaying higher contamination levels which interfere with downstream analysis pipelines. We also note that like DNA, RNA is subject to hydrolytic C > U deamination, and exhibits a unique damage profile. With current emphasis increasing on the *in vivo* process reconstruction of archaeogenomes, we suggest that aRNA might soon become a more viable and powerful analytical tool than previously thought.

Session • Genetic adaptation and evolution ecology and extinction

O–GAE–09
Characterisation of extinct bison methylomes using bisulphite sequencing

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Epigenetics encompasses a suite of mechanisms that potentially enable the adaptation of species to rapidly changing environments. We propose that mammal populations from the Quaternary—the current geological period characterised by dramatic climate oscillations—represent a unique model to study epigenetic responses to environmental cues, and their role in adaptation and extinction. Statistical methods have recently been developed to infer the methylation status of cytosines from ancient mammalian genome datasets, albeit at a relatively low resolution. On the other hand, experimental studies of ancient DNA methylation have been restricted to a limited number of target loci and a small sample size, due to pronounced DNA degradation and low levels of endogenous DNA in sub-fossil remains. Here, we present a method to perform whole-genome bisulphite sequencing of ancient DNA extracts. To demonstrate the power of this method, we characterised methylomes at a single nucleotide resolution using 10 extinct and 14 modern bison samples from North America, which span a time range of more than 50,000 years that includes key climate cooling and warming events. Amongst all identified differentially methylated regions, an intron of the *MET* oncogene shows consistent differential methylation between extinct and modern bison samples. Our method provides a unique opportunity to study the methylomes of extinct mammals at an unprecedented level of resolution.

Session • Deep human population prehistory

O–DHP–01
Genome-wide data from a first-generation Neandertal/Denisovan offspring

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This abstract is not available before the conference.

O–DHP–02
Modelling early human lineages in Africa

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Admixture graph models of population history provide a comprehensive framework to reconstruct the ancestry of ancient and present-day genomes. However, current approaches for admixture graph inference of population history from larger sets of populations rely on limited searches of the full possible space of graph models, usually based on *a priori* historical hypotheses. We introduce a new approach for automated searches of admixture graph space through the high-throughput simulation and evaluation of random graphs, allowing the interrogation of potentially millions of graphs even for larger sets of populations. We apply this heuristic framework to reconstruct the diversification of early modern human lineages using ancient genomes from Africa, and find support for previous evidence of deep structure within west African ancestry that may reflect some of the earliest diversifications of population lineages contributing to present-day populations. However, we also find that modelling early African and non-African lineages using ascertained SNP data captured in ancient samples is complicated by ascertainment schemes biasing comparisons between populations. Specifically, such ascertainment schemes—including ascertainment in African populations—overestimate the genetic differentiation of African- and non-African populations and distort population relationships compared to high-quality genomes. Instead, we show that outgroup-ascertainment of polymorphisms in Neandertal & Denisovan populations provides a largely unbiased set of ancestral variants for studying population structure in present-day human populations. This ascertainment scheme and set of variants provides a future resource for ancient genome-wide capture of ancient DNA inside and outside of Africa.

O–DHP–03
Pleistocene North Africans show dual genetic ancestry from the ancient Near East and sub-Saharan Africa

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

Session • Deep human population prehistory

Here we present genomic data from seven individuals, directly dated to ~15,000-year-ago, from Grotte des Pigeons, Taforalt in Morocco. Uni-parental marker analyses show mitochondrial haplogroup U6a for six individuals and M1b for one individual, and Y-chromosome haplogroup E-M78 (E1b1b1a1) for males. We find a strong genetic affinity of the Taforalt individuals with ancient Near Easterners, best represented by ~12,000 year old Levantine Natufians, that made the transition from complex hunter-gathering to more sedentary food production. This suggests that genetic connections between Africa and the Near East predate the introduction of agriculture in North Africa by several millennia. Notably, we do not find evidence for gene flow from Paleolithic Europeans into the ~15,000 year old North Africans as previously suggested based on archaeological similarities. Finally, the Taforalt individuals derive one third of their ancestry from sub-Saharan Africans, best approximated by a mixture of genetic components preserved in present-day West Africans (Yoruba, Mende) and Africans from Tanzania (Hadza). In contrast, modern North Africans have a much smaller sub-Saharan African component with no apparent link to Hadza. Our results provide the earliest direct evidence for genetic interactions between modern humans across Africa and Eurasia.

Fig 1

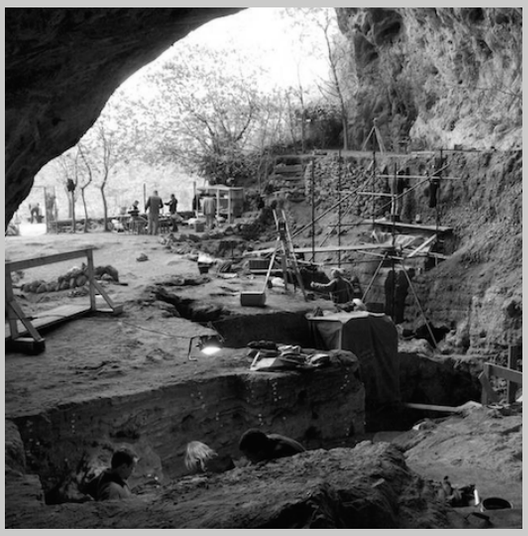
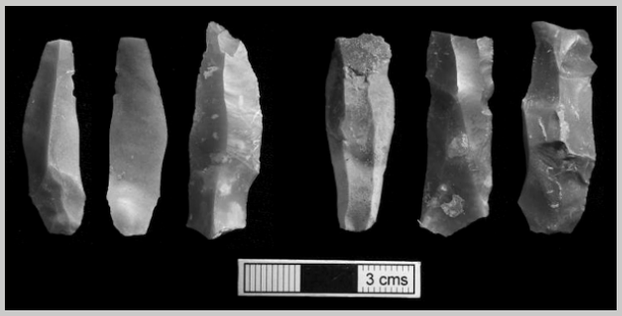


Fig 2

Fig 3



Session • Deep human population prehistory

O–DHP–04

Genomic Analysis of an early *Homo sapiens* from Europe increases complexity of early European demographic structure

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The first modern humans are believed to have entered Europe roughly 45,000 years ago. Recent genomic studies have shown that two of the oldest *sapiens* remains in Eurasia, a 37,000-42,000 year old individual from present-day Peştera cu Oase, Romania (Fu et al., 2015), and a 45,000 year old man from Ust'-Ishim in Western Siberia (Fu et al., 2014), share no direct lineage with modern Europeans, while a few thousand years later, individuals such as the 37,000 year old remains from Kostenki, Russia (Fu, et al., 2016), 35,000 year old remains from Goyet in Belgium (Fu et al., 2016), and all subsequent remains are ancestral to present-day European populations. This early foundation of the current population structure is supported in East Asia by the 40,000-year-old Tianyuan, who is more closely related to modern East Asians than to ancient or modern Europeans (Yang, et al., 2017).

These individuals represent at least four distinct populations inhabiting Eurasia 37,000 years ago. However, with so little data, their true number and the interactions between these early migrant populations during this key period of prehistory is difficult to discern. In addition, poor DNA preservation and the rarity of skeletal material from this region and time make analyses challenging. We present genomic data from a 37,000-year-old European, recovered from poorly preserved material (the DNA having a 40 base pair average fragment length and very low endogenous content) using a combination of several recent advancements in DNA extraction, purification and library construction techniques. These results enrich our current understanding of human migrations into Eurasia, early European population structures, and the roots of Upper Paleolithic industries, and serve to bring into better focus our picture of Europe"s first *Homo sapiens* inhabitants.

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Session • Deep human population prehistory

O–DHP–05

The aboriginal heritage project and the modern human colonization of Australia

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A. Abdullah-Highfold[4], S. Agius[4], A. O'Donoghue[4], I. O'Loughlin[4], P. Sutton[4], F. Zilio[4], K. Walshe[4], A. Williams[5], C. Turney[5]
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The Aboriginal Heritage Project is a collaboration between the Australian Centre for Ancient DNA (ACAD), the South Australian Museum (SAM), and Aboriginal communities across Australia, which aims to reconstruct the genetic history of Aboriginal Australia. The project leverages SAM"s unique collection of >5000 hair samples and extensive ethnographic and genealogical data collected during the University of Adelaide Board for Anthropology Expeditions between 1926-1963. A family and community based consultation program encouraging participation has received overwhelming support, and allows informed consent to be gained from hair sample donors, or their descendants. This dataset therefore provides a unique opportunity to address the population history of Aboriginal Australians, from the Out-of-Africa migration until arrival and settlement in Sahul ~50kya. Our prior analysis of 140 mitochondrial genomes from hair samples collected in Queensland, South Australia and New South Wales revealed that the initial peopling of Sahul comprised a single, rapid migration along the east and west coasts that reached southern Australia by >49-45 kya – producing pronounced regional patterns still evident today that suggest the continuous presence of populations in discrete areas since the original colonisation. Here, we present novel key results to unveil the detailed population genetic history of Aboriginal Australians. First, Y-chromosome analysis reveals that there are differences in male- and female-specific migration patterns across Australia, with males moving more often across the continent. Furthermore, we analyse whole-genome low coverage sequencing data for ~60 unrelated individuals and integrated this with genetic data from populations in PNG and Indonesia, shedding new light on the migration routes traced by the first human occupants of Sahul.

Session • Diet and nutrition I

O–DAN–01
Reevaluating Neanderthal subsistence

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Interpretations of Neanderthal diet from plant microfossils contrast those from nitrogen isotope values of bone collagen. The temporal scales of dietary information from microfossil or biomarker sources are much shorter than that represented in bone collagen isotopes. The nitrogen isotopic interpretations (Richards et al, 2000; Bocherens et al, 2005; Richards and Trinkaus, 2009) of Neanderthal bone collagen have held primacy due to the integrated, long term signal that the data represents. It has led to the impression that Neanderthals were super carnivores because the $\delta^{15}N$ of the Neanderthal collagen is higher than co-occurring herbivores and similar to carnivores such as hyenas. Recent compound specific individual amino acids nitrogen isotopes from Neanderthal and early anatomically modern human collagen (Naito et al, 2016 Drucker et al, 2017) also suggest a substantially meat based diet.
The approaches and interpretations that treat the light isotope values of carbon and nitrogen in bone collagen as an uncomplicated proxy for diet are in error. We suggest that such isotopic fractionation data are better analyzed as a metabolic phenotype that has significant environmental input. We present evidence to suggest that direct open flame cooking of meat or tubers would have produced significant amounts of heterocyclic amines (HCA). Both the organic extractable HCAs and the meat tissue have much higher nitrogen isotope ratios compared to the uncooked product. In addition, some of compound specific amino acid $\delta^{15}N$ values in cooked meat are elevated over the uncooked meat, while others are unaffected by high heat application. The pattern of nitrogen isotope alteration in amino acids from cooked meat could alter interpretations of meat intake in either bulk collagen or compound specific Glu-Phe trophic level placement. The genus Homo likely had a variety of behaviors and a transformation in gut physiology that should be part of the consideration in interpreting natural abundance isotopes.

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Session • Diet and nutrition I

O–DAN–02

Isotopic evidence for high mammoth consumption by late Neandertals and early modern humans in Europe and its possible ecological impact

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Introduction: Exploitation of woolly mammoth (*Mammuthus primigenius*) by late Neandertals and early anatomical modern humans (AMHs) in Europe has been regularly documented in zooarchaeology. If quantitatively significant, mammoth consumption by hominins could have impacted the whole ecosystem.

Objectives: Our goal is to quantify mammoth meat consumption as well as the possible impact of this predation on Late Pleistocene ecosystems.

Methods: Carbon and nitrogen isotopic composition of bone collagen in ancient hominins, compared to those of possible prey including woolly mammoth and to animal predators, is used to directly track the contribution of mammoth in the protein part of their diet. Quantitative estimates were made using the Bayesian model SIAR. Amino acid specific nitrogen isotopic compositions were used to disentangle the respective consumption of freshwater fish and mammoth. Moreover, variations in the isotopic composition of herbivorous species were monitored to document possible changes in the ecological niche of mammoth competitors during periods of different intensities of mammoth predation.

Results: Late Neandertals from Belgium (Spy, Goyet) and France (Saint-Césaire) as well as AMHs from Crimea (Buran Kaya BK III) and from the Czech Republic (Predmosti I) yielded high nitrogen isotopic ratios. In Spy and BK III, 15N abundances in amino acids rule out fish as a significant food source, therefore mammoth meat was the main protein source, representing up to 60% of the protein diet of these hominins. No other animal predator exhibited such high mammoth consumption. During the period between 50,000 and 25,000 years ago, mammoths have systematically higher 15N abundances than all other herbivores, due to high grass consumption. With the onset of the Upper Paleolithic in SW Germany, horses shifted their isotopic composition and overlapped with mammoths, suggesting that the mammoth niche was not intensively occupied and could be used by some horses, possibly a consequence of a decline in the mammoth population caused by AMHs.

Conclusion: Late Neandertals and early modern humans in Europe were the only predators heavily relying on mammoth meat. In some regions, it seems to have impacted on the structure of the ecosystem and the niche partitioning with other herbivores. Since the mammoth was a keystone species, a population decline due to their hunting upon by hominins probably had cascading effects on Late Pleistocene ecosystems.

Fig 1

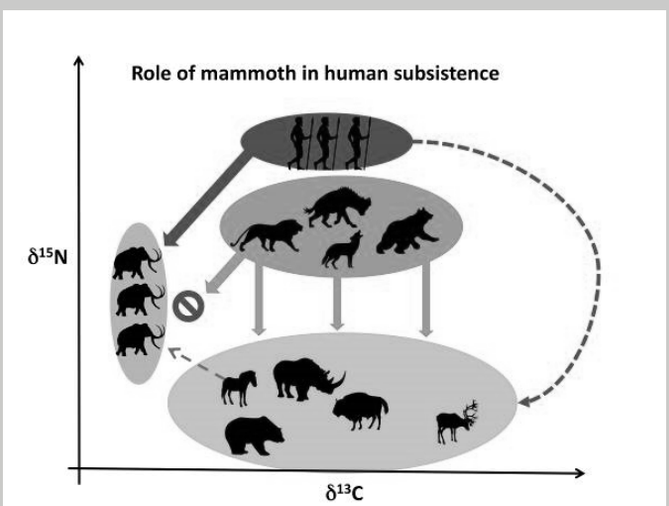
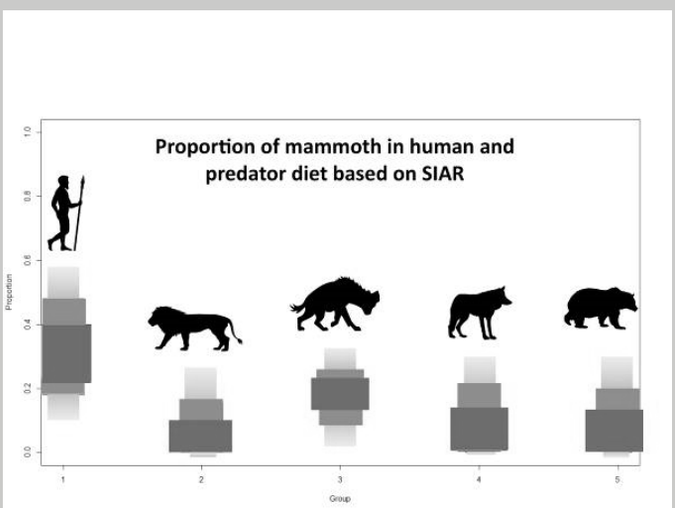


Fig 2



Session • Diet and nutrition I

O–DAN–03
Back to Basics – introducing a model calculus system to test fundamental aspects of dental calculus research

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In recent years, analysis of dental calculus has experienced a surge in popularity due to its ability to store and preserve markers of past diet. However, little is known about the processes by which these markers are incorporated into the dental calculus, and to what extent the data obtained by various methods (e.g. aDNA analysis, palaeoproteomics, and microscopy) are an accurate depiction of past diets and behaviours; if they have unidentified sources of bias causing that would cause under- and overrepresentation of some markers, or others to be missed entirely.

The primary objective of this study was to develop a protocol for a model calculus system that can provide a means of testing the accuracy of current methods used for the extraction and analysis of dietary markers, and address future questions pertaining to dietary research on dental calculus.
Dental plaque was grown for 10 days based on the ACTA active attachment (AAA) biofilm model, and then mineralised for 10 days using a calcium-phosphate-monofluorophosphate-urea (CPMU) solution. Known quantities of starches were added to the calculus during daily "feedings". These were assessed to evaluate the extent of incorporation of starches in the dental calculus, the efficiency of extraction protocols, and the accuracy of microscopic analysis of starch quantities.
Multiple replicates of dental calculus samples were successfully grown, each containing ca. 12 mg of calculus, demonstrating the efficacy of this method for creating a model calculus system. As expected, the overall number and ratio of starches decreased over the course of extraction, dissolution in EDTA and/or HCl, and analysis by microscopy. The dietary image depicted by the final starch quantities was inconsistent with the quantity and ratio of starch that was originally "fed" to the calculus.
There remains a lot to learn about the incorporation of dietary markers in calculus, both ante-mortem and post-mortem, and the biases of various analytical methods. The *in vitro* model calculus system presented here provides a controlled environment for assessing the loss of calculus due to potentially biased sampling and analysis methods, contributing valuable information to facilitate the most efficient methodological approaches to future research questions on diet and dental calculus.

O–DAN–04
Isotopic variation in Foxtail Millet (*Setaria Italica*) with variety and watering regime

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Isotopic palaeodietary studies generally focus on bone collagen from human and/or animal remains. While plant remains are rarely analysed, it is well known that plant isotope values can vary greatly as a result of numerous factors, including the environment and type of plant. The millets were important food crops in prehistoric Eurasia, yet little is known about the isotopic differences within particular millet species. As C_4 plants, the expectation is that the millets will be relatively unaffected by environmental parameters and therefore C_3 plants have been the focus of environmental reconstruction using archaeobotanical remains. Nevertheless, some (modern) studies show a correlation between millet $\delta^{13}C$ values and rainfall.
This paper presents the results from two growth experiments using a controlled environment chamber which investigate isotopic variation in *Setaria italica* with landrace (as a proxy for genetic variety) and watering regime. In the first experiment, we find significant isotopic variability within single leaves and panicles, and between leaves and panicles within the same plant. We find that the leaves and grains from the different accessions have a *c.* 2‰ range in $\delta^{13}C$ values, while the nitrogen isotope values in the grains have a *c.* 6‰ range. We also find an average offset of 0.9‰ between leaves and grains in $\delta^{13}C$ value. In the second experiment, we grew four replicates of twelve of these accessions and subjected them to different watering regimes. Contrary to the expectation that C_4 plants are relatively unaffected by environmental parameters, we found significant phenotypic and isotopic variation.
The variation found in both experiments is large enough to have archaeological implications, and within- and between-plant isotope variability should be considered in isotope studies. The range in $\delta^{15}N$ values in the first experiment is particularly significant as it is larger than the typical values quoted for a trophic level enrichment, and as such may lead to erroneous interpretations of the amount of animal protein in human or animal diets. It is therefore necessary to account for the variability in plant stable isotope values during palaeodietary reconstructions. The differences found with watering regime suggest that there is potential for C_4 plants to be used for environmental reconstruction.

Session • Diet and nutrition I

O–DAN–05

From birth to toddling – changes in diet revealed by the novel use of hydrogen isotopes (δ^2H) in combination with other stable isotopes ($\delta^{18}O$, $\delta^{13}C$, $\delta^{15}N$) of tooth dentin

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Unlike the major protein found in bone, primary tooth dentin collagen does not turnover and therefore preserves a time integrated record of dietary changes within the time window of dentin formation. Incremental micro-sampling of dentin and its measurement for nitrogen and carbon isotopes allows for the reconstruction of breastfeeding and weaning practices, as well as dietary and metabolic changes throughout later childhood. This is based on the premise that weaning produces a characteristic curve in $\delta^{15}N$ vs. time, with distinct $\delta^{15}N$ curves resulting from abrupt vs. gradual weaning.
It has been proposed that hydrogen isotopes (δ^2H) reflect tropic level in a similar manner to nitrogen isotopes, with a ~40-50 ‰ ^2H enrichment between producer and consumer (Birchall et al. [*J. Anim. Ecol.*, **74**, 877-881 (2005)] Reynard & Hedges [*J. Archaeol. Sci.*, **35**, 1934-1942 (2008)]). Here, we test if δ^2H can be used as an additional proxy for weaning and/or other changes in childhood diet. We have taken 1 mm dentin increments from the first molars of individuals buried in a single tomb at a necropolis in Villamar, Sardinia, dating from 800 to 400 calBC. Individuals appear to have been weaned by approximately two years of age based on their dentin $\delta^{15}N$ and $\delta^{13}C$ values.
A comparison of a first and third molar with the corresponding bone from the same individual shows that the tooth dentin isotope signal equilibrates with the baseline bone values in later childhood/adolescence for $\delta^{15}N$, $\delta^{13}C$ and δ^2H. Hydrogen isotopes vary by ~20 ‰ from birth to late adolescence with a marked, but uneven, pattern of enrichment in ^2H in infancy. We find that hydrogen isotope changes through early development do not fit a simple trophic enrichment model.

O–DAN–06

Food for thought – concentration dependent isotopic mixing models applied to data from early Neolithic Turkey and Greece

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Collagen stable isotopes (d13C, d15N) in archaeological human bones are commonly used to describe the trophic level (d15N) and the food source (C3-plants vs. C4-plants, marine vs. terrestrial; d13C).
The results are interpreted by bivariate plots and univariate statistics. This method permits the assessment of the gross trophic level of an individual or the whole population. However, an isotopic sourcing reveals much more information about the biomass contribution of selected food end-members.
Since it is assumed that the Neolithic transition was accompanied by dietary change, stable isotopic ratios of human and animal bones from the early Neolithic site of Nevalı Çori (Turkey: ca 8500 BCE), and five neolithic sites in Greece (Alepotrypa: ca. 6000-3200 BCE, Franchthi: ca. 6000-3000 BCE, Mavropigi: ca. 6600-6000 BCE, Theopetra: ca. 6500-4000 BCE, Xirolimni: ca. 6100 BCE) were re-interpreted by use of concentration-dependent mixing models provided by IsoConc and SISUS. While the largely vegetarian diet of the humans from Nevalı Çori was confirmed, new staples became visible in the later Greek populations indicative of a changing subsistence economy.

Session • Diet and nutrition II

O–DAN–07
Investigation of Neolithic cattle diet and landscape by intra-tooth amino acid $\delta^{15}N$ analysis

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The natural landscape of central and northern Europe in prehistory is thought to have been dominated by forests, but there is debate over the regional extent of natural woodland and how this would have affected animal management practices by Neolithic farmers, and whether forests were used for pasture or leafy hay to supplement animal diets. We aimed to develop a new nitrogen stable isotope approach, using the $\delta^{15}N$ values of cattle dentine amino acids as a proxy for the plants that constitute cattle diet, in order to answer this question. Our new proxy exploits differences in amino acid $\delta^{15}N$ values between the herbaceous and woody plants at the base of this food web. We determined how these values change between the plants and the tissues of cattle consuming them, thereby enabling the consumption of the different plant types and, hence, the contribution of forest or open landscape resources to the diet of prehistoric cattle to be determined. Sequential analysis of the cattle dental tissues also allows seasonal variation in diet to be detected. Here we present results from compound-specific and bulk stable isotopic analysis of sequentially sampled tooth dentine and enamel of cattle teeth from early Neolithic sites (dating from 5600 to 5000 BCE) from across central and northern Europe. The results show that regional differences in fodder management and/or herding practices exist between LBK sites and that seasonal variation in diet was evident due to winter foddering.

O–DAN–08
Farming vs herding – subsistence economy during the late Neolithic evidenced by stable carbon and nitrogen isotopes in Northern Shaanxi Province, China

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In order to explore subsistence patterns in northern Shaanxi Province around 4,000BP, human and animal bones from the Shimao, and contemporaneous sites nearby were sampled for stable carbon and nitrogen isotope ratio analysis. The results show that most people primarily subsisted on C4 resources, e.g. millet and millet-related animal products, despite the fact that there was some intake of C3 plants by some individuals. Stable nitrogen isotope values indicate that there were differences in meat consumption between individuals at the site. Pigs were mainly foddered with millet and millet byproducts, as well as some cattle, according to their high δ13C values. However, the sheep/goats consumed wild C3 plants at those sites. Our above findings indicates that subsistence patterns in northern Shaanxi around 4,000BP were characterized by millet farming, while the grassland animal husbandry, e.g. cattle and sheep/goats raising, displayed very little contribution to local economy. The intensive millet farming in northern Shaanxi provided enough food for population growth, ensured the accumulation of wealth, and consequently accelerated social differentiation and complexity.

Session • Diet and nutrition I

O–DAN–09

The diversity in C4 crop consumption across Kazakhstan during the Bronze and Iron Ages based on stable isotope analysis of human and animal collagen

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Stable isotope analysis of bone collagen has proven itself as a valuable technique in reconstruction of past human diets in Central Asia, especially in the region that is situated away from marine environments. Previous investigations in Kazakhstan employed the stable isotope analysis to demonstrate the increasing importance of C4 plants in this region at the end of the Bronze Age (BA) and the beginning of the Iron Age (IA).

Growing body of archaeobotanical evidence across Kazakhstan has shown the variety of plants that people used to cultivate starting from the mid-third millennium BC (e.g. Doumani et al., 2015; Frachetti et al., 2010; Spengler et al., 2014). During the Late BA and IA periods the crop assemblages mainly consist of wheats, barley, green peas and broomcorn millet. The former, however, remains the only C4 crops found at BA and IA sites of Kazakhstan, which allows associating elevated δ13C values indicative of C4 consumption with the presence of millet in the diet.

By the beginning of the IA the elevated δ13C values become quite widespread not only across Central Asia but also across Southern Siberia, South-Eastern Asia and Europe (e.g. Lightfoot et al., 2013; Spengler et al., 2016). The Chinese millets are considered to be the cause of it. The pattern of millet consumption however, is very diverse across Kazakhstan during the IA. Some communities do not seem to rely on C4 plants for subsistence at all, while in other populations only certain individuals seem to consume millet.

In this paper, the new isotopic data collected from various regions of Kazakhstan together with the previously published isotopic results will be examined to analyze the diversity in the millet consumption across Kazakhstan in the BA and IA and to understand the reasoning of such pattern. The isotopic values of nitrogen and carbon will be discussed in relation to spatial and intra-group variations in the diet. New isotopic results from the Sarmatian-time kurgans of Taksai located in the previously unstudied region of western Kazakhstan will be presented along with the new isotopic data from Northern, Central and Southern regions of the country.

O–DAN–10

A new approach to trace cereal agriculture based on absorbed lipid residues in archaeological pottery

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The adoption of farming in the Neolithic has led to some of the most fundamental changes in later human history. Although it is undisputed that farming started in the Fertile Crescent of the Near East before spreading out across Europe, the exact timing and mode of adoption of farming in many regions is still not fully understood on the basis of currently available evidence. We developed a new method based on Organic Residue Analysis to complement the existing methods and improve the understanding about cereal agriculture in Europe.

Organic Residue Analysis is based on the requisite that cooking of food in unglazed ceramic containers leads to the absorption of lipids and others food constituents (sugars, proteins and DNA) into the porous ceramic fabric of the pots. Once absorbed, lipids are relatively protected against degradation and water leaching and a small fraction, that often contains source-characteristic degradation compounds, can be preserved over millennia. Analysis of these specific biomarkers and the isotopic composition can be used to infer the original lipid source(s) and reconstruct dietary pattern. Unfortunately, cereals have largely been invisible using this approach due to their generally low lipid content and a lack of established and robust biomarkers.

To overcome this, we developed a set of robust biomarkers by lipid profiling of modern cereals using GC-MS, performing laboratory cooking experiments to investigate the transfer of lipids into the ceramic fabric as well as incubation experiments to evaluate the resilience against microbial decay. We could show that a small but detectable fraction of cereal-specific lipids (plant sterols and alkylresorcinols) is transferred into the pots during cooking. Furthermore, once absorbed the biomarkers were relatively resilient against microbial decay, particularly under anoxic conditions. Finally, a targeted method to isolate the cereal biomarkers was developed and could be used to detect these compounds in pottery samples from Roman Britain. Further results from the reference experiments and the first applications of the new technique for the analysis of archaeological samples will be presented.

Session • Diet and nutrition II

O–DAN–11
Inverstigating Early Celtic consumption practices using organic residue analyses on local and imported pottery

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This study documented chemical signatures of eating and drinking practices during the Early Iron Age in Central Europe (7th-5th cent. BC) by extracting and characterising lipid residues absorbed within local and imported vessels from two key sites, the Heuneburg in Baden-Württemberg and the Vix-Mont-Lassois in Burgundy. The ceramics tested originated from different contexts within these two sites including settlement areas on the hilltops and lower towns, as well as the outer settlement and rampart area which may have included craft activities area. This enabled us to obtain novel insights into dietary practices.
At both sites, the identification of plant oils, in particular olive oil, and wine point towards the importation and consumption of Mediterranean products; a finding that questions whether or not Early Celtic societies appropriated foreign feasting practices. We can show that Mediterranean food products were mostly present in imported vessels from Vix-Mont-Lassois. Evidence for the consumption of wine in locally produced drinking vessels was occasionally found. Moreover, fermentation markers indicate the presence of an alcoholic beverage other than wine in both local and imported drinking vessels. We found a wide variety of probably local products in the local vessels, including animal fats, plant oils, millet, beeswax and dairy products. Beeswax, in particular, was repeatedly present in the local pottery, suggesting that beehive products played a key role in Early Celtic communities. This research enabled us to achieve a better understanding of the meanings and functions of Early Celtic pottery and associated eating and drinking practices.

O–DAN–12
Gender-specific food consumption in conversion period inhumation cemetery at Kukruse, NE-Estonia

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Kukruse cemetery is a 12th–13th century AD burial ground in NE-Estonia in which over 40 inhumations of men, women and children were discovered. Among the variety of burial goods were also 14 ceramic vessels concealed as burial gifts relating to particular individuals. The pots enable to draw direct relationship with individuals, and compare the personalised burial meals in ritual contexts (pots) with their lifetime diet (human bones).
We conducted multiproxy bioarchaeochemical analyses of ceramic vessels and human bones. Pottery related food residues were subject to lipid analysis using gas chromatography-mass spectrometry (GC-MS), bulk isotope ratio mass spectrometry (EA-IRMS), gas chromatography-combustion-isotope ratio mass spectrometry (GC-C-IRMS), and plant microfossil analysis from food-crusts. For human skeletal remains stable isotope analysis (EA-IRMS) was performed.
The results reveal gender-specific food consumption by different community members at Kukruse: men were more prone to eat aquatic and higher trophic level organisms, whilst women fed on lower trophic level animals and their products. Furthermore, dietary practices followed in lifetime (based on human bone analysis) were extended to the concepts of afterlife (pots buried as individual grave goods).
Our paper highlights past food consumption as a highly social phenomenon, and exemplifies the fruitfulness of high-resolution and small-scale ancient dietary analyses, the aspects of which can be best revealed with multiproxy bioarchaeological analysis.

Session • Analytical methods in population genetics

O–AMG–01
Joint estimates of heterozygosity and runs of homozygosity for modern and ancient samples

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The rate of heterozygous sites for individual genomes is informative about the genetic diversity of their population of origin. Ancient DNA samples tend to have specific challenges including molecular damage, fragmentation and low coverage. These effects tend makes the task of estimating heterozygosity a difficult one. In addition, domestic animals tend to be heavily inbred and large runs of homozygosity can be found in their genome which can skew estimates of genome-wide heterozygosity rates. Current computational tools to estimate runs of homozygosity and heterozygosity are not robust to either one of such idiosyncrasies. Here, we introduce ROHan, a probabilistic method which substantially improves the estimate of heterozygosity both at the genome-wide and local level. Our method jointly delineates runs of homozygosity and infers genome-wide heterozygosity for regions identified as outside of such runs. ROHan combines a local Bayesian model and a Hidden Markov Model at the genome-wide and is suited for both modern and ancient samples.
We show that ROHan outperforms currently available methods for predicting heterozygosity rates for ancient samples and is highly robust to the idiosyncrasies of such data. In addition, we apply ROHan on modern and ancient samples and show that relevant estimates can be inferred at various depths of coverage and rates of DNA damage.

O–AMG–02
The impact of reference bias on ancient DNA studies of prehistoric human populations

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High quality reference genomes are an important resource in genomic research projects. In palaeogenomic studies of human populations, mapping against the human reference genome is used to identify endogenous human sequences in sequencing libraries built from ancient human remains. The linear human reference genome represents a single haploid sequence carrying only one allele at each variant site. A consequence is that DNA fragments carrying the reference allele map over-proportionally or with higher quality scores. This reference bias can have effects on population genomic downstream analysis when heterozygous sites are falsely considered homozygous for the reference allele. Due to DNA preservation, ancient DNA studies usually operate with low sequencing coverages where a variant site is often covered by a single sequencing read only. Furthermore, fragmentation of DNA molecules causes a large proportion of the sequenced fragments to be shorter than 50 bp reducing the amount of accepted mismatches between reference and sequenced read. These ancient DNA specific properties represent limitations for calling the allelic state of the individual potentially exacerbating the impact of reference bias on downstream analysis.
I investigate reference bias in published ancient DNA sequence data of prehistoric populations. Comparing different strategies for mapping and data filtering, I illustrate how reference bias can influence the results of downstream analyses such as population affinities and heterozygosity estimates. The goal is to start a discussion on the potential impact as well as strategies to mitigate reference bias in ancient DNA studies.

Session • Analytical methods in population genetics

O–AMG–03
Estimation of ancient Nuclear DNA contamination using breakdown of Linkage Disequilbrium

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Ancient DNA (aDNA) has been a revolutionary technology for inferring human history, but inferences can be distorted by sample contamination during the excavation and handling of samples. Methods for measuring contamination based on mitochondrial DNA can provide inaccurate assessments of contamination due to high variability across DNA extracts in the ratio of mitochondrial to nuclear DNA; thus, direct nuclear contamination estimates are important. The best current method for estimating rates of contamination in aDNA using nuclear genome data focuses on detecting polymorphism on the X chromosome in males, but this is not effective in females. Methods based on autosomal DNA have been developed for modern DNA, but these require genotype array data of uncontaminated samples, accurate knowledge of the sample"s population allele frequencies and/or knowledge of all potential contaminant individuals" SNP genotypes, which are generally not available for aDNA.
Here we report a novel method for estimating autosomal aDNA contamination using patterns of linkage disequilibrium (LD). Our algorithm is based on the idea that sequences from a contaminating individual will diminish the LD within the sample individual, because they are from different haplotypes and therefore should have no LD with the authentic ancient DNA sample. We use reference panels from 1000 Genomes populations to attain approximate background haplotype and SNP frequencies and estimate contamination by fitting a maximum likelihood model where contamination and the expected test sample"s haplotype distribution produce the observed sample"s haplotype distribution.
Our method accurately infers contamination generated in simulations using widely divergent 1000 Genomes populations and is highly correlated with X chromosome estimates in real ancient samples. The estimates have standard errors less than 2.0% for contamination of 10% or higher in samples with at least 500,000 reads covering SNPs, and we obtained unbiased estimates in samples with as low as 16,000 reads. This tool should allow users to detect samples with 5% or more contamination with high confidence. The software is publicly available online (link to be provided by the time of the meeting).

O–AMG–04
Inferring the selection history of Europe over the last 10000 years using a novel statistical approach

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We describe an efficient new Bayesian statistical model to identify selection in admixed populations using allele counts from Single Nucleotide Polymorphisms (SNPs) in low and/or high coverage ancient and/or modern genome data. This novel approach accounts for demography and variation in coverage across loci and samples, and also infers proportions of ancestry relating populations (*e.g.* due to admixture) and levels of genetic differentiation among groups. The program can provide both selection probabilities for individual SNPs and/or jointly test sets of SNPs (*e.g.*in pathways) for selection effects. We demonstrate the model's utility through simulations, and showcase its ability to identify previous targets of selection using DNA from prehistoric and modern humans.
We apply our method to a large dataset of ancient and modern genomes, including 75 previously unpublished data from ancient genomes, that span hunter-gatherer and Neolithic early farmer populations from 12,000 years BC through until the late Bronze Age. We identify the time periods over which individual SNPs have experienced selection, and we assess the evidence for selection in sets of SNPs associated with diet, immunity, skin pigmentation and the metabolic syndrome, illustrating the evolutionary constraints on populations at critical periods throughout the history of Europe.

Session • Analytical methods in population genetics

O–AMG–05

MitoBench & MitoDB – novel interactive methods for population genetics of human mitochondrial DNA

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Although nuclear human genomes have become more accessible due to modern next-generation sequencing technologies, the survey of mitochondrial DNA (mtDNA) variation in population genetics, especially in ancient DNA studies, remains extremely informative. A plethora of methods and tools for mtDNA analysis exist, but typically rely on different file formats and often require manual interaction with the data for downstream analysis steps that can be rather cumbersome and result in an increased risk of errors in analytical processing. Furthermore, it is typically difficult to obtain suitable comparative data. Although many public and in-house databases are available, they generally encompass only partially overlapping subsets of all available samples, sometimes with different extents of missing information. Moreover, the number of complete mitogenomes is growing exponentially, from both modern and ancient populations, making it difficult for scholars in the field to keep up with the available information. To tackle these issues, we present MitoBench and MitoDB.

MitoBench is a workbench to interactively analyze and visualize complete mitochondrial genomes with a focus on population genetic applications. The graphical user interface is kept simple to make it suitable also for users without prior knowledge of computational methods. Additional information such as metadata and summary statistics are provided. Currently, MitoBench offers automatic file conversion tools to connect the workbench with existing analysis software such as BEAST, Arlequin, and others as well as some basic analysis methods such as Fst calculation and principal component analysis.

Moreover, MitoBench is linked to MitoDB, a database of mitochondrial DNA reference data. The current prototype encompasses 2,504 complete mitogenomes from the 1000 Genome Project and will be extended continuously. MitoDB also offers users to register and upload their own datasets to collaborate and share their data with other researchers.

Our ultimate aim is to provide a central reference database of population genetics studies on mtDNA that can be easily accessed via the workbench, enabling users to perform typical analysis procedures much faster, more reliably and more conveniently than before.

Session • Analytical methods in population genetics

O–AMG–06
DeamMeth, a full probabilistic model for reconstructing ancient methylomes

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Introduction: Recent computational advances in ancient DNA (aDNA) research have revealed that past epigenetic marks, predominantly the methylation of cytosines, can be reconstructed from DNA sequencing data. By leveraging on increased deamination rates of methylated cytosines present in CpG contexts, a simple count statistic of nucleotide mis-incorporations proved sufficient to recover genome-wide methylation profiles reflecting those generated from fresh samples. However, this methodology comes with several limitations. Firstly, it requires high-quality ancient genomes, which represent a limited resource in aDNA research. Secondly, deamination of methylated cytosines can be hard to distinguish from true variants. Lastly, the count statistic is not ideal for comparisons between samples exposed to different magnitudes of post-mortem DNA damage, thus, rescaling using methylation data acquired from fresh material is often required.

Objective: To overcome these challenges, we have developed a probabilistic model aimed at reconstructing genome-wide methylomes from ancient specimens. The model is implemented in C++ in a software named DeamMeth.

Methods: DeamMeth provides a maximum-likelihood estimate (MLE) of the fraction of methylated cells in a genomic window, by introducing three improvements to previous statistics. Firstly, DeamMeth estimates the actual deamination rates of methylated cytosines and unmethylated cytosines per read position. Secondly, building on the actual deamination rates, the model integrates across the entire DNA molecules to recover the MLE estimate of the fraction of methylated cells. Lastly, the model incorporates the probability of observing a true SNP variant in a CpG context.

Results: We have developed DeamMeth, a probabilistic model to reconstruct methylomes of ancient specimens. This tool provides the first statistic of ancient methylation levels that is directly comparable, without rescaling, to the methylome profiles obtained both from fresh samples and ancient samples. We applied DeamMeth to published ancient genomes, with special attention to contrast populations exposed to different lifestyles and environments.

Conclusion: With DeamMeth, we have improved the methodology for reconstructing ancient methylomes substantially with a full probabilistic model to recover the fraction of methylated cells in a genomic window. DeamMeth can prove crucial for future analyses tracking epigenetic changes through space, culture and time.

Session • Archaeology of the invisible

O–AOI–01
Ancient DNA in sediment – a micromorphology approach

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DNA extracted from environmental samples represents an important source of information on past and present biodiversity. Recent evidence that archaic hominin DNA is preserved in sediments from Pleistocene caves has increased the interest in ancient environmental DNA. Screening sediments for human DNA has the potential to become a standard tool in archaeology, since it could help to complete the map of ancient human occupations and to investigate where and when different groups may have overlapped and interacted. However, little is known about the origins and the preservation factors of ancient DNA molecules in archaeological sediments. Ancient mammalian DNA in sediment can stem from micro-traces of organic material from past living individuals, such as bone crumbles or feces that can be found in the complex mixture of archaeological deposit, or through the direct binding to soil compounds like clay minerals, larger organic molecules, and other charged particles, which may shield the adsorbed DNA from nuclease activity. Studying the pattern of ancient DNA preservation in sediments would help develop more targeted sampling approaches, which - in contrast to random sampling - would allow to reduce costs of time, energy, and money, while at the same time recovering substantially more genetic material. To address these questions, we take advantage of undisturbed blocks of sediment, a tool used by geoarchaeologists to study soil micromorphology in thin section sliced from sediment samples hardened with chemical resins. Our results show that ancient DNA can be retrieved from hardened blocks as well as from loose sediment samples. Hence, by sampling directly through an undisturbed sediment block, we are able to accurately target distinct components of an archaeological sediment sample for DNA extraction. The comparison of patterns of DNA preservation and the distribution of sediment components across undisturbed blocks allow us to investigate the sources of ancient DNA in sediments. This work paves the way for a better understanding of ancient DNA preservation in archaeological sediment deposits.

O–AOI–02
Exploring the genomic impact of colonization in north-eastern Siberia

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Yakutia is the coldest region in the northern hemisphere, with winter record temperatures below minus 70°C. The ability of Yakut people to adapt both culturally and biologically to extremely cold temperatures has been key to their subsistence. They are believed to descend from an ancestral population, which left its original homeland in the Lake Baykal area following the Mongol expansion between the 13th and 15th centuries AD. They originally developed a semi-nomadic lifestyle, based on horse and cattle breeding, providing transportation, primary clothing material, meat, and milk. The early colonization by Russians in the first half of the 17th century AD, and their further expansion, have massively impacted indigenous populations. It led not only to massive epidemiological outbreaks, but also to an important dietary shift increasingly relying on carbohydrate-rich resources, and a profound lifestyle transition with the gradual conversion from Shamanism to Christianity and the establishment of new marriage customs. Leveraging an exceptional archaeological collection of more than a hundred of bodies excavated by MAFSO (Mission Archéologique Française en Sibérie Orientale) over the last 15 years and naturally kept frozen by the extreme cold temperatures of Yakutia, we have started to characterize the (epi)genome of indigenous individuals who lived from the 16th to the 20th century AD. Current data include the genome sequence of approximately 50 individuals that lived prior to and after Russian contact, at a coverage from 2 to 40 fold. Combined with data from archaeology and physical anthropology, as well as microbial DNA preserved in the specimens, our unique dataset is aimed at assessing the biological consequences of the social and biological changes undergone by the Yakut people following their neolithisation by Russian colons.

Session • Archaeology of the invisible

O–AOI–03

Cracked it! – dating potsherds using compound-specific radiocarbon analysis of adsorbed lipids

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Radiocarbon dating of pottery vessels is challenging. It relies on obtaining sufficient carbon, free of contamination, which originates either from the use or from the manufacture of the pot. Invisible food residues preserved within vessel walls are of particular interest because of they are close in age to the time of the deposition due to fast metabolic turnover, and their preservation and relative immobility in the burial environment. Degraded animal fats, distinguished by their high content of C16:0 and C18:0 fatty acids, are often recovered in high concentrations in archaeological potsherds. Therefore, compound-specific radiocarbon dating (CSRA) of individual fatty acids is theoretically possible and highly desirable, rather than the analysis of carbonised residues or total lipid extracts, which are more prone to contamination from burial, handling, storage and extraction.

Preparative Capillary Gas Chromatography (PCGC) isolation has proven to be a powerful technique for isolating single compounds from environmental matrices for radiocarbon dating, however improvements were required to obtain the accuracy and precision required for the dating of archaeological materials. After recent investigations, which identified and quantified sources of contamination associated with the isolation procedure and modified laboratory protocols to minimize and/or eliminate these, our new methods have now been successfully applied on archaeological materials.

Initial tests focussed on a corpus of bog butters spanning a 3000-year range. The tests were then further applied to a range of pottery vessels from well dated archaeological contexts. We carefully selected pottery vessels from different ages and burial environments. Compound-specific radiocarbon dates obtained from the lipids showed good agreement with the pre-existing dates available either from dendrochronology or from Bayesian chronological modelling of radiocarbon dates. These results demonstrate the application of our enhanced CSRA methodology to archaeological pottery vessels, and, significantly, represent the first radiocarbon measurements obtained from lipids preserved in pottery vessels with equivalent accuracy to other commonly dated sample types.

Session • Population structure and migration

P–001

Migration and social organisation studies through ancient genomic analysis of multi-faith populations from Medieval Sicily (ERC Project Sicily in Transition, SICTRANSIT)

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Introduction: The Middle Ages (6th to 13th century) in the Mediterranean area witnessed successive conquests bringing with them new social rules, and ideological regimes, whether Christian or Islamic. The SICTRANSIT project examines the impact of these ideological transitions in Sicily, combining archaeological, molecular, anthropological, ceramics and Isotopic studies. Sicily is an ideal location to study these questions: at the confluence of the East, West and Arab world, Sicily has witnessed four major changes from Byzantine to Aghlabid to Fatimid to Norman to Swabian. Each of these transitions potentially brought new networks of exchange, new social rules as well as new groups of migrants with their own genetic patrimony.
Objectives: In this project, we apply ancient DNA analysis to over 50 samples from human remains spanning the 6th to 13th century from different sites in Sicily, in order to: 1) examine evidence for genetic continuity / discontinuity or for large scale population shifts over this key period; 2) identify the relationship between Medieval populations and contemporary Sicilians; 3) to determine to what extent population affinity is linked to faith-based identity (Christians/Muslims cemeteries).
Methods: We extract DNA from petrous bones, long bones or teeth, build double-stranded libraries and sequence them using a whole-genome approach. We characterise the proportion of endogenous DNA, and assess patterns of authenticity based on sequence length and misincorporation patterns. We apply the programs LASER (PCAs) and ADMIXTURE to examine similarity to modern populations (HDGP dataset).
Results: Preliminary analyses of both teeth, long and petrous bones, indicate a range of sample preservation, ranging from 0% to at least 15% endogenous DNA. Average fragment length and damage estimates are consistent with authentic ancient template. For samples with low endogenous DNA preservation, only sex identification could be accomplished. For high quality samples, nuclear data produced estimates of ancestry, including at least one individual of West African descent.
Conclusion: This ongoing project brings new information for reconstructing human migration in the Mediterranean during the Middle Ages and its consequences on spatial allele variation in the modern population, as well as new insight into faith-based identity.

P–002

Kinship relationships and genomic origins of the peoples buried in an early Medieval cemetery in central Europe

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Historical cemeteries represent valuable sites to study the economic, political and social structures of the populations living on an specific epoch in time and in a particular geographical location. The richness of archaeological finds and wealthy artifacts that have been found in this early Medieval cemetery in central Europe, including high-quality jewelry, ornaments, coins and amulets, suggest that those buried there probably had a high social status. At the same time, many of the burials seemed to be composed of couples, suggesting that the cemetery was used for an elite of dwellers and their families in the context of important trading routes. In this study we used ancient DNA techniques to sequence the complete nuclear genomes of more than 20 individuals buried in a cemetery that was used for a period comprising about a hundred years (950-1050 AD). We analyze the social structure and funerary practices of the population they represent by disentangling close kinship relationships between the individuals. We also use this data together with an extensive panel of European reference samples, evidence from archaeological material, and patterns of strontium isotopes, to explore the origins and genetic affinities of the peoples buried in the cemetery, and to place them in the broader genetic context of the peoples of the Middle Ages in Europe.

Session • Population structure and migration

P–003
Ancient genomes from Iceland reveal the making of a human population

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Opportunities to directly study the founding of a human population and its subsequent evolutionary history are rare. Using genome sequence data from 27 ancient Icelanders, we demonstrate that they are a combination of Norse, Gaelic, and admixed individuals. We further show that these ancient Icelanders are markedly more similar to their source populations in Scandinavia and the British-Irish Isles than to contemporary Icelanders, who have been shaped by 1100 years of extensive genetic drift. Finally, we report evidence of unequal contributions from the ancient founders to the contemporary Icelandic gene pool. These results provide detailed insights into the making of a human population that has proven extraordinarily useful for the discovery of genotype-phenotype associations.

P–004
Ancient genome-wide analysis of the early Neolithic mass grave individuals from Talheim, Germany

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The Talheim mass grave is one of the earliest evidence of violent massacres of Early Neolithic Farmers in Europe. An excavation in 1983 unearthed 34 individuals dated to the Linearbandkeramik Culture (LBK, approx. 5000 BC). Two-thirds of the individuals displayed severe head trauma, in positions to the back and right of the skull indicating that they were attacked from behind. Individuals of all age groups and both sexes were discovered suggesting that the mass grave contained an entire population, killed and buried at the same time. Anthropological analyses suggested a possible kinship between the individuals, and a strontium isotope analysis showed that at least three of the adult individuals had been born in another geographical location. Altogether, the current data point to the massacre of a complete community from a late LBK village.
In this study, we perform a molecular analysis of the Talheim individuals aiming to determine their genetic sex and to infer a possible kinship structure. First shotgun data of petrous bone samples from 29 of the individuals indicate the presence of ancient human DNA (up to 61% endogenous content) with relatively low overall mitochondrial contamination rates. Preliminary analyses of the uniparental markers indicate possible paternal as well as maternal relationships among some of the individuals. In order to extend the kinship analysis, we will combine high throughput sequencing with an enrichment capture to analyse both autosomal genetic variants and the complete mitochondrial genomes. The planned in-depth genetic characterisation of the Talheim individuals will provide a unique snapshot of the family structure of an LBK population which may further help to understand this violent massacre.

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P–005

The Lady from Barfüsser Church – identity reconstruction of a mummy through the mtDNA of living relatives

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In 1975, an almost complete female mummy was found in the Barfüsser church in Basel, Switzerland. She was buried without a gravestone next to the choir screen at the middle corridor in close neighbourhood to influential families. The wealthy clothes, her well-fed body and a mercury treatment imply that the mummy belonged to the upper class of post-reformed Basel. An international research group, led by the Natural History Museum of Basel, is currently analysing the mummy to reconstruct her individual life history and to possibly discover her identity. The archaeological findings together with historical documents revealed a possible candidate for the identity of the mummy, Anna Catharina Bischoff, who died in Basel in 1787.

With the help of genealogists it became possible to trace her maternal family tree and thereby to locate two living relatives in Basel (two siblings, separated by 22 generations). Here we present the results of our molecular analysis of the mitochondrial DNA (mtDNA) of the mummy and her possible living relatives.

We processed a premolar of the mummy in our aDNA laboratory in Bolzano. The complete mtDNA was reconstructed by next generation sequencing (NGS) methods and a target enrichment capture achieving a 697.74-fold coverage. Modern contamination was low and the authenticity of the ancient DNA was confirmed further by ancient DNA damage patterns. By using haplogrep the mitochondrial haplogroup was assigned to U5a1+!16192.

The mitochondrial hypervariable region (HVR) 1 (16024-16500) and HVR2 (60-340) of the modern saliva samples from the possible relatives were Sanger sequenced. The results showed a total match to the haplotype of the mummy including nine known SNP positions. In parallel, the saliva samples were sequenced in a forensic genetics laboratory in Lausanne, where identical results were achieved.

The findings strongly support the assumption that the mummy and the living persons belong to the same matriline and that the Lady from Barfüsser church could indeed be Anna Catharina Bischoff.

However, it has to be noted that 6.7% of the modern Swiss population belongs to the haplogroup U5. Therefore, we are planning to analyse the complete mtDNA of the living relatives and possibly another family branch in the USA to further verify the identity of the mummy.

P–006

Why were 17 people buried in a well in 12th century Norwich? – genome-wide analysis of Medieval human remains from Chapelfield, Norwich, UK

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In 2004 human remains were recovered from a spoil heap of construction work on the Chapelfield shopping centre in Norwich, UK. Archaeological investigations discovered that the bones had come from a circular shaft that had probably constituted the bottom of a well. Excavation of the well shaft produced a disarticulated comingled assemblage of human remains representing at least 17 individuals (six adults and 11 children). The stratigraphic relationships between the skeletons combined with radiocarbon dating and pottery typology indicated that the bodies had been buried over a short period of time in 12th-13th Centuries AD, and possibly deposited in a single event. The well was located close to the Jewish quarter of the Medieval city, which may be significant given that late-12th Century Britain is notorious for documented incidents of violence towards Jewish communities. However, there were no detectable signs of trauma on the Chapelfield bones. Possible alternative explanations for this unusual burial event include a local epidemic, famine or a divergent form of funerary treatment afforded to certain individuals because of their economic, social or religious circumstances.

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Here we present genome-wide shotgun and capture data from the Chapelfield human remains. All individuals analysed show greatest affinities with modern Ashkenazi Jewish and Southern European populations. Chronological modelling of radiocarbon dates using Bayesian inferences produce a range centred on 1190 AD, the date of a historical massacre of Jews in Norwich. We infer that the individuals recovered from the Chapelfield site do indeed represent victims of a documented anti-Semitic pogrom. Most recent palaeogenomic studies have been concerned with demographic processes that took place over hundreds or thousands of years, but this result demonstrates their power in producing dramatic material evidence of single historical events. In providing information on a European Jewish people who lived before the Medieval population bottleneck, these data will also facilitate novel insight into their ancient population history, including admixture with other European groups.

P–007
Ancient DNA from Misión Salesiana, Tierra del Fuego

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Beginning in 1492 and lasting even today, the encounters between Europeans and Native American populations have had major demographic, social, biological and ecological impacts. While first discovered by Europeans in 1520, European settlement of Tierra del Fuego did not begin until the second half of the 19th century. Analysis of biological data from a cemetery population at Misión Salesiana ("Nuestra Señora de la Candelaria") in Tierra del Fuego provides insight into the local population history in this region of South America after contact. Misión Salesiana was established in 1893 to assimilate and Christianize the remaining local indigenous population, the Selk"nam. The mission cemetery includes burials from the community as well as the mission, averaging ~100 years old. Samples of tooth and bone from 32 individuals were used for DNA extraction. In-solution hybridization capture was successfully used to recover the mitochondrial genomes from 25 individuals. Mitochondrial lineages C and D are predominately represented in the sample (appearing in 50% and 41% of the individuals, respectively). Two individuals have haplotypes which are found in European populations, which is reflective of either admixture or interment of European individuals in the mission cemetery. The whole mitochondrial genome data were analyzed for measures of diversity and the cemetery population was compared to other South American populations, both ancient and modern. These studies of diversity yield insight into both inter and intra group variation in Native South American populations. Genome-wide SNP analyses are currently in progress.

P–008
A new targeted enrichment method, BAC-double capture, for ancient DNA analysis

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To analyze a specific region of genome using next-generation sequencing technologies, we usually take a strategy of targeted capture using "baits" designed for the target region. In ancient genome researches, mtDNA (16.6kbp) has often been examined, which is enriched by using PCR amplicons of mtDNA as baits. Thus, when the target regions are not so large region, PCR-amplicons or synthesized oligos are used as baits. However, when the targets are around hundreds kbp, such baits are not so efficient in ancient DNA because of its damaged status. Here we present a new method, "BAC Double Capture (BDC)". The BDC can capture target-regions of hundreds kbp by using BAC fragments as baits. In this poster, we show the optimized conditions targeting Ring finger protein 213 (RNF213) gene (140kbp), including a risk mutation of Moyamoya disease. To evaluate the reliability of BDC, experimental cost and data quality were compared with those of a commercial kit, MYbaits. The results showed, though the ratio of duplicate reads was slightly higher, the cost was less than that of the kit. The data quality was sufficiently the same as that of the kit. Thus, BDC method can be a low-cost, and useful method for analyzing hundreds kbp genomic regions.

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P–009

Reconstructing the demographic history of dingoes using ancient genomic data

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The dingo is a dog-like quadrupedal mammal native to Australia. Due to its morphological similarity to modern domestic dogs, it is generally considered to be either a member of Canis familiaris (the domestic dog) or a separate but closely related species within the Canis genus. However, the precise taxonomy and evolutionary history of the dingo remain a subject of controversy. It has been challenging to reconstruct the demographic history of dingoes using modern genomic data due to recent admixture with European dogs. Here we present whole-genome data (17X) from a dingo fossil dated between 993-1146 CE (95% CI) excavated from a cave beneath the Nullarbor Plain. Population genomic analyses of our ancient data place the dingo within the diversity of various modern village dog breeds from Island South-East Asia (ISEA), and in particular suggest that the dingo is closely related to village dogs from Vietnam and Borneo in addition to the New Guinea Singing Dog (a wild dog population). Our results confirm the dingo"s status as a member of Canis familiaris, settling a decades long debate about the dingo"s taxonomy. Further, we suggest that the ancestor of the dingo originated in central Africa and migrated across Asia into South Asia, finally arriving in northern Australia via islands including Borneo. From that point, the species began to proliferate across the Australian continent. To determine the dingo"s population split time from ISEA dogs we computed the FAB statistic using our ancient dingo data along with genomic data from modern New Guinea Singing Dogs and Basenji (a domestic dog breed). Simulated data were generated via msprime and Approximate Bayesian Computation was used to compute a 95% credible interval of the population split time. From this we constructed an informed demographic model depicting the dingo"s evolutionary history from the common ancestor of dogs.

P–010

Maternal genetic origin of the Avar period (7th century) nomadic elite in the Carpathian Basin

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A nomadic group known as Avars migrated from the Inner-Asian steppes and arrived at the Carpathian Basin in 568 AD, where they have founded the empire called as Avar Khaganate. The Avar population were heterogeneous in anthropological and archaeological characters, while the debate about their Asian connection is long present in the archaeological research and their genetic origin is still unknown. The previous studies of the control region of mitochondrial DNA of a small Avar groups showed mixed Eurasian genetic composition with predominant European elements.

In our study we investigated 27 Avar period individuals from Danube–Tisza Interfluve with a primary focus on the elite, distinguished by richly furnished burials and certain prestige artefacts. The skulls of these individuals showed Mongoloid craniometric traits in different extent. The aim of our research was to describe the maternal genetic composition–based on whole mitochondrial genomes–of the leading stratum of the 7th century Avar population.

The isolation and DNA-library preparation, as well as the capture methods and sequencing on Illumina MiSeq platform were performed in the Laboratory of Archaeogenetics of IA RCH of Hungarian Academy of Sciences in Budapest. The results were evaluated with descriptive population genetic and statistical methods, as well as with phylogenetic analyses.

The mitochondrial genome sequences of the investigated samples from 11 different cemeteries encompass the entire range of the Eurasian haplogroups with a dominance of Asian lineages, which represent 64 % of the variance. The haplogroup based analyses (PCA and Ward-type clustering) shows Asian, especially Central-Asian character of the Avar period elite. The sequence based analyses (MDS) and also phylogenetic results reflect the East-Asian and Central-Asian genetic connections as well.

Our results correspond to the anthropological and archaeological, historical assumptions about the Central-Asian connection of the Avar elite, that has been attested by certain artefact types known from the Eurasian steppe and appearing in the Carpathian Basin only after the Avar conquest. Moreover, it provides even more detailed information, how a nomadic elite even after settling, remained part of the connection network of the Eurasian steppe and valued its tradition by preserving its maternal genetic ancestry through generations.

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P–011

First genetic data from the Holocene Green Sahara – new insights into the human mitochondrial phylogeny

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Ancient DNA studies give us the possibility to directly observe the genetic variation through time and to explore the history of anatomically modern human populations with a high level of resolution. While genetic data from a high number of individuals are available for almost all the geographical areas in Eurasia covering a wide temporal range, information from Africa is limited due to climate conditions that are not favourable to the DNA preservation in most of the continent. For this reason, the knowledge of African genetic variability was restricted to modern data until recently, when studies focused on samples from south and east Africa, Egypt and Morocco were published. Filling the gaps in space and time is extremely important since present-day genetic variability could not properly reflect the past situation: different population genetics dynamics may have occurred in different times and with specific regional impacts, modifying haplotype distribution and frequencies. Here we present the first genetic data for the Saharan region, characterized by severe climate oscillations that could have driven population expansion and contractions, migrations, admixture or isolation in the past. We analysed two ~7000-year-old female individuals with signs of natural mummification from Takarkori Rockshelter, Libya. The mitochondrial genomes show a novel mutation motif phylogenetically linked to the haplogroup N root. The divergence of this haplogroup from L3 lineage is commonly dated around 50-65 ka, probably located in the Arabian Peninsula and linked to the exit of AMH from Africa. The presence of this haplotype in Takarkori can represent a past relic of an African origin of haplogroup N or a trace of an ancient migration from Eurasia not previously documented. Our finding highlights the importance to increase genetic data for past African populations in order to detect lineages nowadays possibly disappeared or whose geographical distribution and frequencies changed during time.

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P–012

Genetic continuity in the western Eurasian Steppe broken not due to Scythian dominance, but rather at the transition to the Chernyakhov culture (Ostrogoths)

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The long-held archaeological view sees the **Early Iron Age nomadic Scythians** expanding west from their Altai region homeland across the Eurasian Steppe until they reached the Ponto-Caspian region north of the Black and Caspian Seas by around 2,900 BP[1,2]. However, the migration theory has not found support from ancient DNA evidence[3], and it is still unclear how much of the Scythian dominance in the Eurasian Steppe was due to movements of people and how much reflected cultural diffusion and elite dominance. We present new whole-genome results of **31 ancient Western and Eastern Scythians as well as samples pre- and postdating them** that allow us to set the Scythians in a temporal context by comparing the Western Scythians to samples before and after within the Ponto-Caspian region. We detect no significant contribution of the Scythians to the Early Iron Age Ponto-Caspian gene pool, inferring instead a **genetic continuity in the western Eurasian Steppe that persisted from at least 4,800–4,400 cal BP to 2,700–2,100 cal BP** (based on our radiocarbon dated samples), i.e. from the Yamnaya through the Scythian period.
However, the **transition from the Scythian to the Chernyakhov culture between 2,100 and 1,700 cal BP does mark a shift in the Ponto-Caspian genetic landscape**, with various analyses showing that Chernyakhov culture samples share more drift and derived alleles with Bronze/Iron Age and modern Europeans, while the Scythians position outside modern European variation. Our results agree well with the Ostrogothic origins of the Chernyakhov culture and support the hypothesis that the Scythian dominance was cultural rather than achieved through population replacement.

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P–013
Indian genetic heritage in Southeast Asian populations

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Mainland Southeast Asia (MSEA) is a region which has a high linguistic diversity and complex population history. Over a hundred of languages from 5 language families are spoken in MSEA. Anthropological and archaeological evidence suggested multiple waves of migration into this region. Early states in MSEA were established with a substantial cultural influence from India. Indian influence persisted and became fundamental for the regional cultures. Here we analyzed new genome-wide genotype data for 12 populations from Thailand, along with published data for other MSEA populations. Results of allele frequency-based and haplotype-based methods reveal Indian admixture in Thai, Cambodians, Mon, Khmer, and some other Austroasiatic speakers which are historically linked to the early Indianised states, while Indian admixture is absent in Austroasiatic speakers which are hill tribes (Htin) and hunter-gatherer populations (Mlabri and Maniq). The results support the hypothesis that the Indian gene flow actually came with Indian culture. We further constructed admixture graphs to investigate the spread of Tai-Kadai languages in MSEA. A best-fitting model among more than 10,000 models tested showed that the present-day Central Thai originated via admixture of a local population closely related to present-day Austroasiatic speakers (already having Indian admixture) and a population closely related to Tai-Kadai speakers from South China, with the later population contributing slightly more than 50%. After this admixture event, the descendant population received a further pulse of Indian gene flow. Thus, the Central Thai population has an elevated Indian admixture proportion, as compared to local Austroasiatic-speaking groups. We were not able to model the Central Thai population without a local Austroasiatic-speaking population as an ancestry source. This result clearly contradicts previous studies based on uniparental markers (mitochondrial DNA and Y chromosome) which suggested demic diffusion of Tai-Kadai-speaking populations from China with a minimal level of admixture with local MSEA populations.

P–014
Genetic identity and relatedness of pre-Dogon and early Dogon populations (Mali)

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For over two millennia, the Dogon Country in central Mali has experienced constant interactions of groups of people from different cultural domains. The subject of identity of these early inhabitants of the region, before the arrival of the Dogon people around the 15th century AD, remains unclear. Our current bio-archaeological research focuses on questions concerning the identities, genetic relationships and relatedness of pre-Dogon and modern Dogon populations, as well as their mobility, ways of life, diet and health.
Within this research, we also evaluate the genetic contribution of the ancient pre-Dogon populations on current Dogon people. To address this question, 48 ancient DNA samples belonging pre-Dogon and early Dogon individuals dating between the 13th and 16th c. AD are currently being analysed. All samples come from Cave C, the largest of the sepulchral burial caves found in the Bandiagara Escarpment, containing more than 3 000 buried individuals. This paper will present the results of the aDNA analyses in order to shed light on people"s origins and relatedness.

Session • Population structure and migration

P–015

How spread of agriculture and historic trade have affected the genetic diversity of emmer wheat landraces

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Emmer wheat was a founder crop of early agriculture in the Fertile Crescent of southwest Asia and one of the first crops to spread across Europe and Asia during the early Neolithic. It remained the principal crop of Old World agriculture until the early Bronze Age when it was gradually superseded by emmer derivatives such as durum wheat and by hexaploid wheats. Although the broad routes for the spread of agriculture through Europe and west Asia have been mapped by archaeological and archaeobotanical studies, we still lack a detailed understanding of the trajectories in certain regions and how the initial pattern of spread was overlaid by subsequent crop movements. Here we present a population genetic analysis of genome-wide SNPs obtained by genotyping-by-sequencing (GBS) of 189 emmer landraces (historic cultivated varieties) from various sites in Europe and southwest Asia. We use archaeological and historic information to formulate scenarios for the spread of emmer cultivation and explore, using approximate Bayesian computation techniques, the relative roles of founder effects and subsequent migration and trade in explaining the present day patterns of genetic diversity of this cereal.

P–016

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

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

Objectives: We are addressing a long-standing question on the origin of the Chachapoya people given the fact that culturally they have received influence from Andean and Amazonian societies in ancient times. Additionally, the study aims to assess whether the high diversity levels we have observed in the Chachapoya area nowadays (1) reflects an ancient demographic signature or the result of more recent phenomena.
Methods and preliminary results DNA was extracted from 43 ancient individuals belonging to eight Chachapoya sites and one Cajamarca site. Double stranded next-generation sequencing libraries (Half-UDG) were generated for all individuals which subsequently were shotgun sequenced following standard protocols. After shotgun sequencing, samples showed a varied degree of endogenous DNA, ranging from 0.76% to 88.17%. A total of 34 individuals that had more than 5% of endogenous DNA and a cluster factor of around 1, were selected for downstream 1240K genome capture.

Downstream analyses: We are currently performing the human quality control pipeline implemented at Max Planck Institute for the Science of Human History in order to proceed with PCA and clustering-based analyses. Subsequently, our dataset and other worldwide refence data will be analyzed in a population genetic framework in order to answer questions regarding substructure within Chachapoya area and populations origins.

Session • Population structure and migration

P–017
Genome-wide data describe Siberian ancestry in ancient Fennoscandia

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Northeastern Europe has so far remained understudied from the perspective of ancient DNA, especially compared to mainland Europe, for which studies of ancient population genetics have provided remarkable findings in the last years. In this study, we explore the genetic connections and migrations in the eastern Fennoscandian by analysing ancient genomes from archaeological human remains of Finnish and Northwest Russian origin.

A genome-wide sequencing dataset was analysed for 11 ancient individuals, consisting of six individuals from the 3,500-year-old site of Bolshoy Oleni Ostrov, in Russian Kola Peninsula, three from an Iron-Age lake burial of Levänluhta in Ostrobothnia, Finland and two from an 18th century Saami cemetery of Chalmny Varre. The ancestral components in modern and ancient populations were investigated using F4 statistics and admixture analysis. The ancestry proportions for populations were estimated using *qpAdm*. A relative date for the admixture events of interest was obtained based on admixture linkage disequilibrium decay, as implemented in the alder program.

Both modern and ancient populations of northeastern Europe support models of mixture between European and North Siberian ancestry, the latter best proxied by the modern-day Nganasan population in the Taimyr Peninsula. A Siberian ancestry component was observed forming a gradient through time. It comprised more than a half of the genomes of the earliest individuals, from 3,500 years ago (Bolshoy). The component was present in considerable amounts in the samples from Iron-Age Finland and both modern and ancient Saami individuals, whereas lower proportions were observed in other modern Finno-Ugrian populations and their close relatives.

The arrival of the Siberian component in the population ancestral to the Bolshoy individuals was dated roughly to 4000 years before present, signaling an early migration and admixture event between Siberia and Europe. However, multiple waves of immigration have likely carried the Siberian ancestry component to its westernmost extremity in Fennoscandia. The particular prevalence of this component in the Uralic language speakers may be associated with the spread of the language group.

P–018
New chronology for Late Upper Palaeolithic sites in Belgium

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The UP-NORTH project is using a range of techniques, including stable isotope, radiocarbon and ancient DNA analyses, to examine the dispersal of people and animal populations into Northern Europe after the Last Glacial Maximum. Our goal is to establish local chronological, palaeoclimatic, and palaeoecological frameworks in which links between cultural innovation under changing environments can be explored. Here we present results from Belgium, which is home to several Late Upper Palaeolithic sites that were occupied around the time of the Lateglacial interstadial, and thus the area is key to understanding wider human migration within northern Europe at this time of rapid and large-scale climate change. The timing of human presence in the area and the specifics of the local environmental conditions have been subject to debate. The majority of sites were excavated in the late 19th and early 20th centuries. The available radiocarbon dates from these sites are mostly conventional or AMS dates made using pre-treatment methods that have now been shown to be problematic. Furthermore, previous dates were made on material which was often not securely linked to the archaeology. Here we present over 20 new AMS radiocarbon dates along with additional stable isotope measurements of humanly modified faunal remains from Trou du Chaleux, Goyet Cave, Trou de Nutons, and Bois Laterie. Together the radiocarbon and stable isotope results are providing a clearer picture of the local climate and timing of faunal and human presence in the region.

Session • Paleoproteomics

P–019
Proteomic evidence of dairy consumption in Neolithic Sudan

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Animal milk has been an important food source for humans in various regions of Africa for millennia but many questions remain about the origins and spread of its consumption, as well as which animal species where utilised. Evidence for dairying can stem from rock art images, faunal remains and lipid residues on pottery, which offer important insights at the community-level. In contrast, the proteomic analysis of human dental calculus can provide direct evidence of milk consumption at the individual-level. Ancient dental calculus is a rich source of information, encapsulating pathogens, food debris and other dietary biomolecules, including animal milk. Moreover, variations in amino acid residues between species mean it is often possible to establish which animal the milk derived from. This study investigates patterns of milk consumption in Sudan during the Neolithic and Kerma periods through the proteomic analysis of ancient dental calculus. The identification of the milk protein beta-lactoglobulin (BLG) contributes new, direct evidence for milk consumption in the Nile Valley. These findings also explore new limits for dietary protein preservation in ancient dental calculus and the application of proteomics to archaeological materials from hot, dry climates.

P–020
New insights into British Neolithic milk consumption

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There has long been debate over the origins of milk drinking and dairy product consumption within European populations. Whilst it has previously been assumed that lactase persistence (LP) was positively selected for following the advent of agriculture – as the ability to consume raw milk may have provided a selective advantage due to its nutritional qualities – recent genetic studies of prehistoric human remains have revealed that LP may have only emerged in Europe in the last 4,000 years, and that Neolithic populations would likely not have had LP. This is in contrast to organic residue analysis of Neolithic pottery indicating the utilisation of dairy, and zooarchaeological mortality profiles indicative of dairying herds recovered from Neolithic sites. The recent discovery of the preservation of the milk protein β-lactoglobulin (BLG) in human dental calculus however presents a new way in which we can explore dairy use in the archaeological past – and provides direct evidence of milk consumption. Here, we present the results of proteomic analysis of human dental calculus samples from a number of British Neolithic sites which has revealed the presence of BLG peptides – but in individuals who are unlikely to have had LP. The protein results can help us to explore the use of dairy in the British Neolithic, potential processing of milk by Neolithic populations, and possible production of new forms of dairy products.

Session • Paleoproteomics

P–021
Fossil collagen – still not easy to get it pure – Is MIP the solution?

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Researchers in the fields of Radiocarbon, Stable Isotopes, ZooMS and Amino Acid Racemization (AAR) studies, they all need Fossil Collagen (FC) in it's purest possible form. But the isolation and cleaning of this FC is very time consuming and these procedures may introduce or reduce contaminations, which may, as a consequence, produce erroneous results. Synthesizing and optimizing a "Molecularly Imprinted Polymer" (MIP) for collagen/gelatin can make this isolation procedure much faster and more specific. This method goes for the shape of this very specific target molecule, instead of its size. The application of MIP in AAR studies on FC is described for the first time. By optimizing the sample preparation over all steps from the fossil bone to analyzing the enantiomers of aspartic acid from the FC by Gas Chromatography (GC), results are now available within one day. Included is a measure of the quality of the FC by the pattern of the single amino acids from the GC chromatogram, which is very characteristic. At the same time, the AAR can give an estimate of the relative age of the fossil bones.

P–022
Using Proteomics to understand the conservation history of a painting

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Protein-based materials have been used extensively in artistic and cultural heritage objects, not just in the original creation of the object, but also during later conservation. Their identification can provide valuable insight into artistic, such as paint binders, or conservation techniques, such as protective coatings, which helps understand the history of the object studied. This knowledge is very useful in defining the most appropriate display and storage conditions, as well as the most effective further conservation protocols.
Current technologies often found in galleries and museums, such as Fourier transform infrared spectroscopy (FTIR), can help identify presence of proteins in these objects, but often cannot distinguish between different proteins or their biological source (species). Therefore, mass spectrometry and paleoproteomics can provide insight into these cultural heritage objects by identifying proteins and their sources, with the added ability to also identify the post-translational modifications (PTMs) that have occurred. As an example, we present recent work done to understand the conservation history of a 14th century Italian wall painting, "A Group of Four Poor Clares" by Ambrogio Lorenzetti (active 1319, died 1348/9), from the National Gallery, London. In an unknown proteinaceous "layer", two protein sources were determined: glue and egg white. Additionally, these proteins were identified to certain species: sheep and cow collagen in the glue, and chicken and duck egg white proteins. Since these two protein components were likely not mixed together, it was then discovered that there were actually two protein layers on the wall painting.
In addition, analysis of PTMs detected several photo-oxidation products, which suggest that the egg layer experienced prolonged exposure to UV light, meaning it was likely applied long before the glue layer. We, therefore, propose that paleoproteomics can provide important information for understanding not just the composition of cultural heritage and artistic objects, but also for elucidating the history of a piece, both important for informing proposed conservation treatments.

Session • Paleoproteomics

P–023

Bottom up and top down proteomics applied to tempera paints: focus on chemical modifications and crosslinking

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In art paintings, protein materials such as egg or milk (e.g. Tempera technique), are implemented as binding media to ensure the cohesion among pigment particles and their adhesion to the paint support. Nevertheless, over time these organic compounds undergo to processes of degradation both spontaneously (ageing) and induced by external factors such as local environment, interaction with pigments or inappropriate conservation/restoration conditions. The presented work aims to study, through proteomics analysis, the mechanisms and products of this decay, investigating protein truncations, processes of reticulation and chemical modifications. Precisely, the identification and localization of native protein cross-linking (i.e., inter- or intraproteic covalent bonds) are principally considered. The research is being conducted on both naturally aged (ten years) and fresh paint mock-up formulated with lysozyme, an egg white protein, mixed with lead white pigment ($2PbCO_3 \cdot Pb(OH)_2$). The effects of other chemical and physical oxidizing agents such as PbO_2, H_2O_2 or UV rays are also studied. To detect and investigate the cross-linked structures, protein separation based on gel electrophoresis has been combined with both bottom up and top down experiments (MALDI TOF-TOF and nanoESI-Orbitrap). The observation of multimers in the gel electrophoresis of samples after protein reduction and alkylation suggests the existence of crosslinks (disulfide bonds excluded). The MS patterns of the lysozyme dimer show various changes compared to monomer in terms of both chemical modifications and structural modifications. For example, the various forms of tryptophan oxidation are pointed out. This study also highlights a peptide involved in the lysozyme crosslinking using the combination of multiple enzymatic digestions (such as trypsin and AspN). The presentation will show the whole analytical strategy and discuss the results obtained on crosslinking and chemical modifications towards the understanding of chemical process and protein reticulation inside the painting.

P–024

Understanding the craft of parchment production using proteomics

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Collagen is one of the most abundant proteins in Cultural Heritage and, as such, an invaluable source of information. Here, we seek to assess the processing history of skins, specifically the use of lime, and the chemical changes that occur when skins are de-haired and processed, using proteomics. Collagen was extracted from parchment samples prepared by different methods and these were analysed by ZooMS (MALDI-TOF) and LC-MS/MS. By measuring glutamine deamidation we expect to gain an understanding of collagen degradation pathways, and the chemical markers associated to skin processing, in order to develop improved and rapid methods to detect parchment production methods and history, and damage caused by skin processing and degradation.

Session • Paleoproteomics

P–025

Components of human Palaeolithic diet identified using proteomic analysis of dental calculus from Southern Italy

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During Pleistocene-Holocene transition, Palaeolithic human populations in Italy are known to exploit several food sources including marine ones. Overall, collagen stable isotopes analysis and microscopic observation of dental calculus residues confirmed the archaeological model indicating hunter-gatherer economic system was based mostly on proteins consumption. However, stable isotope analysis cannot identify the animal and vegetable species used as diet resources. In order to more accurately identify which species were consumed, we present the results obtained using mass spectrometry-based proteomic analysis of mineralised human dental plaque, i.e. calculus, from the sites of San Teodoro (Sicily) and Romito (Calabria) in Southern Italy.

Consistently with the archaeological record, bovine and equine collagen sequences were confidently identified, confirming consumption of meat from these mammalian species. The calculus associated with one individual from San Teodoro cave also returned traces of leguminous proteins. These results demonstrated that recovery of dietary animal and plant proteins from Palaeolithic dental calculus can be achieved with good taxonomic resolution. We demonstrate palaeoproteomics can be used to improve the reconstruction of Palaeolithic human diet, confirming and integrating the results previously obtained by other experimental approaches.

Session • Domestication

P–026

Early Holocene dispersal of Near Eastern Domesticates into High Mountain Central Asia – Zooarchaeology by Mass Spectrometry (ZooMS) analysis of archaeofaunal remains from Obishir V, Kyrgyzstan

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The domestication of sheep and goat, and subsequent continent-scale migrations by Near Eastern pastoralists transformed the ecology of western Eurasia during the initial Holocene, very little is known about the early history of pastoralism in the continental interior. Summarizing recent scholarship from other regions of Central Asia, we present new evidence for early migration of pastoral peoples into the Ferghana region (modern day Kyrgyzstan and Uzbekistan) based on zooarchaeological and biomolecular analysis of animal bones from Obishir V – one of the only stratified and well-documented archaeological sites from the early Holocene in the region. Although the assemblage is largely fragmented, Zooarchaeology by Mass Spectrometry (ZooMS) permits taxonomic identifications of otherwise morphologically unidentifiable bone from this important assemblage. Our results suggest that the earliest occupants of the site had a strong dietary emphasis on ovicaprids, which, when considered alongside contextual archaeological and genomic data we interpret as strong evidence for an early dispersal of domestic animals and pastoral lifeways deep into the Eurasian interior.

P–027

Bronze Age meat industry –ancient mitochondrial DNA analyses of pig (*Sus scrofa*) bones from the prehistoric salt mines of Hallstatt (Austria)

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Question: Large-scale underground salt mining in Hallstatt ('Salzkammergut' region, Upper Austria) dates back to the Middle Bronze Age, approx. 1500 years BC. However, salt mining was not the only production branch located in this remote alpine valley. Archaeological finds from the surface of the Hallstatt High Valley evidence a substantial meat industry mainly based on pig (*S. scrofa* f. domestica). Significant amounts of bone and teeth, as well as large log basins, used to cure the meat in low-grade salt, were excavated. The archaeological and archaeozoological findings demonstrate a well-organized and efficient system capable of providing hundreds of pigs on a yearly basis. This sheds a fascinating light on the organizational capabilities of these Bronze Age communities and raises several questions as to provisioning structures, trade routes and breeding regions. To better understand management of the early pig populations and meat production in Hallstatt and surrounding areas, we aim to perform a genetic analysis to establish a phylogeographic network based on DNA sequence variation among modern pigs, wild boars and prehistoric (likely) domestic pigs.

Methods: In the present pilot study, we extracted ancient DNA from 10 prehistoric porcine teeth specimens for the analysis of mitochondrial DNA sequence variation. Eight samples allowed amplification of a partial sequence of the mitochondrial (mt) control region (CR), and from seven the complete CR marker sequence of 637 base pairs in length could be obtained. **Results**: Five unique mt CR haplotypes ranging within the variation of modern domestic pig and wild boar lineages were found and shared haplotypes between prehistoric and modern domestic pigs and wild boars were observed. Genetic variation found in the mt CR of prehistoric pigs is almost as high as found among present day *S. scrofa* (Wild boar and breeds). With the exception of one intermediate haplotype, all prehistoric pigs from Hallstatt are closely related to haplotypes derived from European breeds or wild boars.

Conclusions: The results proved teeth as suitable material to obtain genetic information from prehistoric domestic pigs from Hallstatt. Although the data are still preliminary, they support the assumption that the 'Hallstatt pigs' were derived from large herds and/or various husbandries. Next, we will test nuclear markers with the tooth material as well as with bones to assess the potential success of genomic analyses.

Session • Domestication

P–028

Ancient DNA and archaeology as tools for understanding the domestication of south american camelids

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One of the most debated topics in SouthAmerican Zooarchaeology has been the domestication and evolution of the four camelid species that live along the Andes: two wild species, guanaco (*Lama guanicoe)* and vicuña (*Vicugna vicugna*) and two domesticated species, llama (*Lama glama*) and alpaca (*Lama pacos)*.

Around 7000 yr. ago two new species llama (Lama glama) and alpaca (Vicugna pacos), appeared because the artificial selection and behavioural features as result of an Andean domestication process. Over years, human-camelids relationship evolved, as human groups went from hunters-gatherer economy to a new economy where they combined of hunting, gathering with herding and crop activities. Osteometry has been widely used to distinguish camelids species. However, osteometrics can only separates species in two size groups, large (guanaco and llama) and small size (vicuña and alpaca), which are not informative of the domestication process. We have generated 61 mitochondrial genomes of ancient camelids using enrichment by capture and NGS and combined this genetic information with morphological data to understand evolutionary processes of the camelids and the domestication of guanaco and vicuña. The sampled remains were recovered from two archaeological sites located in Northern Chile, Tulán-54 and Tulán-85 (Early Formative period, 3200-2300 yaB.P.). In the south eastern border of the Salar de Atacama during this period groups developed a mixed economy sustained by hunting, gathering and camelid breeding. While integrating an important ritual component, new technologies and the development of ceremonial and architecture. These sites have previously been associated with an early herding and hunting economy. Mitogenomic bayesian phylogenies were created, as well as D-loop region haplotypes networks to compare our samples with a panel of published sequences.

Results show two big monophyletic clades, one of them only including small size specimens clustered with modern vicuñas, while the other clade consist of small and large ancient specimens grouped with modern llamas, guanacos and alpacas. The clustering of ancient mitogenomics with domesticated species suggest that some of Tulán-54 and Tulán-85 camelids had already been domesticated. Haplotype temporal networks show that some ancient haplotypes are still present in modern populations and that ancient camelids were less hybridized that modern specimens.

P–029

Unveiling early horse domestication and mule production with ancient genome-scale data

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Despite being one of the last large herbivores to be domesticated, the horse has deeply transformed human civilizations. It provided not only important primary domestication products including both meat and milk, but also invaluable secondary products, such as fast transportation, which impacted patterns of human movements and facilitated the spread of vast cultural and political units across the Old World. The steps underpinning early horse domestication are, however, difficult to track in the archaeological record, especially due to (1) the relative scarcity of horse bone assemblages until the Neolithic and Bronze Age transition, and (2) the absence of clear patterns of size differentiation prior to the Iron Age. Some of the more recent steps accompanying horse domestication, and in particular how it was transformed to fit a range of utilizations in different human groups, are also poorly documented. One such step pertains to the development of mules, and other kinds of F1-hybrids, which are difficult to identify on fragmentary remains using morphology alone. Within the course of the ERC PEGASUS project, we have generated genome-scale sequence information from hundreds of equine archaeological remains spread across Eurasia and spanning the last ~40,000 years. These data helped us test the extent to which candidate domestication centres in Central Asia and Europe contributed to the genetic makeup of the modern domestic horse and propose a minimal time boundary for the earliest utilization of mules by mankind.

Session • Plagues and pathogens

P–030
Molecular screening for historical diseases in Mechelen, Belgium

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In ancient DNA analysis, combining sensitive laboratory techniques and automated computational analyses allows large numbers of individuals to be analyzed reliably and concurrently, permitting pattern analysis within population-size collections of data. These recent advances have also provided researchers in molecular paleopathology with valuable tools for understanding diseases in past populations, which can be critical when reliable historical documentation is incomplete or absent or where etiological agents of illness are unknown. Here, we report on our approach for microbial pathogen screening of skeletal material from St. Rombout's parish cemetery in Mechelen, Belgium. This cemetery in the city's center was used from the 10th to the 18th century CE, and hence spans a period of epidemiological relevance from the Medieval through post-Medieval eras. A recent excavation of a portion of the cemetery yielded a skeletal collection of more than 4000 individuals. Metagenomic data from teeth (n=151) are being analyzed for the presence of pathogen DNA using next-generation shotgun sequencing in parallel with an in-house computational pathogen detection pipeline. These teeth were harvested from individuals interred in multiple burials, as simultaneous deposition in a single grave can be indicative of an outbreak of disease. The preliminary analysis approach is non-targeted, which is beneficial for initial screenings for unknown diseases. Where DNA from organisms of interest is putatively identified, targeted approaches can be applied to further enrich the genetic information obtained. This substantial longitudinal sampling set will contribute to our understanding of the health of this population over an eight-century time transect, and has the potential to illuminate further aspects of the changing disease landscape in Western Europe.

P–031
Screen pathogens from ancient remains and reconstruct the phylogenetic history of ancient pathogens

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Detection and identification the microorganisms in ancient remains were important for tracing the past infections. However, our previous studies were mainly focused on morphological observations and PCR-based molecular techniques aimed to detect infections, which were prone to have false positives and false negatives results. Today, the metagenomic sequencing has significantly increased the analytical resolution and permits parallel analyses of host and microbial communities. In this study, we applied metagenomic sequencing on 10 dental pulp samples recovered from the Bronze Age site in our laboratory. The libraries of soil sample from this site and the blank control were also included in this study. The data generated for all samples were screened for ancient bacteria pathogen DNA using two bioinformatics tools including MALT (Megan Alignment Tool) and MetaPhlAn2 (metagenomic phylogenetic analysis). Using the MetaPhlAn2 tool, we successfully detected the salmonella enterica specific markers in 6 individuals. To verify the results, we constructed the reference database including all complete bacterial genomes and plasmids from the NCBI and screened the pathogens using the MALT. We found six samples showed strong positive signal of salmonella enterica. Damage plot analysis for six positive individuals showed C to T transitions on the 5" end and G to A transitions on the 3" end of fragments and revealed the characteristic pattern of damage expected of ancient DNA. The analysis of physical anthropology showed these samples were underage individuals which absence of skeletal trauma. We considered that salmonella enterica could be a leading cause of underage individuals" death due to low immunity in this site. In the next stage, in order to reconstruct the genomes of salmonella bacteria, identify potentially co-infected bacteria and analysis the phylogenetic history, the target capture probes will be designed and synthesized based on the modern salmonella bacterial strains. Our study will help to understand the evolutionary history and provide an important theoretical basis of infectious diseases.

Session • Plagues and pathogens

P–032
Molecular Archaeoparasitology as a novel archaeological tool

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Parasites are common in many archaeological contexts. Historically, parasitological research in archaeological contexts has relied upon time-consuming microscopic diagnostic methodologies that are constrained by the sensitivity and specificity of morphological diagnosis. We have
developed a suite of molecular tools that offer a new insight into these studies, allowing reliable, highly specific diagnosis and providing additional information on the genetic diversity of parasites over space and time. The application of these methods will be discussed in the
context of the use of parasites to interrogate issues related to hygiene, diet and socio-economic characters. These new approaches will be widely applicable, contributing a novel perspective that can be integrated within a variety of historical and archaeological studies.

P–033
Revisiting the evolutionary history of Yersinia pestis during the second pandemic

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Over the last few years, genomic studies on *Yersinia pestis*, the causative agent of all known plague epidemics, have considerably increased in numbers, focusing on strains attributed to the second pandemic (14th-18th c.). We carried out a comprehensive revision of the current phylogeny of *Y. pestis* strains from recent isolates back to Bronze Age samples, spanning a period of about 5,000 years.
Two scenarios have been suggested to explain the epidemics recorded throughout Europe for centuries following the Black Death: (i) plague periodically erupted from one or more reservoirs located in pre-industrial Europe and (ii) plague was repeatedly imported to Europe from non-European reservoirs. The few ancient genomes of *Y. pestis* that are available to date proved insufficient to confidently distinguish these two scenarios. We believe that the question regarding the possible establishment of a plague European reservoir was never addressed properly using an integrative approach combining history, genomics and ecology. By identifying and sequencing several additional ancient genomes from the second half of the 14th century, we set up an integrative approach where phylogenetic tree reconstruction is interpreted by considering available historical records to determine the likelihood of either of the two scenarios on plague establishment or reintroduction in Medieval Europe.

Session • Plagues and pathogens

P–034
Search for *Plasmodium* spp. in ancient Sardinian Populations

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Robust evidence indicates that malaria has exerted a strong selective pressure on the human genome, leading to the emergence of multiple resistance alleles across human populations. The historical record attests to the presence of malaria throughout large parts of the Mediterranean until the modern era; in Italy, for example, malaria remained endemic until the 20th century, when government-sponsored interventions eradicated *P. falciparum* from its last reservoirs in Palermo province in Sicily.[1] Despite the evolutionary and historical importance of this pathogen, genomic evidence regarding the distribution of *Plasmodium* spp. in the ancient world remains limited. Previous studies have identified *P. falciparum* DNA in skeletal remains from two Roman sites in southern Italy (Vagnari, 1st-4th century CE, and Velia, 1st-2nd century CE),[2] and a PCR-based investigation reported a *P. falciparum* amplicon from a 5th century site in Umbria.[3] Given these successes and the long history of malarial endemicity in Italy, this study investigates the presence of *Plasmodium* DNA in individuals from ancient Sardinia.
This study includes samples from two sites, Villamar and Monte Sirai, located in south-central and southern Sardinia, respectively. Both sites date to the Punic period, with radiocarbon dating of samples ranging from 805-540 calBCE for Monte Sirai and from ~800-400 calBCE for Villamar. At Monte Sirai, 14C dates for multiple burials appear to fall within the same temporal interval, raising the possibility of a pathogenic cause of death. To investigate the presence of malaria at these sites, DNA from dental pulp was extracted, prepared into libraries, and sequenced via next generation shotgun sequencing. Metagenomic data was processed using MALT to identify reads matching to known pathogen species. If present, identification of *Plasmodium* species will add knowledge regarding the geographic and temporal distribution of malaria in the ancient world.

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Session • Microbiomes

P–035

Clinical metagenomics applied to the Iceman and other mummified human remains

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Clinical metagenomics (CM) combines high throughput sequencing methods with bioinformatics approaches to analyze modern patient samples. It is considered to be one major component of future clinical analyses that contribute to the diagnosis and management of several diseases. Beside its potential in the identification of pathogens, CM can identify community shifts in the human microbiota indicating disease developments such as obesity or cancer.

In a recent study, we screened gastrointestinal (GI) tract biopsies of the Iceman, a 5300-year-old European Copper Age mummy, for the presence of *Helicobacter pylori*. By using CM diagnostics and targeted genome capture, we determined the presence of *H. pylori* and reconstructed its complete genome. Our study provided, beside the indication for a possible disease manifestation in the mummy, interesting new details on the origin of the stomach pathogen in Europe. The application of technological and conceptual advances in the Iceman study has paved the way for future studies on *H. pylori* in other ancient human remains. Currently, we are analyzing coprolite material and GI content of precious historical mummies from the American, African and Asian continents. Furthermore, the Iceman GI tract data indicates the presence of other intestinal microbiome members, possibly allowing for future reconstruction of a majority of the original GI tract microbiome of the Iceman.

The application of CM on dated ancient specimens opens a window into the past that enables scientists to address unique evolutionary research questions. Both reconstructed ancient pathogen genomes, and the composition of ancient microbiomes will provide new insights into the evolutionary history of bacterial-mediated diseases.

P–036

A complete metagenomic analysis from a single mummy to assess microbiome differences in distinct body parts

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Based on the latest advances in the field of palaeogenomics, the metagenomics nature of ancient DNA samples can be fully analyzed, including human DNA as well as DNA from associated bacteria. In the last decades, not only whole genomes for pathogens like *Mycobacterium tuberculosis* or *M. leprae* have been reconstructed and analyzed in its evolutionary context, but also sets of genomes corresponding to commensal microorganisms or microbiome. This provides valuable information for the diet, lifestyle, and health of past populations.

As in any ancient DNA study, choosing an adequate sample material is vital for generating valid genomic data. Whereas mineralized tissues such as teeth or bone are openly used to access endogenous human and pathogen DNA, microbiome studies often rely on soft tissues and coprolites, with the exception of calcified plaque (or dental calculus) in the surface of teeth. This supposes an extra challenge in terms of DNA preservation, and a variety of extraction methods can be found in the literature depending on the sample. In addition, the sequencing platform and the tools used for downstream analysis usually differ between studies. The lack of consistency in both laboratory and analysis techniques hinder the comparison of different microbiomes as it could introduce a bias depending on the method used. In an attempt to circumvent this issue, we present here a comprehensive study based on a single individual, a natural Mongolian mummy from the Medieval Period that is remarkably preserved, allowing an assessment of various tissues. We analyzed a total of 14 tissues plus three soil samples in order to compare microbial profiles between body parts. To complement the results, also proteomic, histological and radiological analyses were performed.

Our aim is to use a common methodology to produce reliable and solid metagenomic data for studying microbiomes. By performing these analyses in samples from the same individual we can test if the differences are genuine or due to a methodological bias, a crucial step to generate data that can be used for establishing comparisons between different individuals and databases.

Session • Microbiomes

P–037
The microbiome and isotopic fractionation

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The paper explores the effect the microbiome has on the observed nitrogen isotopic comosition of gut contents. Using germ free and conventionalized mice, developmental differences in both the bulk and the individaul amino acid d15N of gut contents are documented. Further, the involvement of ammonia from microorganisms that populate the gut in the biosynthesis of host protein will be discussed. These results provide one source of proof that even in the transfer of food to consumer, there are intervening organisms that are involved in the fractionation processes. As food choice is known to alter not only the microbial consortia of the gut, but also the physiology of the organ (Daniel et al, 2014), we can anticipate ongoing complexity in interpreting the isotopic composition of consumer tissues.
Daniel, Hannelore, et al. "High-fat diet alters gut microbiota physiology in mice." *The ISME journal* 8.2 (2014): 295.

P–038
The application of historic dental calculus for reconstructing killer whale ecotypes

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Biomolecules in human dental calculus have been used to investigate life history, including dietary reconstruction and pathogen evolution, however its broader utility to study other animals has been underexplored. Here we use historic dental calculus samples obtained from marine mammal strandings and research collections to assess the preservation of an oral microbiome signature and investigate its potential for pathogen reconstruction. We conducted metagenomic screening of dental calculus from fourteen killer whales (*Orcinus orca*). The whale samples were collected between 1961 and 2015 and represent two different killer whale ecotypes. These two ecotypes are known to have dietary and cultural differences and dental calculus may be a way of distinguishing ecotype in the archaeological record. DNA extraction was performed following protocols optimized for human dental calculus and yielded between 0.73 and 121.3 ng/mg of DNA. Despite sample ages ranging from 56 years old to 2 years old, the average fragment lengths were short (91±17 basepairs). Fragment length is correlated (ρ=0.52) with age as expected with degraded DNA. Preliminary analysis shows the presence of several taxa known to inhabit the oral cavity including *Methanobrevibacter*, *Neisseria, Jeotgalicoccus, Corynebacterium*, and *Mogibacterium*. The offshore killer whale ecotype is routinely associated with worn and abscessed teeth. We recovered *Staphylococcus* reads from one of our offshore specimens and members of this genus are known to cause dental abscesses in humans. These data demonstrate the feasibility of reconstructing the oral microbiome from non-primate dental calculus and open the possibility for investigating oral health in response to environmental change.

Session • Microremains and residues

P–042
A multiomic approach to stone tool residues

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Archaeological residue analysis has been around for well over 30 years now and while the analysis of organic residue on ceramic material has produced great results, organic residue on lithic material has been more challenging. In this research, we have applied analytical methods to the study of organic residue on several sets of stone tools in order to determine the reliability of identification. A multiomic approach has been employed to try and capture the information in the various biomolecules that may be present in the organic residues. In part, this has allowed us to re-assess methods that have been applied to residue analysis in the past and to re-evaluate the interpretations from some of these previous studies. While the inadequacies of some of these previous methods has been well documented in the literature and come to no surprise, the importance for a more reliable interpretation of the residues on these artefacts cannot be understated.

Session • Advances in metagenomics

P–044

Using sedaDNA from North Sea sediment cores to reconstruct the early Holocene palaeoenvironment

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Until around 7000-8000 years ago, much of the southern North Sea was a coastal plain now named Doggerland. Evidence from surrounding countries and occasional artefact finds suggest that Doggerland was inhabited, and it is expected to be a rich source of archaeological information. However, the seabed does not facilitate typical archaeological excavation. This study aims to reconstruct the early Holocene landscape using the palaeoenvironmental proxy of sedimentary ancient DNA (sedaDNA) from seabed cores.

Previous studies have found sedaDNA to be complementary to the traditional proxies of pollen, microfossils and macrofossils. Marine sediment is available in large quantities, so is suitable for destructive sampling, and the constant low temperatures and high ionic strength should facilitate good DNA preservation. Preliminary results from Doggerland and a pilot study at Bouldnor Cliff demonstrate the utility of sedaDNA in this context.

We will use next-generation sequencing to generate a list of taxa present in each sediment sample. These will be combined with dates, mapping and traditional palaeoenvironmental proxy data from other teams to reconstruct the landscape through time. We will track the transition from coastal plain to inundation by the sea, and search for evidence of Mesolithic activity as well as proxies of Neolithisation. The timing of Neolithisation in northwest Europe is still uncertain; it may have been in progress before inundation was complete. New information from Doggerland could help to fill this gap.

Session • Mobility

P–045

A new bioavailable strontium isoscape for Northwest Europe – using machine learning approaches

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Strontium isotope ratios (87Sr/86Sr) are increasingly utilized as a geolocation tool in archaeology, ecology, and forensic research. Their application to provenance research, however, requires the development of models predicting baseline 87Sr/86Sr variations in bioavailable strontium (Sr). A wide range of empirical and process-based models have been proposed to build terrestrial strontium isoscapes but these models are not capable of being integrated with continuous-probability surface models used in geographic assignment limiting their applicability in provenance studies. This study aims to overcome these limitations and to predict 87Sr/86Sr variations across Western Europe by combining process-based models and a series of geospatial products into a regression framework. Comparing the results of different approaches, we find that random forest regression significantly outperforms other regression and interpolation methods, and efficiently predicts the multi-scale patterning of 87Sr/86Sr variations by accounting for atmospheric, geological, and geomorphological controls. Random forest regression also provides an easily interpretable and flexible framework to integrate various types of auxiliary environmental variables. The method is transferable to different scales and resolutions and can use the large collection of currently available geospatial data available at local and global levels. The strontium (87Sr/86Sr) isoscape of Northwest Europe generated in this study provides the most accurate 87Sr/86Sr predictions in bioavailable (R2=0.58 and RMSE=0.0023) to date, as well as a conservative estimate of spatial uncertainty by applying quantile regression forest. We anticipate that the method presented in this study, combined with the growing amount and coverage of bioavailable 87Sr/86Sr data and satellite geospatial products, will greatly enhance the applicability of the 87Sr/86Sr geo-profiling tool in provenance applications.

P–046

Analytical review of oxygen isotope analyses for sourcing human and animal skeletal remains

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Investigating the origins of people and items by means of isotopes is increasingly popular in archaeological research. In the last few years there has been a dramatic expansion of these type of applications in the literature. Oxygen isotope ratios in human and animal remains are used with this purpose to track populations and herds mobility. The premises for these studies are that the isotopic ratios of this element are assimilated in human tissues from the environment through food and drink, and diversified in one individual compared to another based on the features of the places where they lived.

The increased availability of instrumental facilities, coupled with the improved sensitivity and measurement capacity, has contributed to the proliferation of new databases in the field but this has not always been followed by the necessary rigorousness in the way data are reported and/or interpreted.

A number of complications can affect the isotopic ratios measured in fossil bone and teeth, and these should carefully be assessed during sample analysis and pondered in the subsequent data mining. These complications include post-mortem alterations, due for example to diagenesis, isotopic modifications during sample preparation, erroneous data calibration, problems in converting the raw data to comparable datasets, mathematical errors, or wrong interpretation of the environmental background to which skeletal isotopes are compared. The effects of these complications are often underestimated, with the risk that the reported results are partially, if not totally independent from the original biological signature. The aim of this presentation is to describe and discuss these complications and present the effects on the interpretation of the results.

Session • Mobility

P–047

Ancient DNA and isotopic analysis of archaeological remains from Guam

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Guam, located in the tropical north-western Pacific, is the largest island in Micronesia and the most southerly of the Mariana Islands. While linguistic and modern DNA studies have inferred that the ancestors of the indigenous Chamorros were south-east Asian migrants who arrived as early as 2,000 BC, geology and archaeology indicate that the first human groups arrived 500 years later.

Marianas prehistory is divided by archaeologists into two main periods: Pre-Latte (c. 1,500 BC to AD 1000) and Latte (AD 1000–1521). For the first thousand years of the Pre-Latte Period, human interment was not practiced. The Naton Beach Site, on Guam's leeward west coast, represents the earliest dated burial and permanent settlement.

Stable isotopic analyses on bone collagen carbon and nitrogen, and tooth enamel oxygen, carbon and strontium, have been completed on seven ancient individuals from the Naton Beach Site. One of these individuals has been radiocarbon dated to the late Pre-Latte period, 774–509 cal. BC; a time associated with a distinctive pottery style that disappeared from the archaeological record around 900 years later. After a "transitional" era of several centuries, the Latte Period began, characterised by different ceramics, uniquely shaped stone pillar house foundations, and the cultivation of rice – all cultural traits that were not found elsewhere in Oceania at that time.

Genome-wide analysis is currently underway for two individuals from the Naton Beach cemetery. The resulting data will be the first ancient DNA from Guam's oldest burial site. Both uni-parental and autosomal genetic information will be used to assess possible migration routes of the first settlers of Guam. The resulting data will be compared to the modern Chamorro population (n = 14) and other Micronesian populations (10 Nauru and 10 Kiribati) to determine potential genetic continuity, as well as the possible source of the people bringing the Latte culture to Guam. Mitochondrial haplotypes will be compared to 80 full mitogenomes from modern Micronesian populations, including previously published data from the western Pacific.

Session • Pathogen genomics

P–048

Investigating ancient syphilis – macroscopic suspicions and molecular detection of *Treponema pallidum* subspecies *pallidum* in 150-year-old foetal remains, Marseille, France

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Syphilis has been known since the late XVth century for being a chronic, ubiquitous infectious disease among ancient populations and, consequently, a severe health burden. In theory, the presence of treponemal spirochetes in bones allows their DNA detection in ancient skeletal material by molecular approaches. However, since its first isolation on an archaeological specimen in 1999, and despite multiple published research articles reporting attempts to isolate treponemal ancient DNA (aDNA), little success was encountered in molecular studies of syphilis.
Our study aimed to investigate several 150-year-old French foetal and infant specimens exhibiting palaeopathological signs of probable congenital syphilis.
We performed macroscopic and molecular investigations of *Treponema pallidum* on six infant remains from the cemetery "Les Crottes" in Marseille city (XVIII-XIXth century). PCR-based amplification methods developed from previous clinical and palaeomicrobiological studies were used for molecular investigations, following strict protocols warranting absence of contaminations and result authenticity. Positive PCR products were processed by Sanger sequencing, and sequence analysis was performed using NCBI"s online Basic Local Alignment Search Tool (BLAST).
Studied specimens, buried between 1837 and 1867, showed widespread osteoporotic lesions across the skeleton, possibly related to a systemic infectious disease, including congenital syphilis. Among them, specimen SP332 yielded positive results for all the tested amplification systems, subsequent sequences analysis supporting strong evidence for the effective detection of *Treponema pallidum* subspecies *pallidum* aDNA.
This individual is the first PCR-confirmed palaeopathological case of syphilis identified in France, and the youngest specimen ever to be diagnosed with certainty for congenital syphilis (29 amenorrhea weeks, approximately 7 months in utero). This study allows better insights on congenital syphilis manifestations among very young immatures. Those results illustrate that osteoarchaeological remains of immature individuals are indeed a valuable material for molecular investigations targeting ancient syphilis.

P–049

Analysis of a 17th century *Mycobacterium tuberculosis* genome from Lund, Sweden extracted from a lung nodule

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Ancient pathogen genomics has opened a new avenue for directly studying the temporal and spatial history of certain infectious diseases. Tuberculosis is an intense focus of modern medical and microbiological research, but questions persist regarding its origin and earliest association with its human host. Based on analysis of modern *Mycobacterium tuberculosis* complex (MTBC) genomes, one hypothesis suggests their most recent common ancestor (MRCA) followed modern human Pleistocene migrations out of Africa ~70,000 years ago. However, studies using ancient genomes to calibrate the molecular clock have indicated a much younger MRCA date of less than 6,000 years. The difference in estimated ages is complicated by evidence for tuberculosis from paleopathology and PCR-based paleogenetics that pre-dates 6,000 ya. This discrepancy can be addressed by continued sampling of diverse, high-quality, ancient tuberculosis complex genomes that provide numerous calibration points to account for potential rate heterogeneity between different MTBC lineages and over time. Here, we contribute by presenting a *Mycobacterium tuberculosis* genome extracted from a calcified lung nodule from the remains of Bishop Peder Winstrup of Lund (b. 1605 – d. 1679). The results of initial shotgun sequencing showed that human DNA and MTBC DNA made up 87.98% and 0.045% of the metagenomic reads respectively. Analysis revealed no mycobacterial diversity outside the MTBC, which is often a confounding factor in the reconstruction of ancient tuberculosis genomes. Enrichment of the preserved tuberculosis DNA was accomplished with a custom-designed in-solution capture method, which increased the endogenous content to 44.92% and allowed us to reconstruct a 141-fold coverage genome. This study shows the promise of lung nodules as an archaeological source for MTBC and host DNA, and contributes a new, high-quality and securely dated calibration point for the dating of the MTBC, which we attempt here through Bayesian phylogenetic methods.

Session • Pathogen genomics

P–050

An automated pipeline for detection and characterization of recombination patterns in bacterial genomes

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Phylogenetic trees elucidate the evolutionary histories of bacteria. Bacteria can take up and integrate DNA through transformation, transduction and conjugation. This phenomenon of recombination tends to distort phylogenetic signals and induces incongruences in the tree topologies. Identifying regions of recombination is a major challenge in deciphering the evolutionary processes in bacteria.

Here we present an automated pipeline for detection of recombination in bacterial genomes with application to *Treponema pallidum* and *Helicobacter pylori* as examples. The three subspecies of *Treponema pallidum pallidum, pertenue* and *endemicum* cause the diseases Syphilis, Yaws, and Bejel, respectively. Though *T. pallidum* is considered a clonal species, there is evidence for recombination between the subspecies. On the other hand *H. pylori* is a highly recombinant gut bacterium that has co-evolved with humans for a long time as represented by its phylogeographic patterns. Certain strains of *H. pylori* form mosaic structures with exchange of genomic regions between strains of the 7 lineages.

By application of our pipeline for a chosen target strain, a maximum likelihood tree is constructed for representative strains of the bacterial species excluding a chosen target sequence. In a next step tree models are created on this tree backbone by placing the chosen target on all possible positions. Using a sliding window or an annotation of protein coding genes our pipeline calculates for each genomic region, which of the model tree topologies are not consistent with the data.

We demonstrate the application of our pipeline using one target genome each for *T. pallidum* and *H. pylori* species. 94B is an ancient *T. pallidum* genome isolated from human remains from colonial Mexico. 94B branches with syphilis causing *pallidum* strains, but with various genomic regions contradicting the topology of the whole-genome phylogeny. PeCan4 is a strain of *H. pylori* isolated from Peru. Phylogenetically, PeCan4 is located between strains of hpAsia2 (predominantly found in Central and Southeast Asian populations) and hspAmerind (found in indigenous North and South American populations) unlike other Peruvian strains that clearly branch with the hspAmerind lineage.By this procedure our pipeline not only highlights genomic candidate regions for recombination events but also estimates their effect on phylogenetic reconstruction.

Session • Genetic adaptation and evolution and extinction

P–051

Isotopic evidence on foraging ecology of *Elephas maximus* and *Stegodon orientalis* in South China during late Pleistocene

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Introduction: Proboscidea feeding ecology plays a significant role in their evolution history, which is possibly related to their dental morphology. Proboscidea are often considered as a keystone species with high plant consumption, so it will be useful to understand their survival strategy through reconstructing foraging ecology of two coexisting proboscidea, one extinct (*Stegodon orientalis)* and one surviving until today (*Elephas maximus)*. In south China, both coexisted during the Pleistocene.

Objectives: We want to explore the ecological niche partitioning of these two coexisting species in their dominated late Pleistocene, and also review their dietary history.

Methods: Quzai Cave and Baxian Cave are located in Chongzuo, Guangxi in south China. Both sites are estimated to be early Late Pleistocene. More than ten mammal species were chosen for enamel carbon and oxygen isotope analysis, 77 samples for bulk samples analysis and 3 *E. maximus* molars for sequential analysis.

Results: The bulk isotope results of the two sites are quite similar. All the carbon isotopic data represent pure C_3 diets with a range of -19.9‰ ~ -11.1‰. The $\delta^{13}C$ values of *E. maximus* are widely distributed (-17.9‰~-11.9‰, n=21) in both sites, reflecting a wide food resource use typical of a mixed feeder. Besides, two groups of Asian elephants are observed in Baxian Cave on the basis of isotopic data, which may relate to age, seasonal variation and/or subspecies differences. Serial analysis allowed to exclude weaning and seasonal dietary influence, so the possible reason might be social structure. The $\delta^{13}C$ of *S. orientalis* ranged from only -16.7‰ ~ -14.7‰ (n=9), which might represent narrow browsing behavior. The $\delta^{18}O$ values of both are all largely varied between -9‰~ -4.1‰, which may be mainly caused by different water sources.

Conclusion: Based on all the published bioapatite $\delta^{13}C$ values from *Stegodon* and *Elephas*, we conclude that *Stegodon* (n=33) mainly fed on C_3 plants during all their evolution time, only include small part of C_4 plants during 6~2 Ma, reflecting their mainly browsing diet. *Elephas* (n=60) fed purely on C_4 plants before 1Ma, coinciding with the global expansion of C_4 grass. Since the middle Pleistocene until nowadays, their diet shifted in south Asia to C_3 tropical forest vegetation. The dietary flexibility of *Elephas* with strong hypsodont molars could be an important factor in its survival during the end-Pleistocene megafauna extinction event.

Session • Genetic adaptation and evolution and extinction

P–052

An aukward tale of extinction – the demise of the great auk

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The flightless great auk was once abundant and distributed across the North Atlantic. It is now extinct, having been heavily exploited for its eggs, meat and feathers. We investigated the relative impacts of climate-driven environmental change and human hunting on the demise of the great auk by integrating genetic data, GPS based ocean current data, and population viability analyses. We sequenced complete mitochondrial genomes of 41 individuals that had been sampled from across the species" Late Pleistocene and Holocene geographic range. Our analyses show a lack of population differentiation, consistent with a lack of barriers to gene flow as revealed by ocean current data from GPS-equipped drifting capsules. Demographic reconstructions suggest a stable effective population size leading up to the extinction of the great auk. Population viability analysis revealed that harvesting 5–7% of the population annually would have been sufficient to drive the great auk to extinction in fewer than 350 years. Our findings are consistent with hunting as the primary cause of the great auks' extinction and emphasise the vulnerability of even abundant and widespread species to intense and localised exploitation.

Session • Genetic adaptation and evolution and extinction

P–053
Time-dependent molecular evolution in ancient DNA

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Introduction Estimating rates of molecular evolution is necessary in order to infer demographic dynamics and evolutionary timescales from genetic data that had been sampled at specific points in time. For phylogenetic analysis of time-structured data, ages of the ancient DNA sequences can be drawn from radiocarbon-dated samples to calibrate the molecular clock. The hypothesis of time-dependent molecular evolution states that the rate of observable evolution varies depending on the timeframe over which the rate is measured. Domestic animals and their wild progenitors are an excellent to proxy to test the hypothesis of time dependency given their relatively short generation time and their ubiquity in the archaeological record.

Objectives The hypothesis of time-dependent molecular evolution will be tested by comparing the directly-dated mitochondrial genomes of multiple ancient archaeological samples across a balanced temporal distribution. By analysing these data using dated molecular clock analyses, changes in the molecular substitution rate across different time scales can be estimated.

Methods Hundreds of samples from at least five vertebrate species used for analyses were either radiocarbon dated or are associated with archaeological sites with high confidence. From these directly-dated samples, high-coverage full mitochondrial genomes used for analysis. We used different phylogenetic methods in estimating the rates from time-structured data, including root-to-tip regression, scalable relaxed clock dating, and approximate Maximum Likelihood inference.

Results Preliminary results from ancient suid and bison datasets suggest evidence of time-dependent molecular evolution within timeframes that span between the present day to 14,000 BP, and from the present day to 128,000 BP, respectively. There is a negative relationship between rate and time, where as the sample age increases, there is a corresponding decline in estimated substitution rate.

Conclusion To our knowledge, this study will be the largest meta-analysis yet using ancient DNA in testing the hypothesis of time-dependent molecular evolution, and preliminary results suggest that the observed time-dependency is a biological phenomenon. In addition, this study may yield interesting observations on the genetic processes of domestication within and between the different animal populations of study, as well as inform and improve fossil calibration of current molecular clock models.

Session • Genetic adaptation and evolution and extinction

P–054

Reconstructing local palaeoseasonality and palaeoclimate at Middle Palaeolithic sites in Western Europe – sampling, data handling, and temperature conversion in oxygen isotope seasonality models

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Adaptation to changing and sometimes harsh climatic conditions are a key aspect in the discussion of Neanderthal behaviour, their success in different environments and even their eventual demise. Oxygen isotope ($\delta^{18}O$) analysis of sequentially sampled faunal tooth enamel from archaeological contexts have the potential to allow high resolution reconstruction of seasonal temperatures that can be spatially and chronologically directly linked with the archaeological record of Neanderthal behaviour. These techniques therefore can enable the examination of environmental impacts on local and regional patterns of site use, mobility and faunal resource exploitation. However, consensus on different aspects of sample selection, data generation and data handling – including temperature conversions – is required. Utilising new and previously published sequential oxygen isotope data from a number of Western European Middle Palaeolithic sites, here we describe a protocol for generating site-specific isotope seasonality using non-linear statistical models. We examine the influence of different regression approaches to drinking water $\delta^{18}O$ and temperature reconstruction and their impact on temperature estimate uncertainty. Keeping such uncertainty in mind, we use diachronic comparisons to statistically evaluate the sensitivity of oxygen isotope data in faunal enamel to climatic changes over time and make recommendations for sampling and data handling strategies to optimise future study designs.

P–055

An epistatic effect of Asian-specific nonsynonymous variants of *ABCC11* and *EDAR* on the amount of facial bacteria

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Population genomics studies scanning for recent positive selection have revealed that nonsynonymous variants of *ABCC11* and *EDAR* were targets of strong positive selection in East Asian populations. These genetic variants are associated with several Asian-specific phenotypes: The *ABCC11* variation is involved in apocrine secretion and associated with wet/dry types of earwax and body odor, whereas the *EDAR* variation has pleiotropic effects on the morphology of hair, tooth, ear, and mandible and on the density of eccrine sweat glands and mammary glands. However, what selective pressures acted on these genes are still unknown. In this study, focusing on effects of these genes on skin functions, we examined the association of the Asian-specific variants with skin phenotypes. The subjects were 244 healthy Japanese living in Okinawa. We measured skin hydration and sebum, skin color, and the amount of facial follicular porphyrin, which are mainly produced by Propionibacterium acnes, and collected saliva specimens for DNA preparation. *ABCC11* G180R and *EDAR* V370A were genotyped. For 130 subjects, we also examined skin microbiome profiles by 16S rRNA analysis. As results, confirming that the amount of facial porphyrins is correlated with the proportion of Propionibacterium, this study suggested an interactive effect of *ABCC11* and *EDAR* variants on the amount of facial porphyrins. This may indicate a possibility of coevolution of these genes against dermal troubles such as pimples in the ancestors of East Asian populations.

Session • Genetic adaptation and evolution and extinction

P–056
Phenotypic inference based on ancient DNA of Iron Age individuals from Luistari in Southern Finland

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Introduction: Among the potential uses of ancient DNA (aDNA) data is the prediction of ancient individuals' phenotypes. Such knowledge can complement the insights gained from archaeological, osteological and stable isotope analyses, thus illuminating for example the morphology, health and disease of past populations and individuals.
Objectives: The aims of our study are threefold: first, expanding the set of phenotypes typically inferred from aDNA data; secondly, estimating the effect of various factors - such as sequencing coverage and the genetic architecture of the phenotypes - on the confidence of the phenotype prediction; and third, applying these insights in the phenotype inference of ancient individuals from Finland.
Methods: We studied six individuals (5 males, 1 female) from the archaeological site of Luistari, Eura in Southern Finland. Based on radiocarbon dating, these individuals originate from the 8th to 13th centuries AD. After DNA extraction, indexed libraries were prepared, enriched for a genome-wide set of 1.2 million single-nucleotide polymorphisms (SNPs) using in-solution capture, and sequenced on an Illumina HighSeq 4000 instrument. A set of 118 SNPs were chosen from this dataset, including loci for frequently inferred phenotypes such as hair or eye color and lactose tolerance as well as loci contributing to other potentially interesting phenotypes. The genotypes of these SNPs were obtained by samtools command mpileup, and the phenotype inference was done by manual inspection of the genotypes of each individual. Genotype probabilities were calculated based on the read depth of the observed variant(s) and the variant frequencies from the modern Finnish population.
Results: The number of successfully genotyped SNPs was 10-43 per individual. Despite the low sequencing coverage (average read depth 1.7 for the genotyped SNPs), 50% of these genotypes could be inferred with reasonably high certainty (> 85%). The corresponding phenotypes range from physical appearance (hair and eye color) to diseases and metabolic features.
Conclusion: Phenotype estimation based on ancient DNA can produce information that is potentially highly relevant both individually and in the context of population history. However, the availability of such insights is limited by a combination of data quality (low sequencing coverage) and the true complexity of phenotypes.

P–057
Caving for ancient DNA – looking for human impact on the environment

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The first successful use of sediment as a source of DNA was back in 2003, when researchers showed that it was possible to use DNA trapped in sediment to track changes in both taxonomic diversity and composition of Beringian vegetation and fauna. DNA has since then been extracted from ice, lake sediments, soils and coprolites. With the introduction of Next Generation Sequencing this subfield of ancient DNA research has gained a lot of traction. Different studies have found evidence of both extinct and current animals and traces of plants no longer found in the region. Complete reconstructions of long lost environments are now possible.
Hall"s Cave is a unique paleo environment archeological site. It is an underground cave located in central Texas. It is a remarkable site due to its prime location on the central Edwards Plateau, the bedrock consists primarily of limestone hence DNA preservation is excellent. The site has been excavated extensively and the oldest layers has been proven to be at least 18,000 years old. Native Americans used the cave and surrounding area intermittently from the late Paleo Indian period to the Late Prehistoric period. This means that this site represents a unique place to investigate any human impact on the surrounding environment. Samples have been taken across the stratigraphy, thus representing both before and after human entered the cave and the surrounding environment. Initial results show a remarkable change in both flora and fauna at several distinct time periods.

Session • Genetic adaptation and evolution and extinction

P–058
The genetic makeup of enslaved Africans from early Colonial Mexico City

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The multiple ethnic roots of the modern day Mexican populations are largely a result of genetic admixture among Africans, Europeans, Native Americans and Asians during the New Spain period. Although the presence of people of African origin and their descendants in diverse historical periods in Mexico is documented through exhaustive historical studies, little has been done to look into the African roots that came into the Americas from a genetic perspective, especially outside of the populations bearing the most African ancestry according to modern DNA data. Here we used an archaeogenetic approach, by analyzing ancient human genomes, including uniparental markers, together with strontium isotopes and ethnohistorical information to track down the origins of three enslaved Africans from Mexico City buried at the San José de los Naturales Royal Hospital (Hospital Real de San José de los Naturales). Uniparental markers, HLA haplotypes and admixture estimates point to a common West African origin for the three individuals, whereas D-statistics show that despite their genetic relationship to human groups speaking Niger-Congo languages, they all have different genetic origins. When taken together, the molecular evidence allowed us to provide insights into the origin of these three individuals who were probably among the first enslaved Africans to reach the central plateau of New Spain in the 16th century.

P–060
Signatures of High-Altitude Adaptation in Ancient Andeans

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High-altitude adapted individuals show distinct circulatory, respiratory, and hematological adaptations to chronic hypoxia. Emerging genetic data support an evolutionary origin and a genetic basis for these observed physiological adaptations to high altitude. However, the history of this adaptation remains poorly understood. We performed a locus-specific branch length (LSBL) analysis of pair-wise Fst values comparing ancient high-altitude Andeans (n=20), modern Mexicans (MXL, n=67), and modern Han Chinese (CHS, n=108) from the 1000 Genomes Project. Our top LSBL hits were associated with alternative splicing (RBFOX1), the myosin superfamily (MYO10), and NF-kappaB binding (COMMD7). Interestingly, we found nine SNPs in the gene EGLN1, which is known to be under selection in modern Tibetans and Andeans, that were significant at the p-value<0.05, and showed an increase in frequency of the minor allele in modern Peruvians PEL compared to the Ancient Andeans. Taken together, our results suggest a potential genetic signature of adaptation to high altitude in the Ancient Andeans.
This project was funded by the National Science Foundation BCS-Archaeology, the Leakey Foundation, the Department of Anthropology at the University of Michigan, the College of Arts and Science at Vanderbilt University.

Session • Genetic adaptation and evolution and extinction

P–061

Giant deer (*Megaloceros giganteus*) phylogeography and population dynamics – insights from Late Quaternary mitogenomes from Eurasia

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The climatic fluctuations of the Late Quaternary in the northern hemisphere led to distributional changes in large mammal species: range expansions, range shifts, contractions, and extinctions. The giant deer (*Megaloceros giganteus*) was one of the megafaunal species that became extinct in the Holocene (ca. 7,660 cal. yr BP). The range of the species spanned from Western Europe to Central Asia. However, during the Holocene, it became contracted to Western and South-Western Siberia and European Russia, where the last populations of the species survived. For the first time, our study addresses the phylogeography and population dynamics of this extinct species using ancient DNA. We have combined in-solution capture enrichment and NGS technologies to generate 35 mitochondrial genomes from giant deer specimens spanning from the Late Pleistocene, beyond the 14C radiocarbon limit, to 7,660 cal. yr BP from Europe and Western Asia. Bayesian phylogenetic analyses of these mitogenomes were used to estimate phylogenetic relationships, divergence dates, as well as population dynamics through the Late Quaternary. Our results suggest five main clades for the species: three pre-LGM clades that do not appear in the post-LGM genetic pool, and two clades that show continuity into the Holocene. All the clades include samples from Russia (Urals, Western and South-Western Siberia); this high diversity within the region suggest that it was the main area for giant deer origin and diversification. Our study also identified a decrease in genetic diversity starting in the Marine Isotope Stage 3 and culminating during the Last Glacial Maximum.

P–062

Ancient genomics of the Baltic harp seal

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This PhD project investigates questions related to the genetic composition of the ancient harp seal population in the Baltic Sea in a diachronic perspective. From an outstanding zooarchaeological collection of harp seal bones, ancient DNA are being extracted and analyzed in order to investigate the colonization history and geographical origin of the Baltic harp seal, and to further assess genetic, life history and demographic processes associated with the gradual decline and eventually extinction of harp seals in the Baltic Sea.
Today the harp seal is categorized as a subarctic pelagic species. Due to their strong dependence on good quality pack ice in order to breed successfully, the presences of a harp seal breeding population in the Baltic Sea during the middle Holocene have been much debated and many questions still remain unanswered. Firstly, it still remains unclear whether climatic changes or the extensive seal hunting by contemporary hunter-gatherer societies was the main driver of the presumed extinction of the Baltic harp seal. Secondly, it is still not known from which geographical area the harp seals that colonized the Baltic originated from and whether the Baltic breeding population arrived from a single or multiple colonization events. Another unanswered and interesting observation is the significant reduction in the mean adult body size of the Baltic harp seals from the warmer Atlantic period to the cooler period of the Subboreal. This is likely to be a sign of genetic isolation from the Atlantic population leading to higher levels of inbreeding, which could have been a main factor leading to their extinction, or may as also suggested be local adaptations to southwards migrations.
From a comparative-genetic analysis of the samples, we expect by some level of confidence to be able to pinpoint the most likely ancestral population of the Baltic harp seals and to tell whether a single or multiple colonization events occurred. We eventually also aim to investigate signs of inbreeding, and to provide information on the relative effects of climate and human exploitation on the extinction of the Baltic harp seal.

Session • Deep human population prehistory

P–063
The early history of Neanderthals and Denisovans

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We use Legofit to study the past several hundred thousand years of human evolutionary history. Our results show that (1) Neanderthals and Denisovans separated early in the Middle Pleistocene; (2) their ancestors survived a bottleneck of population size; (3) 3-8% of Denisovan DNA derives from a "hyperarchaic" population that separated from other hominins about 2 mya; (4) about 1% of Neanderthal DNA derives from the ancestors of modern humans. Our results also (5) support previous estimates of gene flow from Neanderthals into modern Eurasians.
This work was supported by grant BCS-638840 from the National Science Foundation and by the Center for High-Performance Computing, University of Utah.

P–064
Patterns of ancient DNA preservation in a Palaeolithic human tooth from Les Cottés Cave, France

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Introduction: The scarcity of human remains from the beginning of the Upper Palaeolithic in Europe, and the small number of individuals from which genome-wide data has been obtained, make it difficult to reconstruct the genetic history of early modern humans and late Neandertals. A particular challenge stems from the small amounts of endogenous DNA and high proportions of microbial and present-day human contamination.

Objectives: The human molar investigated here comes from the backdirt of previous excavations at the Les Cottés cave and cannot be associated with a particular archaeological context. As the site contains a well-dated stratigraphy of Mousterian, Châtelperronian, Protoaurignacian and Early Aurignacian, we aimed to determine to which hominin group the tooth belongs and to reconstruct relationship of this individual to archaic hominins, as well as ancient and present-day humans.

Methods: Initially we removed removed 17.6 mg of dentine for DNA extraction. Three additional samples of 18, 20 and 25 mg of dentine were removed from three different spots in order to investigate whether sampling other parts of the specimen may improve the yield of ancient human DNA.

Results: The mitochondrial genome of the tooth reconstructed from putatively deaminated DNA fragments falls basal to the haplogroup R, and using 10 securely dated ancient modern humans as calibration, we estimated it to be 46,060 years old (95% HPD: 31,098 to 62,221 years BP). Attempts to analyze the nuclear genome of the specimen by direct sequencing of the first sample were hampered given that not more than 0.2 human genomes could be recovered and that 89% of the nuclear sequences derived from modern human contamination. The subsequent DNA extracts varied by several orders of magnitude in their content of nuclear genomes (0.06, 0.17 and 4.3-fold genomes) and the levels of present-day human contamination (13%, 0.2% and 0%). We are currently reconstructing large parts of the nuclear genome from the extract that yielded most ancient DNA, and that illuminate the relationship of this individual to ancient and present-day populations.

Conclusions: Our results illustrate that DNA preservation can vary greatly within one specimen and that the removal of multiple small sub-samples instead of one larger sample, coupled with decontamination procedures can drastically improve the likelihood of isolating sufficiently pure and large enough amounts of DNA for comprehensive genetic analyses.

Session • Diet and nutrition

P–065

Illustration of the sea spray effect detected in $\delta^{13}C_{carbonate}$, $\delta^{18}O_{carbonate}$, and $\delta^{34}S_{collagen}$ using Gaussian Mixture Model (GMM) clustering

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Transport of sea spray in coastal areas ("sea spray" effect) can have a marked influence on the isotopic composition of the terrestrial environment. This effect shifts terrestrial isotopic values towards unusual high values masking the original terrestrial signature. It is unclear so far if and to what extend sea spray influences other stable isotopes besides sulphur. In this study, we examined if the effect was also detectable in carbon, nitrogen, and oxygen stable isotopes of bone collagen and carbonate, respectively.

Multi-isotope data of mammals sampled from the Viking Haithabu and Medieval Schleswig sites in Northern Germany were analyzed according to a previously developed approximation procedure and Gaussian Mixture Model (GMM) clustering in order to quantify the sea spray effect in the isotopes under study.

We were able to approximate a sea spray effect of at least 32.8% and 62.8% in $\delta^{13}C_{carbonate}$ and $\delta^{18}O_{carbonate}$, respectively. However, it was not possible to validate or approximate this effect in $\delta^{13}C_{collagen}$ and $\delta^{15}N_{collagen}$. Indeed, detection of the sea spray effect not only in $\delta^{34}S_{collagen}$ (16.5%), but also in $\delta^{13}C_{carbonate}$ and $\delta^{18}O_{carbonate}$ is of particular importance for studies on both prehistoric and recent material.

Our correction procedure allowed to approximately recalculate the original terrestrial signature. The effect of the sea spray correction is illustrated using GMM clustering. Before correction clustering terrestrial herbivorous and marine mammals resulted in a "mixed" sea spray cluster, while herbivorous and marine mammals were correctly separated into two distinct clusters after correction for the sea spray effect, as expected due to the different diet and habitat of the analysed individuals.

Furthermore, although our study focused on palaeoecology, we suggest that our sea spray approximation and correction procedure as well as GMM clustering also constitutes a very useful tool for modern ecology based on stable isotope analyses.

P–066

Consideration of freshwater and multiple marine reservoir effects – dating of individuals with mixed diets from Northern Sweden

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Human burials from the cemetery at the Rounala church, Northern Sweden, were radiocarbon dated to shed light on the use of the cemetery. Carbon, nitrogen and sulfur stable isotope analysis of bone collagen from 19 distinct individuals indicated that these individuals had a mixed diet consisting of freshwater, marine and terrestrial resources. Dietary modelling using FRUITS was employed to calculate the contributions of the different resources for each individual. These data were then used to calculate individual ΔR values, taking into account freshwater and multiple marine reservoir effects, the latter caused by Baltic and Atlantic marine dietary inputs, respectively. Radiocarbon dating of tissues from modern freshwater fish species demonstrate a lack of a freshwater reservoir effect in the area. Two OxCal models were used to provide endpoint age estimates. The calibrated data suggest that the site"s cemetery was most likely in use already from the 14th century, and perhaps until at least the late 18th century.

Session • Diet and nutrition

P–067
Diet and population mobility in the Early Medieval Alpine area (Italy)

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In the Early Middle Ages, South Tyrol (Alto Adige, Italy) played a key role as strategic territorial junction of relevant geographical and military power. Limited historical sources documented that many nonlocal groups (Germanic and Slavic), after crossing the Alps, entered the South Tyrolean valleys. The material culture showed the mutual cultural exchanges among previously settled and nonlocal people. Besides that, the nature of these migrations and their demographic and socio-cultural impacts are still unknown. Stable isotope (δ13C, δ15N and δ34S) analyses were conducted to explore dietary and migration patterns of individuals living in different valleys. Bone collagen of 91 human samples and 33 faunal remains from nine archaeological sites, located in four valleys at different altitudes (from 395 msl in Adige - 1427 msl in Venosta) were analysed. The results showed significant statistical differences in the isotopic signatures, not only within but also among valleys, indicating variations in subsistence strategies and possible socio-cultural behavior. Highly significant differences in the δ13C values of the individuals found in Venosta indicated a C3 plant based diet (mean and standard deviation: -19.1‰±0.5) compared to Adige, where more positive carbon values (-18‰±0.9) showed a possible intake of C4 plants (e.g. millet). Interestingly, the δ13C data correspond to the different altitudes, with more positive values at lower sites. The δ15N values showed greater protein consumption at higher altitudes and possible differences between sexes in access to dairy products and animal proteins (e.g., meat). The δ34S data supported the identification of nonlocal individuals in all areas, indicating greater mobility in Adige (+8.7‰±2.1). The study suggests that the impact of allochthonous populations in this territory might not lead to cultural exchange only, but also to the settling of these people. Ongoing genomic analyses (BioArchEM project) will provide more information in understanding the origin of Early Medieval populations in South Tyrol.

P–068
Dental microwear analysis and diets of Yanghai Ancient Population in Xinjiang, China

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Dental microwear analysis (DMA) focuses on the microscopic scratches and pits that formed on a tooth's surface as the result of chewing which is a useful approach to reconstruct the diets of animal species and human ancestors. The aim of this study is to use this new method to reconstruct the diets of Yanghai ancient population, whom lived in Turpan area in Xinjiang Uygur Autonomous Region, between the bronze to early iron age. Different microwear patterns of scratches on the buccal surface indicate different dietary composition. All samples from 10 individuals have been observed at 200X magnification by 3D deep field microscope. After scanning and measuring buccal surface microwear features, the ratio between the average length of the horizontal scratches and the average length of the vertical scratches (LH/LV) can be calculated. Comparing with other researches, Yanghai population have a LH/LV ratio of 75.2%, which is similar to Bushmen and Australian Aborigines with a LH/LV ratio of 73.59% and 73.67%, who are originally hunter-gatherers living in a tropical forest environment. It is speculated that the food structure of the Yanghai individuals have a relatively high proportion of meat intake. This result is concordant with the cultural characteristics reflected in the archaeological relics and conclusion of stable isotope analysis.

Session • Diet and nutrition

P–069

Preservation and variation of diet-related zinc isotope in a Pleistocene food web – perspectives on a new dietary tracer

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While measurement of nitrogen stable isotope ratio of bone collagen (expressed as δ15N) allow dietary reconstruction and trophic level assessment, this method unfortunately remains limited by the preservation of protein. However, with recent developments in mass spectrometry, the application of non-traditional stable isotope systems (e.g. Ca, Cu, Fe, Mg, Sr, Zn) opens up new research avenues in archaeological contexts. Among these, zinc (Zn) isotopic composition (66Zn/64Zn, expressed as δ66Zn) of enamel bioapatite, inherently offering a better long-term preservation potential compared to collagen-bound nitrogen, represents a promising dietary indicator as it yields similar information as δ15N.

The aim of this study is to assess whether δ66Zn values and trophic level differences, observed in modern food webs, are preserved in fossil assemblages. To this end, samples from an assemblage from Marklot (Xoneuna city, Laos PDR), a Southeast Asian Pleistocene fossiliferous site, will be analyzed. Various diagenetic tests (diagenetic trace elements and Zn concentration profiles, Zn concentration and stable isotope composition mixing line) will be presented to evaluate the impact of post mortem taphonomic processes. The impact of geology on δ66Zn values, traced through radiogenic isotopes of strontium (87Sr/86Sr), will also be assessed and discussed. Finally, the combined study of δ66Zn and δ13C, carried out for the first time, will be explored in order to attain a higher level of food traceability, both for carnivorous and herbivorous diet.

As expected, trophic level differences in δ66Zn values are observed between herbivores, carnivores and omnivores. This clear trophic spacing and the diagenetic tests performed demonstrate that the impact of post mortem taphonomic processes on the preservation of diet-related zinc isotope values is negligible, if not entirely absent. While 87Sr/86Sr vary markedly between individuals, no relation with δ66Zn values can be discerned. Finally, the combined study of δ66Zn and δ13C further distinguished distinct diets (i.e. amount of ingested animal or plant matter and its type of carbon source from C3 versus C4 biomass) through δ66Zn values within a similar δ13C range, and vice versa.

Our results demonstrate the validity of Zn isotopes and their potential as an additional new dietary and trophic level tracer in archaeology and paleontology. They also shed light on the variations at play behind δ66Zn values in enamel bioapatite.

Session • Diet and nutrition

P–070
Tabula rasa – a new look at light stable isotopes in archaeological contexts

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While light isotope analysis of archaeological remains has settled into a semi-routine procedure, the hydrogen (δ^2H) and oxygen ($\delta^{18}O$) isotopes in bone collagen remain understudied. δ^2H and $\delta^{18}O$ were measured in humans and fauna from six sites spanning 3500 km east-west across the Mediterranean basin. Faunal remains are highly variable in both δ^2H and $\delta^{18}O$, but in some cases group by species. In contrast, human collagen demonstrates very tight δ^2H and $\delta^{18}O$ population means, arguing for a human-specific effect not easily accounted for by existing trophic level-related explanations. We discuss causes for these patterns in the humans and fauna – including food modifications by humans (cooking, storage), environmental influences (aridity), and differences in digestive physiology.
Existing understanding of δ^2H, $\delta^{18}O$, and $\delta^{15}N$ in collagen, particularly with respect to humans and dietary inputs (as well as trophic levels), is inadequate and current interpretations are often overly simplistic. We can improve both the use and the interpretations of these isotopic pairs with an open-minded assessment of the impinging variables and, of course, further investigation.

P–071
A compound specific isotope approach to breastfeeding and weaning in archaeological populations

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Infant care and feeding in the past are widely studied for insights into maternal and infant health, population demographics, diet, and social organization. The onset and conclusion of weaning is identified through a comparison of the stable carbon ($\delta^{13}C$) and nitrogen isotope ($\delta^{15}N$) values of subadult bone or dentine collagen with those of adults. Recent advances in dentine microsampling have circumvented the osteological paradox inherent in these studies by focusing on adults, and have provided higher resolution datasets relating to childhood diet. However, archaeological case studies and longitudinal studies of modern populations are demonstrating that maternal and infant stable isotope values can be influenced by a number of factors including nutritional and physiological stress, maternal diet composition, and diachronic changes in the isotopic composition of maternal milk.
In this paper, we present novel results of compound specific $\delta^{15}N$ analysis of dentine serial samples to characterize the isotopic signature of breastfeeding and weaning on collagen amino acids. We extracted collagen from serial sections of the first molars of eight individuals according to established methods. To evaluate the influence of maternal and weaning diets on the isotopic composition of collagen amino acids, our samples included four marine-adapted individuals from northeastern Siberia (ca. AD 600-1000), and four C_3 consuming individuals from Post-Medieval Britain. The bulk $\delta^{13}C$ and $\delta^{15}N$ values from each serial sample were first measured by EA-IRMS, then selected samples were hydrolysed and the constituent amino acids derivatized for analysis via GC-C-IRMS.
This pilot study represents a significant step towards untangling the variability observed in many infant feeding studies of archaeological populations. By comparing the amino acid $\delta^{15}N$ values between incremental dentine samples we estimate the trophic enrichment of nursing infants. We further assess the suitability of recent trophic calculations employing the $\delta^{15}N$ values of glutamic acid and phenylalanine for identifying the onset of weaning. Finally, we compare the influence of different diets on amino acid routing and trophic enrichment.

Session • Diet and nutrition

P–072

Diet, mobility and dynamism across the long seventh century in Anglo-Saxon Cambridgeshire, a stable isotope study

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Due to the introduction of Christian religious ideology and practices, we begin to see changes in Anglo-Saxon burial practices throughout the seventh century, and much has been made of this in terms of social and cultural implications.This poster explores questions of economic, environmental and cultural change in Anglo-Saxon England by using carbon, nitrogen and oxygen stable isotope analysis alongside funerary archaeology in a multi-scalar and multi-proxy approach. Change in diet and cultural practices over time, both at an individual and a population level are highlighted in stable isotope analyses of human bone collagen, dentine and enamel. We highlight certain individuals with strong Christian connections and imported grave goods to test any links between faith and food, and if the exchange of goods from the continent correlates with migration, burial rites or diet. 75 individuals were included from the Cambridgeshire region, with the majority having both dental and rib samples analysed. This allowed observation of both population and individual change over time and space. These analyses when combined with the material culture and funerary contexts of these individuals will help answer questions about health, societal structure and cultural identities during a highly dynamic time in Anglo-Saxon England alongside environmental questions.

Session • Analytical methods in population genetics

P–073

Struct-f4 – a new method to retrieve high-resolution population affinities from *f4* permutations

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Assessing genetic affinities between ancient and modern specimens entails multiple challenges. Firstly, many true heterozygous sites remain undiscovered in ancient specimens owing to limited depth-of-coverage. Since undetected variation could be interpreted erroneously, as increased drift, ancient DNA studies usually downscale the available sequence data to the same sequencing depth, thereby wasting substantial amounts of data. Additionally, post-mortem DNA damage increase the number of sites that are falsely called at the heterozygous state. Such errors segregate at low frequencies, and are often excluded following MAF filtering. MAF filtering, however, can also remove diversity that only segregates within a few ancient samples, but that could prove essential to the detection of evolutionary relationships not captured in most common sequence variants.

We introduce *Struct-f4*, a novel framework for inferring population affinities from *f4* permutations, calculated at the individual or the population level. Since *f4* statistics measure shared drift, genetic signatures affecting specific populations, including errors or differential sequencing depths, have a minimal contribution to *Struct-f4* inferences. By minimizing lineage-specific signatures, *Struct-f4* magnifies hence ancient population structures, revealing the ancestral components upon which estimating accurate ancestry coefficients. More recent times can be modeled if *f3* permutations, a particular case of the *f4* statistics, are provided instead. From discrepancies between *f4* or *f3* permutations, *Struct-f4* can also co-estimate the underlying error rates. Model fitting is carried out through a genetic algorithm coupled with a constrained L-BFGS-B scheme. Benchmarking by means of coalescent simulations reveals excellent performance and sensitivity, including in the identification of large populations that have diverged only a few generations ago. We finally evaluate the impact of systematic sequencing errors, which are shared by multiple individuals or populations, on the accuracy of *Struct-f4* predictions.

P–074

A stainless-steel mortar, pestle and sleeve design for the efficient fragmentation of ancient bone

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Different types of milling equipment –such as oscillating ball mills, freezer mills, mortar and pestle– can be used to fragment ancient bone prior to DNA extraction. Each of these tools, however, is associated with practical drawbacks. Here, we present the design for a stainless-steel mortar and pestle, with a removable sleeve to contain bone material. The tool is easy to clean, practical and its simplicity allows university workshops equipped with a lathe, boring tools and milling machine to make these components at local expense. We find that this design allows for the efficient fragmentation of ancient bone and improves sample throughput. We recommend this design as a useful, economical addition to existing laboratory equipment for the handling of ancient bone.

Session • Analytical methods in population genetics

P–075
MUSIAL – MUlti Sample varIant AnaLysis

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Mapping-based assembly of genomes from sequencing data allows for a fast and accurate comparative analysis of closely related species when using the same reference for all reconstructions.
After the mapping of the reads of a sample, genotyping programs like the Genome Analysis Toolkit (GATK) (McKenna et al., *Genome Research*, 2010) create a call for each position in the reference genome. This allows a direct comparison of the respective nucleotides between the different samples. These calls can then be used to reconstruct the corresponding genomes, based on the coordinate system of the reference genome.
However, the analysis of these calls can be complicated, as they are only the summary of the mapping. Because of repetitive regions in the genome or missing coverage, they are not always unambiguous for every position. This is further complicated by small insertions or deletions (indels).
Pipelines like EAGER (Peltzer et al., *Genome Biology*, 2016) reconstruct the genomic sequence from NGS data for each sample individually. When allowing for indels, the reconstructed genomes no longer conform to the same coordinate system of the reference genome, which negates the advantages of mapping-based assembly, like the direct comparison of multiple samples. To account for all indels across all samples, we suggest to analyze the genotyping files simultaneously, thus analyzing all samples in a sequencing project together and not individually.
For this, we developed the Java program MUSIAL - MUlti Sample varIant AnaLysis. It can analyze the genotyping information of multiple samples simultaneously, identify single nucleotide variations (SNVs) and indels, create whole genome, as well as gene and SNV only alignments, and report different statistics about the identified SNVs. When analyzing low coverage SNVs, it is possible to allow for a call below the normal threshold, if the SNV was already identified in another sample and thereby increase the base call resolution. Additionally, the program SNPEff (Cingolani et al., *Fly*, 2012) is integrated to identify the functional impact of identified SNVs automatically.
The results created by MUSIAL can be used for phylogenetic and population genetic analyses. We will exemplify this for samples of an ancient leprosy project (Schünemann et al., *Plos athogens*, 2018).

Session • Archaeology of the invisible

P–076

Crop $\delta^{15}N$ values – A tool for reconstructing past soil fertility?

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Nitrogen isotope ($\delta^{15}N$) values of archaeological crop remains are proving a useful tool to directly identify past manuring. The empirical relationship between cereal grain $\delta^{15}N$ values and soil fertility is still little understood, however, since modern ecological studies focus on isotopic analysis of vegetative plant parts whose integration of isotopic signatures may differ.

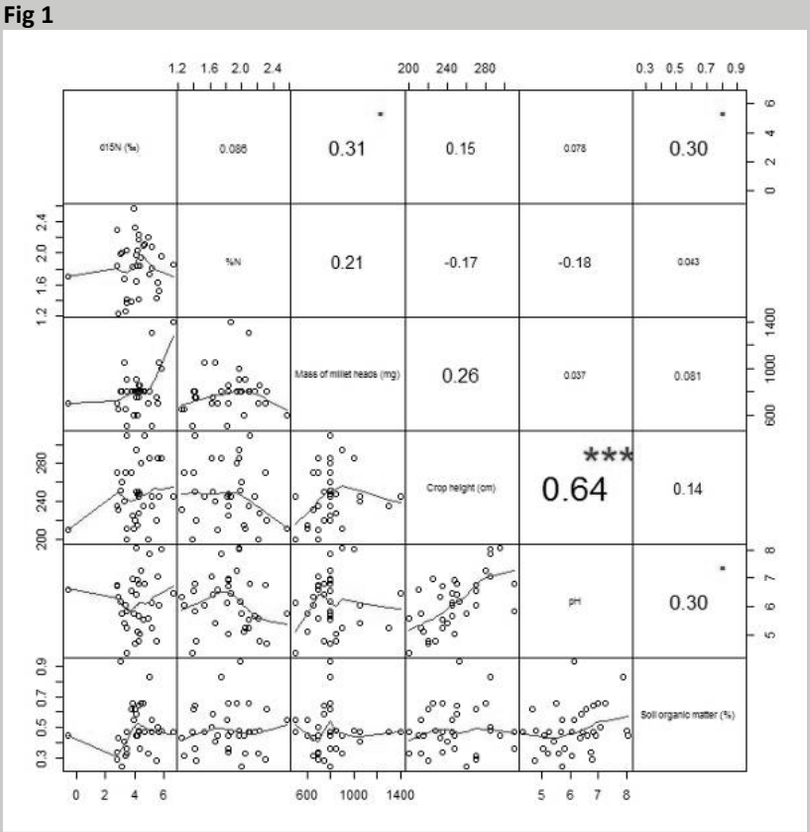
Our aim is to determine the correlation between crop productivity and soil fertility indicators and $\delta^{15}N$ values of pearl millet (*Pennisetum glaucum*) grains grown in soil receiving different quantities of organic matter input in the form of compost or animal manure.

We sampled millet grains and soil (0-10 cm below the surface) from 39 fields in three regions in northwest Senegal. We determined the N content and $\delta^{15}N$ values of millet grains, the pH, organic matter, plant-available phosphorus and exchangeable cation (K, Ca, Mg, Al) content of soils and recorded plant height and average mass of cereal grains and heads. We analyse the relationships between millet grain $\delta^{15}N$ values, soil fertility and crop productivity variables using principle components analysis and multiple regression.

Addition of compost/animal manure resulted in a significant increase in millet grain $\delta^{15}N$ values ($W(38) = 129.5$, $p = .0459$). Figure 1 is a correlation matrix showing that there are no significant correlations between millet grain $\delta^{15}N$ values and mass, crop height, pH or soil organic matter content (significance codes: p = 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1). Analysis of other soil fertility variables is on-going and will reveal whether there is a relationship between a general soil fertility index and millet grain $\delta^{15}N$ values.

The lack of a correlation between millet grain $\delta^{15}N$ values and crop height and mass means that archaeological millet grain $\delta^{15}N$ values cannot be used as an index of past crop productivity/yield. This study thus confirms that crop $\delta^{15}N$ values can be used as an indicator of manuring but that in subsistence farming situations, such as those encountered in this modern study, farmers are managing their limited compost/manure resources to *maintain* crop productivity where this is needed, rather than *enhance* it per se. These modern farming studies are valuable for developing more nuanced insights into how people were being strategic in maintaining long term agricultural sustainability, beyond the binary interpretation of whether they were manuring or not.

Fig 1



Session • Archaeology of the invisible

P–077

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

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Techniques for extracting ancient biomolecules and microremains from archaeological materials have developed at a tremendous pace over the last years. However, archaeological materials are a finite resource, so destructive sampling should be minimized. Ancient dental calculus is a rich source of biomolecules and microremains, harbouring DNA, proteins and microfossils, which often offer complementary lines of evidence. Dental calculus is however often found in small quantities, especially in earlier time periods, and many current standard extraction protocols for DNA, proteins and microfossils are chemically incompatible. A protocol allowing for the simultaneous extraction of several types of information from a single sample would be advantageous, in order to maximise the information gained from this finite resource.

Here we test a new unified protocol for extracting DNA and proteins from a single sample of ancient dental calculus. The protocol was systematically evaluated on archaeological dental calculus of different ages and anticipated states of preservation. The unified protocol yielded on average 40% less DNA than what was recovered through a standard DNA-only protocol, with losses being slightly higher in well preserved samples. The average fragment length or endogenous human DNA content were not significantly altered by extraction through the unified protocol. By contrast, protein yields were unexpectedly on average 74% higher through the unified protocol than through a protein-only protocol. The number of identified proteins was significantly higher through the unified protocol, with identifications including human, bacterial, and putative dietary proteins. The increase in yield and protein identifications was found to be due to a freezing step present only in the unified protocol. Peptide hydrophobicity was higher through the unified protocol, but not affected by freezing samples, which indicates that hydrophilic proteins are present in the aqueous fraction, which is mainly used for DNA extraction in the unified protocol.

Our results indicate that DNA and proteins can be extracted from a single sample of ancient dental calculus, but some hydrophilic proteins may be lost and DNA yields are reduced. However, possible downstream biases in analyses introduced by the unified extraction protocol must also be considered. We conclude with preliminary results on effects of extraction protocol on microbiome and proteome reconstruction.

Session • Archaeology of the invisible

P–079

ArChTES – an investigation of dental enamel mineralization and dental calculus formation combining spectromicroscopy and isotopic analysis

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ArChTES combines Tender-Energy X-ray Absorption Microspectroscopy with stable isotope analyses, to characterise dental calculus and dental enamel (during different stages of enamel mineralisation). The study brings together stable isotope signatures with spatially resolved chemical characterisation, to address questions about enamel and calculus mineralisation. It provides chemical information critical to answering questions that isotopes alone cannot; and addresses a fundamental limitation of X-ray probes, that they are not sensitive to isotopes.

Enamel is well-preserved over long time scales, and is formed at very specific stages of life, thus recording information about not only conditions when and where an animal was alive, but at a particular time in its life. Although enamel of a specific tooth forms at a specific stage of development, and once formed is not altered during life, the sequences and processes of biomineralisation and element incorporation are not uniform during enamel formation. Calculus is also well-preserved over time and is created during the animal's life, from tooth eruption until tooth loss or the animal's death. Trace element chemistry and biogenic isotope signatures in both enamel and calculus have potential to provide information on diet, climate and location. However, for enamel, better understanding of mineralisation and element inclusion processes is needed to guide sampling, thus enabling greater resolution of the timing of life events. Calculus formation is an unbalanced mineralisation process and as a result does not offer the same opportunity of temporal clarity as enamel, but calculus still has potential to offer relevant dietary and life history information once element inclusion and mineralisation are better understood. Our study provides the baseline results to enable future work, through linking enamel and calculus isotope ratio values and trace element chemistry.

Session • Archaeology of the invisible

P–080

Ancient DNA insights into Ivory recovered from 17th century Indian Ocean shipwrecks

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The Dutch Vereenigde Oost-Indische Compagnie (VOC) was the world"s first multinational corporation, dominating maritime trade during the 17th Century. As the VOC played an integral part in the establishment of a global economy, its trade routes reveal a lot about cross-continental human contact during this time. In the 17th Century elephant ivory was highly prized and was a commonly traded into Asia and over 5000 voyages were documented. After 1610 maritime routes followed the westerly winds (Roaring Forties), crossing much of the southern Indian Ocean, before heading north towards Asia. Those ships that travelled to far east flirted with a treacherous West Australian coast line that has claimed over 1500 vessels. This presentation will discuss the 22 mtDNA signatures recovered from ivory tusks excavated from the *Vergulde Draeck* (1656) and *Zeewijk* (1727) wrecks, as well as a tusk of unknown provenance discovered on the Cocos (Keeling) Islands. The data sheds light on the source of ivory in Africa, past biodiversity and suggests the presence of an as yet "undiscovered" shipwreck.

Fig 1

Session • Archaeology of the invisible

P–081

Reconstructing the health landscape of a Medieval hospital cemetery – a holistic interdisciplinary approach

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Established for the care of the poor and infirm, with the exception of pregnant women, lepers, the wounded, crippled and insane, the assemblage of 400 internments (c. 1204-1511) from the Hospital of St. John, Cambridge, provides a laboratory for testing osteological/aDNA methods and for understanding the health and diseases of a broadly representative British Medieval population as it experienced the spread of Black Death from continental Europe during 1347 – 1349. Four hundred skeletons from the cemetery site were assessed for osteological traits and paleopathology. A subset was sampled for isotopic and ancient DNA (aDNA) analysis and compared to a time-transect of sites in the local area. DNA was extracted from teeth, built into double-stranded Illumina-compatible libraries and sequenced on the NextSeq500 75-cycle single-end platform. The raw libraries were screened in collaboration with the Jena Max Planck Institute for the Science of Human History using MALT. Surprisingly, though the cemetery"s prime usage overlaps the main plague period, no skeletons (n = 86, 0%) tested positive for the presence of *Y. pestis* in the teeth, while a contemporaneous site less than 500 meters away contained at least 5 individuals (n = 26, 19%) whose teeth tested positive for *Y. pestis* aDNA. In line with the charter, within the St. John Hospital cemetery, no signs of active *M. leprae* infection (osteologically or aDNA) were found; however, osteological evidence of possible *M. tuberculosis* infection is abundant (post-cranial remains are currently being extracted and screened for pathogen aDNA) as well as a number of trauma. Ancient DNA scans did, however, find evidence of opportunistic infections, pneumonia and septicemia, more indicative of "diseases of the elderly" that effect immunocompromised individuals in today's hospital settings and analyses of the human genome provide insight into heritable disease risk present in the population. By combining the aDNA with dietary isotopic information and skeletal analysis, this collection provides a valuable experiment in holistic Bioarchaeology and an opportunity to explore the relationships between diet, culture, and heritable disease risk on the discovery and expression of heritable and communicable disease in the archaeological record.

P–082

A long journey – aDNA analysis of human samples from the archaeological sites in Croatia

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The application of aDNA analysis on human samples from diverse archaeological sites is a substantial challenge. Altogether, some 50 analysis of autosomal DNA, from several burial sites in Croatia, and wide range – from the Bronze Age to the industrial revolution (from 3000 BC to 1850 AD), were made. Finally, full or partial profiles were obtained for 30 samples. The sampling strategy is based on the anthropological criteria but also on certain aspects of the bones and the DNA success rates. An additional criterion was the taphonomic data because the analyzed samples were excavated from different types of soil and different ph conditions. As for the ancient DNA studies, the analyses of aged bone samples can be hampered by contamination with exogenous DNA. In archaeology, field exploration is often rescue excavation, carried out quickly. We thus assume that every sample had been touched by about a dozen people before it arrived in the DNA laboratory. Hence, a number of measures have been implemented to limit potential contamination of the skeletal samples. After removing soft tissue and dirt from the bones, minimum three sections were sawed. All taken bone sections were soaked overnight in 96% ethanol and in case of harsh contamination bleach was used. After that bone samples were cleaned with ultrafiltrated water and then dried. After each usage, all labware was thoroughly cleaned with bleach and ethanol and exposed under UV light before the next use. In our laboratories, about two dozen cases that involve bone and dental material are processed annually, so that is not a routine work for us. The bones we analyze have not been exposed to the environment for more than 100 years, therefore the obtained results for specimens of the archaeological age give us not only a pleasant surprise but are also a major breakthrough for an understanding of the problem and the development of higher quality and simpler methodology.

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P–083

Mitogenomic data indicate Central Asian origin of the Hungarian conquerors admixed with Srubnaya descendants

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Introduction It has been widely accepted that the Finno-Ugric Hungarian language was brought into the Carpathian Basin in the late 9th century by the conquering Hungarians. Based on linguistic arguments it was expected that the Conquerors may show more genetic affinity to other Uralic speaking groups than modern Hungarians.

Objectives Ancient DNA research makes it possible to trace the origin and genetic relation of prehistoric individuals and populations. In order to shed light on the genetic origin of the Conquerors we sequenced more than 100 mitogenomes from the earliest Conqueror cemeteries and compared them to sequences of all publicly available modern and ancient databases.

Methods We used the Next Generation Sequencing method combined with hybridization enrichment. Phylogenetic method was applied to find the closest matching mitogenome sequences to that of individual Conquerors. We have created ancient and modern Eurasian mitogenome population databases to identify populations with most similar mitogenome composition to the Conquerors. Besides conventional population genetic methods we also used novel algorithms called Shared Haplogroup Distance and MITOMIX, which are especially suitable to uncover past population admixtures.

Results Phylogenetic analysis revealed that about one third the Conqueror maternal lineages derived from Central-Inner Asia, from a territory corresponding to the ancient Xiongnu empire. The most similar population to the Conquerors are modern Volga Tatars, which according to historical and anthropological sources most probably derives from Onogur ancestors of both groups. Population genetic analysis indicated that their East Eurasian component can be traced back to ancestors of modern Tuvans, Buryats and Central Asians, while their West Eurasian component most likely originated from the Bronze Age Potapovka-Poltavka-Srubnaya cultures of the Pontic-Caspian steppe.

Conclusion Our data indicate that all potential ancestors of the Conquerors were steppe nomadic people derived from multiple sources. Their ultimate East Eurasian source may be linked to the Xiongnus, which was brought to the Pontic steppe most probably by Onogur groups, which then admixed there with other nomads. Available data imply that the Conquerors did not have a major contribution to the gene pool of the Carpathian Basin, raising doubts about the Conqueror origin of Hungarian language

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P–084

Maternal lineages from Iron Age to present in Eastern Fennoscandia

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Introduction: aDNA has revealed that the Neolithization involved a turnover of maternal lineages in Europe: haplogroup (hg) U, dominating in hunter-gatherers, was widely replaced by the farmer-associated hgs such as H. As a result, modern European populations show different proportions of these hgs. In Finland, mtDNA diversity resembles that observed in other populations, but holds relatively high frequency of U and shows internal substructure: U is more common in the north-east (NE) Finland and farmer-associated hgs in the south-west (SW). This pattern has been interpreted to reflect the arrival of agriculture from the south-west, most likely associated to the spread of the Corded Ware Culture c. 4,500 ya.

Objectives: To provide insight into the past of Eastern Fennoscandia, complete mtDNA genomes from Iron Age to Medieval Era were obtained from Finland. These derived from five burial grounds, of which Levänluhta (300-800 AD, N=13), Luistari (600-1130 AD, N=10) and Kirkkailanmäki (1100-1200 AD, N=16) are located in SW Finland, and Kylälahti (1200-1400 AD, N=14) and Tuukkala (1200-1400 AD, N=19) sites in south-eastern (SE) Finland.

Methods: Extraction of aDNA was performed as in Meyer *et al.* 2010 and mtDNA capture as in Dabney *et al.* 2013. Raw sequence data processing was performed with EAGER and Schmutzi. Statistical analyses were calculated in Arlequin 3.5.2.2.

Results: The 72 haplotypes obtained belong to hgs observed in modern Finns, but the frequencies differ both from the modern population and between studied sites: the SW sites showed higher frequency of U (60%) than the SE sites (19%) or the modern data (23 %). H showed an opposite trend: 52% in SE and 27% in SW. On sequence level, SW sites have higher affinity to the modern NE, while SE sites cluster with modern SW. Furthermore, within the SW sites the distribution of U subhaplogroups is uneven: Levänluhta has high frequency of U5a and Saami-related hg U5b1b1a whereas other SW sites show relatively high frequencies of U4.

Conclusion: Our results suggest an interpretation that among the studied sites and modern Finns, there are varying levels of admixture of three ancestries: Saami (U5b1b1), possible non-Saami hunter-gatherers (U4, U5a) and farmers (H, J, T, K). The high prevalence of H in the eastern sites might reflect bidirectional arrival of the farming-associated populations into Finland, challenging the traditional assumption of the spread of agriculture from the south-west.

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P–085

Paleogenetic study of ancient archaeological finds related to Kazakh ethnogenesis

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Ethnic history of the Kazakh people is rooted in the ancient period of settling the territory of modern Kazakhstan. The 1st archaeological finds in the territory of Kazakhstan belong to the Paleolithic period. According to archaeological and paleoanthropological data, the ancient tribes spread on the territory of Kazakhstan since the Bronze Age.

We studied the genetic structure of the modern Kazakhs population based on the information about pedigree analysis (shezhire) and Y-chromosome (875 persons) and mtDNA characteristics (130 persons).

The DNA-analysis of two important archaeological finds, which can provide the information about ancient Human migrations and Kazakh ethnogenesis, was conducted: 1) bone remains belonging to the object of Hun elite from Hungarian Natural History Museum, dated to the middle third of the V century CE; 2) a cranium of Eneolithic period human from Botai settlement dated IV-III millennium BC. To the paleo-DNAs analysis the historical data were studied, the archaeological and anthropological evidences were obtained.

It was revealed that Hun period bone remains from Hungary are characterized by R1a haplotype of Y-chromosome and D4j12 haplotype of mtDNA, that testifies the Asian origin of ancient object"s paternal and maternal lines. The phylogenetic and bioinformation analysis determines the genetic proximity of the ancient Hun with ancient and modern populations from Asia and suggests the possibility of ancient people migrations from the Asia Minor to Central and East Asia via Tibet. Comparison of ancient object"s DNA with DNAs of modern descendants of the historically mixed protopopulation Argyn, considering intratribal clans, does not reject the genetic affinity of paternal lines between ancient object and the descendants of Argyn-Meiram (Suindyk and Karakesek) clan, and ancient maternal line with maternal lines of Argyn-Momyn-Sarzhetim clan descendants.

Our results show that Eneolithic period man from settlement Botai, characterizes by Y-chromosome haplotype R1b1a1 and mtDNA haplotype K1b2 and the female individual is Z1mtDNA haplotype. The Eneolithic Botai individuals are closest to each other in the PC space than to any other ancient or present-day individual, and are in proximity to the upper Paleolithic Siberians from the Mal"ta or Afontova Gora archaeological sites. Botai represents a separate group that has genetic similarity with both European and Asian populations.

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P–086

Genetic diversity and social stratification in prehistoric Balkans – genomes, culture and the rise of complex societies

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New whole genomes from Neolithic and Bronze Age Balkan specimens have been sequenced in order to assess intra-population genetic signatures and reconstruct ancestry in the context of social stratification as indicated in the archaeological record. The Balkan Peninsula was an important corridor for the first migrating farmers into Europe, and is a key region for understanding what impact the arrival of Neolithic migrants had on both social organisation and genetic composition in early settlements. A paucity of Balkan specimens means questions remain regarding hunter-gatherer and farmer interactions, and how social stratification developed following the Neolithic transition. Do genetic substructures correlate with intra-cemetery inequalities visible in the funerary record, and how was social status conceived? Almost forty Starčevo inhumations from the Neolithic site of Beli Manastir-Popova Zemlja are found in contracted position with ceramic vessels placed by their head, while a minority are deposited atypically in a channel. In addition, the nearby site of Bronze Age Jagodnjak-Krčevine contains inhumations accompanied by varying numbers and types of grave goods. Aims include identification of SNPs to investigate biogeographic origins, phenotype, admixture, and sex-specific mobility patterns. Furthermore, relationships to other ancient and modern Eurasian samples are investigated, as well as demographic patterns of migration and impacts on human genomic diversity. Petrous bones of 28 specimens were sampled for aDNA and extracts built into libraries. Whole genome shotgun sequencing was performed to above 1X coverage, followed by strict quality control measures and bioinformatic analyses to identify SNPs and perform tests of genomic variation and ancestry. Preliminary results from principal components analysis for nuclear SNP data show Bronze Age samples plotting uniformly, while two Neolithic specimens plot slightly out of expected range. Further measures of genetic diversity including admixture analysis, together with results of haplogroup assignment will be presented to clarify their origin and intra-population genetic substructures. Carbon, nitrogen and strontium stable isotope analysis from the same individuals will complement these results to further investigate dietary status and mobility patterns in relation to the development of social organisation in this understudied area.

P–087

Regional networks, climate change, and cultural interactions as drivers of population expansion in Northwestern Amazonia

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Human populations often exhibit contrasting patterns of genetic diversity in the mtDNA and NRY, which reflect sex-specific cultural behaviors and population histories. Here, we sequenced a region of 2.3 Mb of the NRY from 284 individuals representing more than 30 Native American ethnolinguistic groups from Northwestern Amazonia (NWA) and compared these data to previously generated complete mtDNA sequences from the same ethnolinguistic groups, in order to investigate the impact of cultural practices on their patterns of genetic variation and to gain new insights about their population history. Relevant cultural practices in NWA include patrilocal vs. matrilocal postmarital residential rules, and linguistic exogamy, a marital practice in which men are required to marry women speaking a different language.

In the NRY sequences analyzed, we identified 2969 SNPs, of which only 925 have been previously described. The analysis of NRY and mtDNA sequences showed that males and females experienced different demographic histories. Overall, the female effective population size (Ne) has been larger than that of males through time, and both the mtDNA and NRY lineages show a pronounced increase in lineage diversification beginning about 5000 years ago, with a male-specific expansion occurring about 3500 years ago, after the Mid to Late Holocene climatic transition. As these are too recent to be associated with agriculture, we propose that these changes in population history reflect technological innovations and the expansion of regional trade networks documented in the archaeological evidence. Furthermore, we find that postmarital residential practices and linguistic exogamy have impacted levels of between-population differentiation and within-population diversity.

Overall, our study highlights the importance of analyzing high-resolution mtDNA and NRY sequences to reconstruct population history, since there can be considerable differences between the maternal and paternal lineages, as seen in NWA.

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Characterizing the mesolthic to neolthic transition in central and southern Italy using genome-wide data from 10,000 to 6,000-year-old individuals

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The Mesolithic period in Italy stretches from ~9,000 BC to ~6,200 BC and consists of two main phases, both characterized by different technologies: Mesolithic I (Sauveterrian, ~9,000 BC to ~6,800 BC) and Mesolithic II (Castelnovian, ~6,800 BC to ~6,200 BC). While the archaeological record in northern Italy is abundant and follows a standard transition from Mesolithic I to II, the record from Central/Southern Italy is much more scarce. Additionally, many Mesolithic sites found in the Center/South still display Paleolithic features, and are immediately followed by the Neolithic originating in the Fertile Crescent, which reached the Adriatic coast around 6,200 BC before spreading quickly in the Italian peninsula. Overall, the Paleolithic/Mesolithic/Neolithic transitions within Central/Southern Italy remains poorly understood. In particular, the existence of both possible contacts between Mesolithic hunter-gatherers and Neolithic farmers and possible exchanges between Sicily and Tunisia, as suggested from cultural evidence, remain unclear. In order to answer these questions, we have developed a project aimed at collecting genome-wide sequence data from multiple individuals of the Mesolithic and Neolithic archaeological sites in Central/Southern Italy and Tunisia.

P–089

Investigation of mitochondrial genomes of medieval populations (6-12th centuries AD) lived in the Ural and Volga-Kama region in context with early Hungarian

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Different scientific theories exist about the origin of early Hungarians and their migration from North-Central Asia to Central Europe in the 8-9th centuries. The Hungarian conquerors arrived in the Carpathian Basin 895 AD. Until their arrival they migrated with attached folk elements that joint along the way westwards from the Ural region through the Middle-Volga region on the East-European steppe. The first relics from archaeological cultures that are most probably connected with Hungarian ancestors – the Kusnarenkovo and Karajakupovo cultures – were found in the regions of the Central and Southern Urals. The exact origin, route and chronology of the migration is still unclear and intensively debated by historians, linguists and archaeologists. In our research, we are approaching these issues with archeogenetic methods.
We investigate Medieval (6-12th century) populations from the Ural region, the Carpathian Basin and principal sites of the supposed migration route, which territories had archaeological connections to each other and to early Hungarians. Our test object is the mitochondrial genome (mtDNA), which makes possible to determine the maternal descent line due to its special inheritance. We compare our complete mitochondrial genome sequences with modern and ancient populations, thereby we aim to explore the migration of Hungarian Conquerors.
We examined samples from east side of the Central-Ural, from its west side and from Volga-Kama region. We sequenced the whole mitochondrial DNA of more than 65 samples, and determined mitochondrial DNA haplogroups. Based on our preliminary results, the populations are heterogeneous, in all of them appear both European and Asian haplogroups, but in different proportions. The Uralian populations show Central and Northeast Asian mtDNA composition, whereas the West-Uralian population has more connections to Eastern Europe and to the Caucasus. Certain haplotypes connect the investigated Central Eurasian communities to the first Hungarians in the Carpathian Basin, although the Asian lineages were diluted along the way of migration and during the conquest of the new homeland.
With these new information, we can get closer to understand the migration of Hungarian Conquerors and the maternal genetic composition of the Medieval populations of Central Eurasia.

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Genetic history of longobard migrationsn – a mitochondrial perspective

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From the first century AD, Europe has been interested by population movements, commonly known as Barbarian migrations. Among these processes, the one involving the Longobard culture interested a vast region, but its dynamics and demographic impact remains largely unknown. According to historical records, around the first century CE a Germanic population called "Longobard" was settled in the northern Elbe basin. Around 500 CE the term "Longobard" reoccurs in the region north of the middle Danube, including Pannonia, and three generations later, in 568 CE, a people referred to as Longobards invaded and conquered much of Italy. The geographical spread of the word "Longobard" might evoke a quite large migratory phenomenon; however, the effective impact of the Longobard migration is still highly debated. There is a clear connection between the material culture of Pannonia and Italy at the end of the 6th century, suggesting strong interaction and communication between these two regions.
Archaeological and written sources, however, are open to different interpretations, and are unable to tell us whether such similarities in the material culture result from horizontal cultural transmission and/or trade or from migration. If the latter is the case, a further question arises, namely the relative contribution of immigrants and previously-settled people in the composition of the hybrid population. In this light, the analysis of ancient genetic data is fundamental to obtain a better understanding of past population dynamics and interactions. We report 87 new complete mitochondrial sequences coming from nine early-Medieval cemeteries located along the area interested by the Longobard migration (Czech Republic, Hungary and Italy). From the same locations, we sampled necropolises characterized by cultural markers associated with the Longobard culture (LC) and coeval burials where no such markers were found (NLC). Population genetics analysis and Approximate Bayesian Computation (ABC) modeling highlighted a similarity between LC individuals, as reflected by a certain degree of genetic continuity between these groups, that reached 70% among Hungary and Italy. Models postulating a contact between LC and NLC communities received also high support, indicating a complex dynamics of admixture in Medieval Europe.

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Population dynamics at Late Chalcolithic and Early Bronze Age Arslantepe, Anatolia

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While Anatolia was highlighted as the genetic origin of early Neolithic European farmers, the genetic substructure in Anatolia itself as well as the demographic and cultural changes remain unclear. In eastern Anatolia, the archaeological record reflects influences from North-Central Anatolia, the northeastern sectors of Fertile Crescent and the Caucasus, and suggests that some of these were brought along with the movement of people. Central to this question is the archaeological site of Arslantepe (6th-1st millennium BC), strategically located at the Upper Euphrates, the nexus of all three regions. Arslantepe also developed one of the first state societies of Anatolia along with advanced metal-technologies. Archaeological research suggests that conflicts with surrounding groups of pastoralists affiliated to the Caucasus might have contributed to the collapse of its palatial system at the end of the Chalcolithic period (4th millennium BC). To test if these developments were accompanied by genetic changes, we generated genome-wide data from 18 ancient individuals spanning from the Late Chalcolithic period to the Early Bronze Age of Arslantepe. Our results show no evidence for a major genetic shift between the two time periods. However, we observe that individuals from Arslantepe are very heterogeneous and differentiated from other ancient western and central Anatolians in that they have more Iran/Caucasus related ancestry. Our data also show evidence for an ongoing but also recent confluence of Anatolian/Levantine and Caucasus/Iranian ancestries, highlighting the complexity of the Chalcolithic and Bronze Age periods in this region.

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Preservation of barley genetic integrity stretching over two centuries in southern Sweden

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Introduction: Barley, *Hordeum vulgare*, was introduced to northern Europe and Fennoscandia during the Neolithisation 4000 years BCE. Latitudinally distributed population structure have been detected in 19th century Fennoscandian materials, but the temporal preservation of these structures is not known.

Objectives: We have studied desiccated 17th century materials found in the grave of Bishop Peder Winstrup, Lund, Sweden, to both assess the material itself for suitability for genetic analysis and begin to uncover the temporal patterns of population structures.

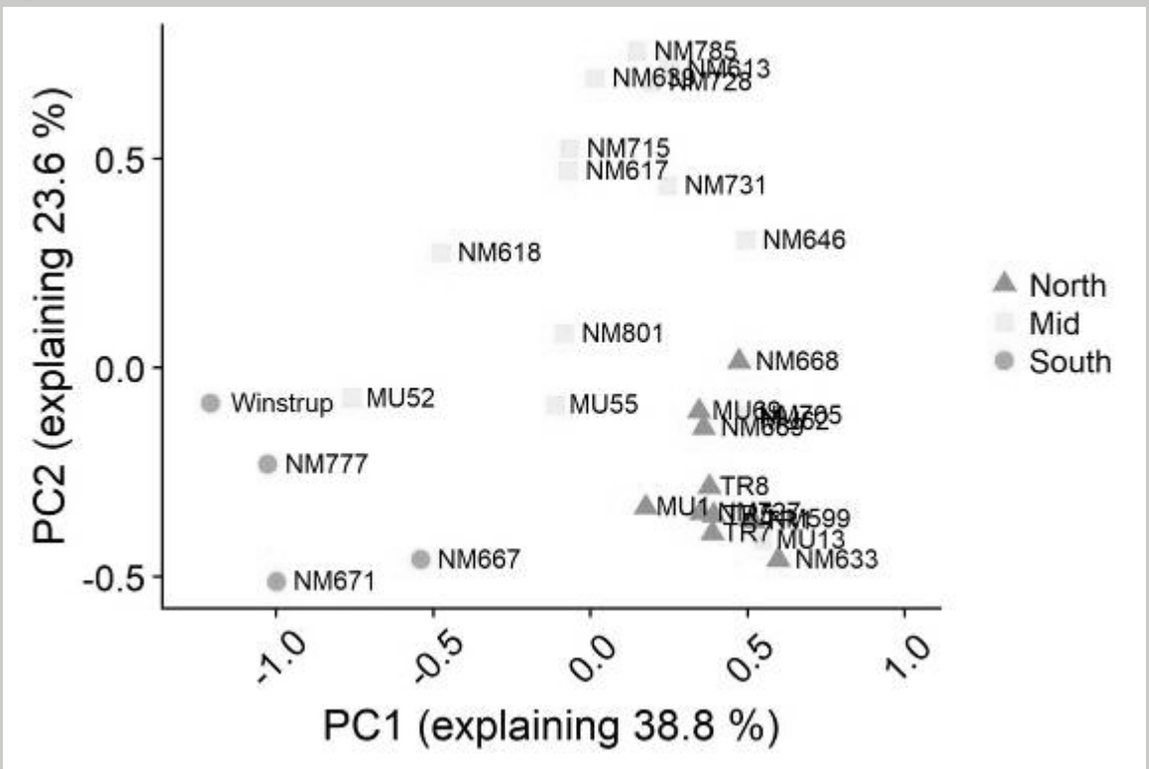
Methods: We extracted DNA from nine barley grains and a negative control and sent part of the extracts for KASP genotyping of 100 SNPs, and part of them for sequencing on Illumina HiSeq 2500. The genotypes were compared to published genotyping data from 29 populations of Fennoscandian barley cultivated in the 19th century.

Results: The success rate for the KASP genotyping was 54% with individual rates ranging from 8 to 94%. STRUCTURE analysis based on genotype data from five samples and 68 SNPs together with data from 19th century Fennoscandian barley showed highest support for 2 or 3 populations; grouping the 17th century samples together with the 19th century ones originating from the nearby geographic region in the south of Sweden. PCoA plots produced a similar pattern, placing the 17th century barley together with 19th century southern populations.

Conclusion: In summary, this suggests that the barley population grown in southern Sweden remained mostly unchanged for a period of at least 200 years.

Figure: PCoA comparing 17th century barley "Winstrup" from Southern Sweden with 29 19th century barley populations from Southern, Mid, and Northern Fennoscandia.

Fig 1



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P–093

Tiwanaku – exploration of the population's characteristics, provenance and changes for the pre-Columbian culture upon the Lake Titicaca using genetic methods

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Tiwanaku was a culture that flourished in the Lake Titicaca Basin between 4th and 11th century AD and made one of the most significant cultures of the Pre-Columbian times. We intend to generate low coverage genomic data and mtDNA genome sequences from human remains excavated from archaeological sites to explore some of the unresolved aspects of Tiwanaku culture such as: (i) Where did the victims of ritual human sacrifices made during religious rituals in the Akapana ceremonial center come from. Archaeological research suggests that the victims were non-locals and most probably warriors captured during military raids. (ii) How and why did the settlement pattern change happen after the demise of Tiwanaku culture. The obtained genetic data will allow to determine the relationships and affinities between the individuals and populations, the provenance of the particular individuals as well as the direction and source of gene flow between the studied populations. To this point we obtained sequences of mitochondrial genomes from 33 individuals representing Tiwanaku and post-Tiwanaku periods. We used this data to test whether there are signs of demographic change after the demise of Tiwanaku culture.

P–094

Paleogenomics of populations in France, from the Neolithic to the Bronze Age

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Expanding from Anatolia into Europe about 7,500 years ago, the Neolithic culture based on agriculture followed two different routes, through the Balkans along the Danube northwards to the Hungarian plain and from there westwards to arrive in the Parisian Basin, and along the coastline of the Mediterranean basin to arrive in Southern France and Spain. Both migration waves eventually reached the territory of present-day France, where the Neolithic culture further evolved and was later replaced by the Bronze Age culture, over the course of the third and second millennia BC. While France is a geographic crossroads that provided multiple opportunities for interaction between populations of different origins, as is well documented by the archaeological record, the underlying demographic processes were not yet explored at a territory-wide scale .

Here we present the complete mitochondrial genomes, Y chromosome markers and genotypes on a number of nuclear loci of interest obtained through a DNA enrichment approach of 163 Mesolithic, Neolithic and Bronze Age individuals sampled from three regions of present-day France, the North, the East, and the South. This study provides, for the first time, a high-resolution 4000-year transect of the dynamics of maternal and paternal lineages in France as well as of autosomal genotypes associated with known phenotypes. This transect that comprises two major cultural transitions (Mesolithic-Neolithic and Neolithic-Bronze Age), reveals contrasting population dynamics between northern and southern France. The study of 120 nuclear SNPs, covering both physical and physiological traits, allowed us to follow the evolution of the allelic frequency over time of several phenotypes that characterize modern Europeans. This study fills a large gap in the understanding of the peopling of western Europe from the Mesolithic to the Bronze Age, completing the knowledge of the global process of the Neolithization of Europe.

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After the plague – genetic history of the human population of Medieval Cambridge

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"After the plague" is a collaborative project that combines methods of archaeology, history, osteoarchaeology, isotopes and ancient DNA of both humans and pathogens for the study of the people of Medieval Cambridge. Low coverage shotgun sequence data has been generated from more than 80 individual samples from an urban cemetery of the Hospital of St John the Evangelist, contextualized with similar data produced from other contemporary local cemeteries, including individuals of various social background, and a time transect of Cambridgeshire, with an aim to understand the effects of the Black Death epidemic(s) of 1347-1351 on the health status and genetic composition of a Medieval town population. Analyses focused on the reads mapping to the human reference genome aimed to explore how the epidemic influenced genetic diversity of the population at the scale of the entire genome and whether individual genes, those associated with immunity in particular, have shown more change than other genes. Genome-wide data has also been used to assess the diversity of urban Medieval Cambridge after the establishment of the university and the level of immigration from continental Europe among various social groups of the town.

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Genomic diversity of ancient individuals from the Iceman´s territory in the Eastern Italian Alps

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Since the prehistory, the Eastern Italian Alps have been a meeting point for people with different origin. Various cultural material as well as funerary rituals documented in this region during the Copper Age (~3700-2200 a.C), suggests several contacts with non-local cultures from east and west Europe during that time. The Tyrolean Iceman (3360-3100 cal. BC) is the best representative of the Copper Age in the Eastern Alps. So far, besides the Tyrolean Iceman, only one Mesolithic sample (Veneto Dolomites) has been genetically analysed from this area. Therefore, there is a lack of regional ancient genomic data to better understand the genomic diversity of prehistoric alpine groups. Comparison with ancient and modern samples, have shown that the Iceman clusters with Early Neolithic farmers from different parts of Europe and with Neolithic individuals from Anatolia. In addition, European individuals contemporary of the Iceman cluster together. These Copper Age individuals also differ from the Iceman in their ancestry and admixture patterns, showing different proportions of Neolithic, hunter gatherers and Eastern (Yamnaya) ancestry components. Since the Iceman alone cannot be considered as representative of the genomic diversity of this alpine area, we are analyzing in this study seven additional prehistoric individuals from the Iceman´s territory. Two samples have approximately the same dating of the Iceman while the other are dating to the Middle Neolithic and to the Copper-Early Bronze Age. The new data will give us the opportunity to better understand the genomic diversity of Eastern Italian Alps and the Iceman´s genetic history. Furthermore, with additional genomic data from this crucial South-eastern European area, we will contribute to know more about the main demographic events that occurred in prehistoric Europe. First shotgun analyses of four pars petrosa samples indicate high percentage of endogenous content (from ~9% to 52%) and low mitochondrial contamination rates. All individual will be now further subjected to deeper sequencing aiming to perform genome-wide comparative analyses with the Iceman and a dataset of European and Near Eastern ancient individuals.

Session • Population structure and migration

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Ancient DNA preservation, genetic diversity and biogeography – a study of desiccated insects from Roman Qasr Ibrim, Aswan, Egypt

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With excellent preservation of organic remains by desiccation and numerous early settlements, Egyptian archaeological sites are a valuable asset in the study of the evolution of synanthropic environments.
This study extracted and analysed ancient DNA from three insect synanthropic species, two storage pests, *Sitophilus granarius* and *Trogoderma granarium,* and the house fly, *Musca domestica,* from Roman Qasr Ibrim, an Egyptian frontier site located in lower Nubia. DNA was amplified from a section of the mitochondrial COI gene, a common barcoding region. Experimental variables were tested for their impact on the efficiency of non-destructive extraction of ancient DNA from desiccated insects with the aim of producing a methodology which can be used as a protocol to maximize successful DNA extraction from other ancient insect samples. Population pairwise Fst distances, shared haplotypes, percentage of different haplotypes, the mean number of pairwise differences and nucleotide diversity were calculated for each population and phylogenetic trees were constructed. Population comparison of sequences obtained from ancient insect samples to modern insects from worldwide populations were used to determine genetic similarity of modern and ancient populations.
DNA was recovered from 64% (9/14) of the *M. domestica* specimens. Successful DNA extraction was influenced by insect species but not other measured variables (e.g which commercial extraction kit was used). Population comparison of Ancient Egyptian and modern housefly populations indicates they were genetically most similar to modern specimens of house flies from Saudi Arabia and Israel and shared a haplotype with modern India. Our research supports the existence of biological invasions and links across the Red Sea from Egypt to the Arabian Peninsula, and exchanges between India and Egypt. The successful extraction of DNA from *M. domestica* specimens provides a proof of concept for a protocol which suggests further non-destructive analysis using ancient insects is likely to yield amplifiable DNA. This research demonstrates the potential uses of insect aDNA in reconstructing biogeographic distribution and better understanding past environments.

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Dutch population history from a genetic perspective

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In this paper we attempt to investigate demographic processes and social structures in the (post) Medieval Netherlands by means of ancient DNA analysis.
For this study we analyzed over 700 Dutch archaeological skeletons from four different urban populations, dating from the Middle Ages to 1850 AD. This data set was examined for autosomal STRs, Y-chromosomal STRs and SNPs and mitochondrial SNPs. The substantial size of this unique historical dataset, in combination with more than 2000 modern Dutch individuals, provides us with sufficient statistical power in estimating heterozygosity, population pairwise differences and population continuity.
We were able to identify subtle but significant differences in time and space. By adding additional bioarchaeological information and connecting each population with its own specific historical context we can also infer detailed information on social aspects of our studied historical populations. This does not only significantly contribute to our knowledge of Dutch (population) history, but is also crucial information for studies on selection in the Dutch population.

Session • Population structure and migration

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Using ancient DNA to identify the ancestry of individuals from a Medieval trading centre in Northern Finland

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Analyzing genomic information from archaeological human remains has proved to be a powerful approach to understand human history. For the archaeological site of Ii Hamina, ancient DNA can be used to infer the ancestries of individuals buried there. Situated approximately 30 km from Oulu, in Northern Finland, Ii Hamina was an important trade place since Medieval times. The historical context indicates that the site could have been a melting pot for different cultures and people of diversified genetic backgrounds. Archaeological and osteological evidence from different individuals suggest a rich diversity. For example, stable isotope analyses indicate that freshwater and marine fish was the dominant protein source for this population. However, one individual proved to be an outlier, with a diet containing relatively more terrestrial meat or vegetables. The variety of artefacts that was found associated with several human remains also points to potential differences in religious beliefs or social status. In this study, we aimed to investigate if such variation could be attributed to different genetic ancestries. Ten of the individuals buried in Ii Hamina's churchyard, dating to between the 15th and 17th century AD, were screened for presence of authentic ancient DNA. We retrieved genome-wide data for six of the individuals and performed downstream analysis. Data authenticity was confirmed by DNA damage patterns and low estimates of mitochondrial contamination. The relatively recent age of these human remains allows for a direct comparison to modern populations. A combination of population genetics methods was undertaken to characterize their genetic structure, and identify potential familiar relationships. We found a high diversity of mitochondrial lineages at the site. In spite of the putatively distant origin of some of the artifacts, most individuals shared a higher affinity to the present-day Finnish or Late Settlement Finnish populations. Interestingly, different methods consistently sugested that the individual with outlier isotopic values had a different genetic origin, being more closely related to reindeer herding Saami. Here we show how data from different sources, such as stable isotopes, can be intersected with ancient DNA in order to get a more comprehensive understanding of the human past.

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Yeniseian hypotheses in light of genome-wide ancient DNA from historical Siberia

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The relevance of ancient DNA data to debates in historical linguistics is an emphatic strand in much recent work on the archaeogenetics of Eurasia, where the discussion has focused heavily on Indo-European (Haak et al. 2015; Narasimhan et al. 2018; de Barros Damgaard et al. 2018a,b). We present new genome-wide ancient DNA data from a historical Siberian individual in relation to Yeniseian, an isolated language "microfamily" (Vajda 2014) that nonetheless sits at the center of numerous controversial proposals in historical linguistics and cultural interaction. Yeniseian's sole surviving representative is Ket, a critically endangered language fluently spoken by only a few dozen individuals near the Middle Yenisei River of Central Siberia.
In strong contrast to the present-day picture, river names and argued substrate influences and loanwords in languages outside the current range of Yeniseian, as well as direct records from the Russian colonial period, indicate that speakers of extinct Yeniseian languages had a formerly much broader presence in the taiga of Central Siberia as well as further south in the mountainous Altai-Sayan region – and perhaps even further afield in Inner Asia (Vajda 2010; Gorbachov 2017; Blažek 2016). The consilience of these proposals with genetic data is not straightforward (Flegontov et al. 2015, 2017) and faces a major obstacle in the lack of genetic information from verifiable speakers of Yeniseian languages other than the Kets, who have had complex ongoing interactions with speakers of non-Yeniseian languages such as the Samoyedic Selkups. We attempt to remedy this with new historical Siberian aDNA data, orienting our search for common denominators and systematic difference in a broader landscape of concordance, discordance, and uncertainty at the interface of diachronic linguistics and genetics.

P–101
The need for a more collaborative archaeological and genomic research framework in the study of Aboriginal Australia

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While close collaboration between archaeologists and molecular biologists are tackling important questions relating to migration, socio-economic change and domestication in Europe and the Americas, such an approach is yet to be applied within Australia. A handful of studies investigating the DNA of the First Australians have been undertaken revealing important insights into Australia"s population history. The research has specifically targeted big questions, e.g. timing of the split from Eurasians, introgression events with archaic hominins, divergence from Papuans etc. The value of genomic research has not yet been considered in relation to key questions from later prehistory. These could, and indeed should be tackled through a collaborative "archaeogenomic" approach to Australia"s prehistory.

A more collaborative approach is now necessary, as it is emerging that archaeological datasets alone do not have the capacity to resolve many of the key socio-economic hypotheses that persist relating to the Australian continent of hunter-gatherers. For example the suggestion that there may have been significant gene flow as a result of the dispersal of the Pama Nyungan languages commencing in the early Holocene, the emergence of increasing socio-economic complexity through "intensification" in the mid to late Holocene, increased contact and trade with the Torres Strait Islands and Papua in north east Australia, and the evolution of the extensive trade and exchange networks around the narcotic pituri in the last 1000 years - theoretically these hypotheses are all testable if targeted regional datasets can be acquired. I outline two regional projects I have initiated combining archaeological, genomic and isotopic datasets that hold great promise for understanding the evolution and complexity of Aboriginal social systems. It is perhaps most important to emphasise that such an approach will only be possible if it is undertaken as part of a genuine partnership with Aboriginal communities.

Session • Paleoproteomics

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Palaeoproteomic analysis of paint binders and adhesives in ancient Egypt

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Proteins from hide, bones, egg and milk have been mentioned to be used as paint binders and adhesives by the ancient Egyptians. A vast artistic production from ancient Egypt is still accessible to us but a limited number of analytical studies have been conducted so far on the organic media. Ancient literature sources provide limited information about the use of proteinaceous materials in ancient Egypt, leaving several questions open: were certain protein-based materials preferred for specific applications? Were the same materials used for different purposes in different periods and geographical areas? How did proteins in paint formulations decay over millennia? Recently, the introduction of high-throughput tandem mass spectrometry (MS)-based protein sequencing allowed confident sequencing of ancient proteins. This new, robust and reliable approach, named palaeoproteomics, can provide very innovative results in the study and preservation of cultural heritage collections.
The objective of this research is to apply palaeoproteomics to confidentially identify the biological species of origin and the molecular damage of the protein-based materials used in ancient Egypt painted artifacts. We investigated micro-samples from different artifacts, such as painted coffins, cartonnage and mural paintings dating 3000 BC – 600 AD coming from several European and North American museum collections. Samples were first screened by Fourier transform infrared spectroscopy in order to understand the nature of the paint binder and confirm the presence of protein-based material. The most promising ones were then subject to proteomic analysis by mean of nano-liquid chromatography coupled with tandem mass spectrometry.
Results revealed animal glue from *Bos* species was used as binder in both the preparation and, occasionally, paint layers. In addition, the first molecular evidence of the possible use of an oil paint binder, at the plant species level, is presented. The accurate identification of the protein species and the characterization of its molecular damage represents a significant step forward in the understanding of the painting materials and techniques used in ancient Egypt, and complements the information from art history and zooarchaeology sources. The results of this research demonstrate how palaeoproteomics provides new evidence to advance understanding of the use of specific protein sources, with potentially strong implications for future conservation treatments.

P–103
Sequencing of ancient protein residues from the ground layer of Danish Golden Age paintings by tandem mass spectrometry

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The recent application of proteomics to cultural heritage objects has proven to have a potential in the characterisation of the damage and the identification of the biological species of origin of ancient protein residues in artistic materials. A protein sequencing protocol, based on tandem mass spectrometry analysis, was tested on a series of mock-up paint samples, containing proteinaceous and non-proteinaceous binding media and different types of pigments. Protein extraction was performed on the solid samples in one step, with a guanidine hydrochloride solution, followed by enzymatic protein digestion. The same protocol was subsequently applied to characterise the proteinaceous residues from the ground layer of a series of easel paintings, dating back to the Danish Golden Age. Five samples have been collected from the tacking edges of five 19th-century artworks by Christen Schiellerup Købke and Christoffer Wilhelm Eckersberg and preserved in the National Gallery of Denmark and the Royal Danish Academy of Fine Arts. The identification of the biological source of the material, as well as a partial characterisation of the damage of the proteins, have been achieved. Animal glue, the most common protein material in preparation layers, from *Bos* species has been confidently identified. The obtained results show the efficacy of proteomics to investigate the history of artworks, leading to a better comprehension of artistic techniques and traditions. The characterisation of protein residues in paint and preparation layers can provide precious information to guide conservation and restoration treatments.

Session • Paleoproteomics

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The FINDER project – identifying hominin bones in the Altai Mountains using collagen fingerprinting

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The recovery of Pleistocene human fossils in general is extremely rare, especially so in Central and Northern Asia where those discovered are often too fragmentary to allow for a secure identification. This is most easily demonstrated by the problem of the Denisovans. Since their initial discovery in 2010, their geographical distribution, genetic history, and admixture into Neandertals and modern humans has been widely researched and discussed however at present they are known only from a single phalanx bone and three teeth from one site.
Using Zooarchaeology by Mass Spectrometry (ZooMS), the ERC-funded FINDER project (finderc.org) aims to address this problem by targeting assemblages of fragmented and morphologically unidentifiable bone assemblages. Over the course of the next five years, the FINDER project will screen 40,000 fragmented bones from ~20 archaeological Eurasian sites using ZooMS. In doing so, this project aims to move the focus of the search for Pleistocene human remains away from morphologically identifiable fossils to the vast numbers of fragmented and non-diagnostic bones regularly excavated from archaeological sites.
Here we describe preliminary results from the Altai sites of Denisova and Strashnaya caves. These represent the first two sites intensively studied as part of the FINDER project"s search for Pleistocene human remains. Both caves are key in understanding the interplay of ancient hominin populations in Northern Asia and significant, if rare, Pleistocene human remains have already been located here.
Thousands of fragmented bones from Denisova and Strashnaya caves which had been previously excavated and stored, as they could not be taxonomically identified on the basis of their morphology, have now been analysed using ZooMS at the newly-established facilities of the Max Planck Institute for the Science of Human History, Jena, Germany. Such large scale identification of previously unutilised bone fragments opens research up to a variety of scientific methods. In order to investigate these fragments to their full potential, the FINDER project will apply a variety of techniques to examine them further, including stable isotopes to investigate diet and consumer-resource systems, radiocarbon dating to secure a direct age estimate of the bone samples, and DNA analysis to understand the genetic history of the individuals analysed.

P–105
MS-based palaeoproteomic evaluation of oxidative damage in artistic objects

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Proteins are known to be the main targets for free radicals and other oxidants due to their high abundance in biological systems and reactivity. Free radicals usually cause extensive damage to the multiple side-chain and backbone sites in proteins, yielding various oxidation products (e.g. carbonyls, commonly used markers of protein damage).
Besides chemical oxidation, UV-mediated oxidation is one of the most frequently-occurring photo-chemical reactions. This type of oxidation produces specific intermediate peroxidic species during photochemical oxidation of chromophoric amino acids - tryptophan (Trp), histidine (His), tyrosine (Tyr), cysteine (Cys), methionine (Met), and phenylalanine (Phe).
Peroxidic species and their tautomeric forms (other di-oxidation products), in their turn, can be considered as marker intermediates distinguishing photo- from chemical-oxidation. Moreover, these intermediates can be used as markers of UV-related damage, enabling the tracing of photo-induced degradation status and conservation history of artistic objects.
The presence of above mentioned photo-oxidative PTMs in cultural heritage materials can be characterized using tandem mass-spectrometry based proteomics. In the current work this technique has been successfully applied to the study of photo-oxidative damage of a Medieval mural painting (Mackie et al., 2018). Remarkably high abundance of His di-oxidation products, compared to the negative control samples, showed that the proteinaceous material had undergone an extensive UV exposure. The obtained results also enabled reconstruction of conservation history of the studied sample revealing the possible sequence of application of the different conservation layers.
Being the first in-depth example of photo-oxidative marker PTM characterization in artistic materials using proteomics, we believe that this methodology has a great potential for further palaeoproteomic applications.

Session • Paleoproteomics

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Sex-specific protein markers as a tool for exploring animal domestication

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Zooarchaeological remains hold a wealth of information and can provide important insights into the relationship between humans and animals in the past. Research into understanding more about the earliest domestication of sheep and goats has focused on the area known as the Fertile Crescent. To gain a deeper understanding of the domestication process, key pieces of information are needed: species ID, sex and age at death. Age can be determined through traditional morphological methods, while species ID and sex can be more problematic as they rely on certain elements of the skeleton surviving and being associated with other morphologically identifiable parts. Ancient DNA (aDNA) analysis can be applied, but it is very dependent on the level of molecular preservation which is known to be poor in areas such as the Fertile Crescent. Zooarchaeology by mass spectrometry (ZooMS) is a proteomic method that can provide good species distinction even in cases where DNA preservation is poor; however the sex of an animal can not currently be identified.
The goal of this research is to develop a new method of sex identification based on nano-liquid chromatography coupled with tandem mass spectrometry (nanoLC-MS/MS) applied to ancient teeth. Enamel, which commonly survives in archaeological sites, is made up of very little protein. However one protein that is present is amelogenin, which is expressed from genes on the X and Y chromosome. The peptide sequences differ between these, and therefore could be used as a possible indicator of sex. Proteomic analysis of modern and subfossil tooth enamels, along with amino acid composition and racemization studies to understand the stability of the signal, is allowing us to understand its potential as an alternative method to aDNA and morphological analysis for sex identification in sheep and goats. This could result in the age, species and sex of an individual being identifiable from one single tooth.

P–107
Strategies for data validation in ancient protein studies using a milk model

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Technological advances in LC-MS/MS technology are increasingly allowing archaeological researchers to gain new insights into past cultures through the analysis of ancient protein residues. This presentation will focus on how optimization of aspects of study design, quality control, and data authentication can improve data reliability and archaeological interpretations from ancient protein remains. The most common focus of quality control and data validation in the field of ancient proteomics is in the final output, whereby data are generally processed using probabilistic scoring algorithms where significance values are given to help us assess the likelihood that results are valid. However, there are additional checks and authentication steps that can be incorporated into the workflow, even prior to sampling, to improve the reliability and confidence of ancient protein identification. Using archaeological milk proteins as a model system, this presentation will focus on how database design, patterns of degradation (e.g., deamidation) and proteotypic peptide recovery, and other factors can be used to assist in protein identification, validation, and authentication. Additionally, critical attention to the possible limitations of our methods or proteins of interest will be addressed. Validation procedures can be time-consuming but they are a vital component of experimental design and should be a routine part of any ancient proteomics workflow.

Session • Domestication

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Phylogeography of the aurochs and of early domestic cattle revealed by ancient mitogenomes

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We studied through ancient mitogenomes the genetic diversity of the aurochs *B. primigenius primigenius* at the beginning of the Neolithic and followed its evolution over time in wild and domestic cattle in southwest Asia and Europe. The obtained genetic data shed light on the population structure of the aurochs, which then allowed us to deduce the key elements of the domestication process from the Neolithic to the Bronze Age. Our study also yielded important insights into the various modalities of the spread of domestic cattle into Europe and Africa.

P–110
Human-mediated dispersal of cats in the Neolithic Central Europe

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Archaeological and genetic evidence suggest that all domestic cats derive from the Near Eastern wildcat (*Felis silvestris lybica*) and were domesticated twice, first in the Near East around 10,000 years ago and for the second time in Ancient Egypt ca. 3,500 years ago. The spread of the domesticated form in Europe occurred much later, primarily mediated by Greek and Phoenician traders and afterwards by Romans who introduced cats to Western and Central Europe around 2,000 years ago. We investigated mtDNA of Holocene Felis remains and provide evidence of an unexpectedly early presence of cats bearing the Near Eastern wildcat mtDNA haplotypes in Central Europe, being ahead of Roman Period by over 2,000 years. The appearance of the Near Eastern wildcats in Central Europe coincide with the peak of Neolithic settlement density, moreover most of those cats belonged to the same mtDNA lineages as those domesticated in the Near East. Thus, although we cannot fully exclude that the Near Eastern wildcats appeared in Central Europe as a result of introgression with European wildcat, our findings support the hypothesis that the Near Eastern wildcats spread across Europe together with the first farmers, perhaps as commensal animals. We also found that cats dated to the Neolithic period belonged to different mtDNA lineages than those brought to Central Europe in Roman times, this support the hypothesis that the gene pool of contemporary European domestic cats might have been established from two different source populations that contributed in different periods.

Session • Domestication

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An ancient DNA study on sheep domestication in Central and Western Anatolia

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Southeastern Anatolia is known as the center of sheep domestication. Sheep domestication started nearly 9000 years before common era (BCE) and then spread by demic diffusion, cultural diffusion or both. In this study, 144 bp long partial mitochondrial DNA (mtDNA) sequences of ancient sheep bones obtained from 9 archaeological sites in central Anatolia, (Tepecik Çiftlik Höyük-Niğde, Boncuklu Höyük-Konya, Çatalhöyük-Konya, Pınarbaşı Höyük-Karaman, Canhasan Höyük-Konya), western Anatolia (Ulucak Höyük-İzmir and Yeşilova Höyük-İzmir) and northwestern Anatolia (Barcın Höyük-Bursa and Aktopraklık Höyüğü-Bursa) were analyzed in order to understand the spread of sheep domestication in Anatolia. Haplogroup (A-E in sheep), haplotype and nucleotide diversities; and sequences of meta populations were analyzed comparatively by permutation and continuity tests over the time spanning before 7500 BCE (early Neolithic) to 5500 BCE (Chalcolithic). Analyses revealed that, around 7000 BCE haplogroup, haplotype and nucleotide diversities dramatically increased in central Anatolia. Sudden appearances of domestic sheep on the west coast of Anatolia may be related with the contributions of seafaring groups. However, sheep of northwestern Anatolia seems to evolve from early sheep of central Anatolia. Results of paleogenetic studies are supporting the previous archeological and archaeozoological observations.

Session • Plagues and pathogens

P–112
Manifestations of tuberculosis on skeletal remains from the EBA cemetery in Mikulovice (Czech Republic)

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Introduction: Tuberculosis remains a serious medical problem today. The palaeopathological studies aimed at monitoring disease changes in skeletal remains of historical populations are also beneficial for the detailed study of the development of this disease, as they present direct evidence of the existence of tuberculosis and its forms in the past.

Objectives: One of the objectives of the palaeopathological analysis of studied skeletal remains from the cemetery in Mikulovice is to obtain a basic overview of the occurrence of tuberculosis in the population of the Early Bronze Age.

Material and Methods: In the past years, skeletal remains of 106 people have been studied (35 females, 34 males, 9 juveniles and 28 children) from Mikulovice (Czech Republic), dating from the Early Bronze Age (2200–1750 BC). Palaeopathological analysis was based on standard anthropological and palaeopathological treatment. The main diagnostic method was macroscopic examination, supplemented by X-ray examination. If necessary, bone samples for genetic testing were collected to detect Mycobacterium tuberculosis DNA.

Results: A total of 19 suspected cases of bone tuberculosis were found in the Mikulovice skeletal collection. Most of these were changes in cranial bones caused by tuberculous meningitis (10 individuals – 3 adults, 3 juveniles and 4 children), Pott disease (8 cases), and in one case tuberculous pleuritis.

Conclusion: The results of the palaeopathological analysis will become the basis for a detailed pilot genetic study.

P–113
Molecular evidence for the etiologic agent of the Tyrolean epidemic of 1636

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Containing major, historical and modern, trans-alpine travel routes, the region of Tyrol has been affected by various epidemics in the past. In August 1636, the Tyrolean village of Naturns (Italy) was struck by a disease referred to as "pest", killing up to 25% of the local population and leading to an increase of burials in the so-called "plague graveyard" of the St. Procolo church on the outskirts of the village. While historical sources indicated that the outbreak was likely a typhus epidemic caused by the bacterium *Rickettsia prowazekii* and not plague and its bacterial pathogen, *Yersinia pestis*, molecular evidence for the etiologic agent of this event was missing.
To clarify the nature and cause of the outbreaks striking Tyrol in the 17th century, we attempted to identify the pathogen responsible for the epidemic by investigating tooth samples from individuals recovered from multiple burials in the graveyard of the St. Procolo church in Naturns dated to 1636.
Human ancient DNA (aDNA) content in teeth from 24 individuals was assessed by quantitative PCR (qPCR). All extracts were screened for the presence of *R. prowazekii* and Y. *pesti*s via PCR and qPCR, respectively, and samples exhibiting amplifications were further investigated via shotgun sequencing and metagenomic profiles.
All teeth (24/24) contained sufficient endogenous DNA for the amplification of the human mitochondrial HVR1 region. qPCR results revealed the presence of *Y. pestis pla* and *caf1* DNA in seven individuals, but no *R. prowazekii* DNA was detected in any of the 24 teeth over the course of the experiment. The metagenomic analyses are still undergoing.
Contrary to historical evidence, which had suggested that the buried individuals had died of epidemic typhus, we have provided clear molecular evidence that the disease having struck Naturns in 1636 was, in fact, plague. Hence, the results of this study have shedded light on the historical past of Naturns and the Tyrolean region in the 17th century, and highlighted the importance of cooperation between archaeologists, historians, and molecular biologists in order to reconstruct the nature of ancient epidemics.

Session • Plagues and pathogens

P–114

Ancient *Yersinia pestis* genomes from Britain, France, Germany and Spain reveal extensive strain diversity during the First Plague Pandemic (541-750 CE)

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The first historically reported pandemic unambiguously assigned to *Yersinia pestis* is the Justinianic Plague (541-544). It was later followed by numerous outbreaks in Europe, North Africa and the Middle East until the mid-8th century, often referred to as the "First Pandemic". Despite the lack of historical records in southern Germany, the identification and characterization of the causative lineage has thus far been based solely on ancient genomes found in two early Medieval cemeteries in this region. These two genomes, that are identical, occupy a distinct phylogenetic position in the modern diversity of *Y. pestis* on a now extinct or undocumented branch.

We aim to elucidate the evolutionary history of *Y. pestis* during the "First Pandemic" by sampling on a broader spatial and temporal scale, including the Mediterranean basin that is known to have been heavily affected by plague as well as more questionable regions such as Britain. After screening of more than 150 samples and performing targeted DNA enrichment of positive candidates, we recovered three new genomes from Germany, and one from each of Britain, France and Spain with 5 to 10-fold mean coverage. Only two of the genomes were identical to those previously published, having stemmed from relatively nearby cemeteries.

The newly sequenced strains reveal a rapid diversification of strains during the Justinianic Plague, similar to the radiation events described in association with the "Second" (14th to 18th c.) and "Third" (19th to 20th c.) Pandemics. At least four independent strains seem to have emerged during this event, two of which were found in southern Germany. The British genome substantiates the bacterium"s presence in this region already at, likely, the onset of the "First Pandemic". However, the genomes recovered from Spain and France appear phylogenetically distinct, reflecting historical records that testify that *Y. pestis* affected the western Mediterranean basin multiple times during the late 6th and 7th centuries. In addition, the French genome falls in the most derived position on this branch, and seems to lack a genomic region that includes two previously identified virulence genes.

Overall, the genomes we present substantially contribute to the understanding of the "First Pandemic" which remains, to, date comparatively understudied by the field of archaeogenetics.

Session • Plagues and pathogens

P–115

16th-century *Yersinia pestis* genome from Logroño, Spain underlines plague persistence in Europe during the Second Pandemic

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The Black Death caused by *Yersinia pestis* ravaged Europe between 1346-1353 AD and was followed in numerous places by further major outbreaks until the 18th century. It is still under discussion whether these were due to reintroductions of the pathogen from Asia or its persistence in local reservoirs within Europe.
Here, we analyzed 55 teeth from individuals buried in the necropolis of *La Inquisición* at Logroño, Spain, an important station along one of the main pilgrim routes of the Camino de Santiago. From the 13th century until 1512 this site was a pilgrim hospital (*Hospital de Santa María de Rocamador*) and included a cemetery that probably maintained its funerary function in the following decades. In 1564, the city of Logroño was struck by a mass mortality event that is referred to as *pestilencia* in written historical records. During this event a great number of corpses were buried in the cemetery of the abandoned hospital. Through a qPCR based assay specific to the *Yersinia pestis pla* gene, located on the pPCP1 plasmid, ten of these teeth showed possible preservation of this pathogen"s DNA. Subsequently, UDG-treated DNA libraries from these extracts were prepared and were whole-genome captured for *Yersinia pestis* DNA. After high throughput sequencing, the data were mapped against the *Yersinia pestis* CO92 reference genome for authentication, as well as SNP and phylogenetic analyses.
We present here a post-Black Death genome retrieved from the Iberian pensinsula and are able to show that the 1564 outbreak of *pestilencia* at Logroño was caused by *Yersinia pestis*. Phylogenetic analysis shows that the Logroño genome occupies a position within the European *Yersinia pestis* cluster in close relation to the previously published genomes of Ellwangen, Germany and Marseilles, France. Our data provide further support for the hypothesis of a western Eurasian focus of post-Black Death plague instead of a re-introduction from Asia and provide insights into the local diversification of *Yersinia pestis* during the second pandemic.

P–116

Drought, disease and decline of the Wari Empire – contextualizing tuberculosis in the Peruvian Andes

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Mycobacterium tuberculosis complex (MTBC) is one of the most successful and deadly group of bacterial pathogens. Its spread is promoted through migration, population crowding, drought, malnutrition, and poverty. In 2014, recovery of pre-contact MTBC genomes from coastal Peruvian human material revealed circulation of a MTBC strain currently adapted to pinnipeds (*M. pinnipedii*), suggesting transmission of the bacteria between seals and humans before European presence in the region. Throughout Peru, there exists evidence of major networks facilitating interaction and exchange, both ideological and biological, between groups of people across a large geographical expanse, most notably established by the Wari Empire that ruled during the Middle Horizon (600 -1000 CE). In the Terminal Wari (ca. 1050 CE) and post-Wari era, known as the Late Intermediate Period (LIP, 1000-1400 CE) there were extended droughts and the political decline of the Wari, as well as the onset of skeletal signs consistent with tuberculosis. To examine the relationship of MTBC strains in this region to others circulating in contemporary southern Peru, we genetically analyzed skeletal material from three contexts from the capital city of Huari. Here we present data from 104 skeletal elements recovered from commingled assemblages largely from the late LIP but also some representative of the Terminal Wari era of the early LIP. Using high throughput methods of DNA recovery and detection-based DNA analysis, we were able to identify and recover full MTBCgenomes from 6 individuals. Our results reveal the challenges in recovering ancient MTBC genomes in samples rich with environmental mycobacterial backgrounds. Our analysis provides insight into the ecology, geographic range, and evolutionary history of MTBC in the Andes and the possible relationship between infectious disease and the climatic and political shifts experienced by the population of Huari.

Session • Microbiomes

P–117

Dental calculus microbiome from Medieval populations in prague castle and Pilsen

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Dental calculus becomes a valuable material of choice for retrospective studies aimed to investigate health status and dietary habits of past populations. In a course of the large multidisciplinary project, we aimed to compare dental calculus microbiomes from Medieval human remains obtained from burial sites in Pilsen, Prague castle and settlement surrounding Prague castle. Besides osteological and paleopathological analyses of the human remains, we collected dental calculi for the investigation of microbial DNA. Dental calculi from teeth found freely and without any context in the burial sites were used for the method development. Used methods and results obtained from microbiome analyses as well as analyses of other DNA found in dental calculi will be discussed.

P–118

Combining different methodologies for gaining much information from ancient dental calculus – the case of the Porticus Octaviae in Rome (Italy)

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Over the past two decades, dental calculus has become object of an increasing number of investigations which concern different research fields in biology. Thanks to its chemical nature and way of forming, tartar represents a mineralized archive of multisource materials deriving from the oral cavity such as mucosa cells, components of the bacterial flora, minute fragments of various materials which entered the mouth. Indeed, acting as a trap for various materials, dental calculus keeps information about human state of health, hygiene, behaviors and activities which characterized recent or ancient cultural contexts. Focusing on different contents (DNA, proteins, food residues, …), the laboratory procedures require specific treatments which are often alternatives. Therefore, the amount of tartar recovered from ancient teeth has become the main limiting factor for gathering data, particularly when working on prehistoric and protohistoric samples. In order to maximize the information which can be obtained from the same sample of dental calculus, we tested different combinations of laboratory procedures in order to identify the best strategy for simultaneously extracting DNA and isolating plant residue. Preliminary tests were performed on fresh plant materials for verifying the effects of the DNA extraction protocols on starch grains and phytoliths. Successively, different combined experimental procedures were applied the dental calculus of three individuals recovered at the Porticus Octaviae in Rome. The different procedures was proven to only provoke negligible affections on the starch grain morphology, while no effect was observed on phytoliths. When combined procedures were applied to ancient calculus samples, only a reduction in the quantity of the plant microresidues was observed compared to the reference method, while the quality of the observations was unaltered. DNA yield did not show appreciable variations compared to the strategy used. Sequencing analysis confirmed that the DNA extracted from the ancient calculus samples was mainly derived from oral microbial populations. Our results confirmed that authentic genetic data could be successfully recovered from ancient dental calculus using protocols commonly used for extracting DNA from ancient bones and teeth. Moreover we showed that the residual pellet can be successfully used for morphological characterization of plant residues without significant alterations or loss of information.

Session • Microbiomes

P–119

Biomolecular preservation in dental calculus from the Teotihuacan ritual landscape

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The population at the ancient city of Teotihuacan dramatically increased during the Classic Period (AD 1-550) with estimates of more than 100,000 people. This growth accompanied urban development, such as ceremonial precincts, large pyramids and thousands of residential compounds. While archaeological and isotopic evidence indicate that many Teotihuacan residents emigrated from regions across Mesoamerica, little information about health and diet exists for the city. Although interdisciplinary approaches have filled some gaps, genetic studies in ancient Mesoamerica remain scarce due to the lack of biomolecule preservation. Calculus provides a new source of ancient biomolecules that may be more robust to contamination and degradation and may prove valuable in addressing questions about human biology in areas with poor biomolecular preservation.

In this study, we apply shotgun sequencing techniques to four dental calculus samples from two localities at Teotihuacan to investigate biomolecular preservation. Three of these individuals date to AD 350-400 and were interred within the Moon Pyramid (PPL), a prominent religious complex at Teotihuacan. These individuals likely held a high social status due to their placement inside the pyramid and internment with green stone pendants of Maya origin. Previous analysis of strontium and oxygen isotopes suggest that some of the Moon Pyramid human sacrifices were foreigners and genetic data may be useful in exploring the ancestry of these sacrificial victims. An additional individual was identified in ongoing excavations at the nearby Plaza of the Columns Complex (PPCC). The calculus samples were processed at the University of Oklahoma"s Laboratories of Molecular Anthropology and Microbiome Research (LMAMR). DNA yields ranged from zero to 73 ng/mg with the PPL samples having very low DNA yields. Following shotgun Illumina sequencing (2 x 150 bp), an intact oral microbiome was recovered in the PPCC sample but the PPL samples did not have intact ecologies. Human endogenous content for the PPCC calculus sample was 0.001% and the reads showed the characteristic patterns of damaged DNA molecules. Preliminary analysis suggests that biomolecular preservation is sufficient for downstream analyses at the PPCC but poor at the Moon Pyramid. This study is the first to reconstruct the oral microbiome of Teotihuacanos and suggests that biomolecular preservation in dental calculus is context-dependent within a site.

Session • Microremains and residues

P–120
Rapid, cost-effective lipid analysis of small samples of archaeological ceramic by pyrolysis GC-MS

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Here we evaluate a potentially rapid, cost-effective method of characterizing lipids on small samples of archaeological ceramic. Lipid residue analysis of ceramics is frequently applied in many parts of the world with the number of applications continuing to broaden. One challenge is that this method requires destruction of pottery itself (1-2 g) and fairly lengthy sample preparation and extraction times (8-9 h). These have prevented the application of the technique to rare and valuable samples or object on display in museum collections. Due to the sample preparation time, and associated costs, studies are also limited to selecting a small number of vessels from larger assemblages raising questions of representativity. To circumvent these issues, here we present a new approach for lipid analysis from just 1-5 mg of pottery sherds and associated charred deposits by thermally assisted hydrolysis and methylation (THM)-GC/MS using tetramethylammonium hydroxide (TMAH) reagent with a multi-shot pyrolyzer (Frontier Laboratories Ltd., model EGA/PY-3030D). The approach involves direct pyrolysis of the organic residues of the ceramic matrix and therefore negating the need to extract. Here we compare this approach with routine lipid analysis through parallel analysis of East Asian Neolithic-Bronze Age pottery. We show that this method can be used for identification of various kinds of biomarkers such as alkylphenylalkanoic acids, isoprenoid fatty acids and the pentacyclic triterpene methyl ether, miliacin, a diagnostic compound for broomcorn millet. In short, this method will enable us to reduce the sampling time three to four fold, using thousandth part of the quantity of ceramic powder samples.

P–121
Use or manufacture? – experimental insight into the origin of aquatic lipids in Alaskan pottery

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During the manufacture of pottery a wide range of organic materials can be used as temper. Historic and ethnographic sources describe the use of fibrous materials, such as bone, hair and feathers but also lipid-rich materials such as resins, waxes and oils as tempering-agents. If these organic materials were not entirely removed during the firing process, then there is the potential that they could complicate efforts to reconstruct pottery function based on organic residue analysis, i.e. making it difficult to ascribe the chemical signal to the use versus the manufacture of the ceramic vessel.
Firing temperatures play a key role in this issue as exposure to temperatures above 500℃ would be expected to ash any organic material with little retained in the clay. Although most ceramics required firing at temperatures in excess of this value, this can"t be assumed in all cases. Many examples of hunter-gatherer pottery were probably fired at temperatures below 600℃. In some areas of Alaska archaeological pottery was fired at particularly low temperatures due to a lack of fuel. Ethnographic information has indicated that in order to make these low-fired pots waterproof people used (sea mammal) oil and blood which they then mixed in with the clay, or applied as a coating.
In order to test the degree of this problem for the interpretation of lipid residue results, we designed an experiment where we mixed salmon oil with clay, as well as coated clay briquettes with salmon oil. The experimental ceramics were subsequently fired at different temperatures ranging from 200℃ to 800℃. Here we present the results of this experiment and discuss its implications for the interpretation of lipid residue results of nearly 60 ceramic vessels from Southwest Alaska.

Session • Microremains and residues

P–123

Dietary practice of Middle Copper Age populations in Eastern Croatia – evidence fromorganic residue analysis

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This research aims to contribute to our knowledge of dietary practices in the Middle Copper Age populations of Eastern Croatia. The Retz-Gajary culture dates to the second quarter of the 4th millennium BC in this region, and is part of a larger cultural complex typified by pottery having furrowed incision. The pottery assemblage is characterised by various jugs, deep pots and bowls which were decorated with incised or furrowed incised decorations, as well as apliqués. Handles are often present. Analised pots come from Retz-Gajary settlements located in the vicinity of the town of Osijek. Rescue excavations were carried out during the construction of the motorway and revealed settlements with large pit dwellings. Ceramic vessels and animal bones are abundant in the settlements, and complementary evidence from the zooarchaeological analysis and organic residue analysis (ORA) provided an excellent opportunity to study the dietary practice of the inhabitants.

Vessels were selected for ORA from three Retz-Gajary settlements, targeting different vessel typologies and vessel parts to potentially obtain a better understanding of function of the various pottery types. Lipids were extracted by direct acid extraction and extracts analysed using Gas Chromatography - Mass Spectrometry (GC-MS) and Gas Chromatography-combustion-Isotope Ratio Mass Spectrometry (GC-c- IRMS). Results show traces of possible ruminant animal fats, dairy fats and plant lipids. The presence of ruminant animal fats as well as dairy fats shows the importance of herding practices in these populations. Their subsistence economies were based on livestock breeding for meat and possibly dairy products as well as farming.

Session • Advances in metagenomics

P–124

Metagenomic analysis of dental calculus and teeth in ancient Egyptian baboons

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Recent studies have demonstrated that shotgun metagenomics of ancient dental calculus represents a thriving source to characterize the oral microbiota of hominins and humans, representing a track record of dietary behaviour and health status of ancient specimens. Dental calculus is known to form in a wide range of animals, such as domestic pets and non-human primates. Characterization of the animal oral microbiome has several implications, potentially informing on dietary shifts associated to feeding within the human food web on one hand, and on the origin and diffusion of zoonotic diseases on the other.

Here we show the preliminary results of shotgun sequencing analysis of dental calculus and tooth samples of 15 ancient Egyptian mummies of hamadryas baboons (*Papio hamadryas*) and olive baboons (*Papio anubis*) dated to the Late Period. Egyptians were renowned for their worship of animals and for keeping them as pets. Baboons and monkeys were sacred animals and object of a cult dedicated to the divinity Thot. The investigated specimens, that are curated at the Musée des Confluences in Lyon, originate from Gabbanat el-Qurud where they were held captive in temples. Palaeopathological analyses on the skeletal remains have shown that these baboons were not always treated well (healed fractures) and that the poor health conditions resulted in metabolic diseases (amongst others rachitis). As baboons did not occur naturally in Egypt, questions remain open about the place from which they were imported, either Nubia, the Horn of Africa or the Arabian Peninsula.

Our objective is to characterize the oral microbiome of captive baboons in ancient Egypt and investigate how the anthropogenic forces linked to captivity and disruption of baboons" social life in the wild affected the animals" biology.

Session • Mobility

P–125
Movement around a busy Byzantine Port City

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Stable isotope ratios of human remains have long been utilized by archaeologists as a pathway for studying topics such as migration and diet at the scale of the individual. Importantly, these data allow for the analysis of in-group variation in archaeological populations, something which often remains difficult to approach from the archaeology alone. Here, we analyze the δ13C, δ15N, δ2H and δ18O of human remains from Elaiussa Sebaste, a Byzantine harbor site in present day Turkey. Previous osteological research has suggested that the individuals in our sample—dated to the 6th century AD—were exposed to high levels of physical trauma and subsistence stress (Equini Schneider, 2010). Analysis of δ2H and δ18O will allow for the identification of possible migrants within the population, and the correlation of these data with δ13C, δ15N and osteological results will allow us to further investigate the relationship between mobility and chronic stressors in a population that lived at the fringe of the Byzantine empire.
Equini Schneider, E. (2010). Elaiussa Sebaste. III, L'Agora romana. Istanbul: Ege Yayınları.

P–126
No genomes, no genes – mtDNA d-loop diversity in Bronze Age alpine cattle

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During Bronze Age decisive economic and agricultural changes took place, which is also reflected in different crop plant and domestic animal compositions as before (e.g. millets, spelt, lentil, horse). In the Alps (Italy, Austria, Switzerland), settlements related to mining activities were established at high altitudes, their inhabitants in need of food resources. Whether this was accompanied by farming at high altitudes, increased transhumance of animals, adaptation/import of e.g. cattle specialized in grazing on alpine meadows, or transport of meat from the valley, is a matter of debate.
Here we use domestic animals as proxies for human actions and sequenced short fragments of mtDNA d-loop in 34 cattle from metallurgic sites in the Eisack valley, Italy and Savognin-Padnal, Switzerland. We found high diversity measures, the presence of cattle belonging to the main European T3 haplogroup variants but also to the rare T2 and Q haplogroups. Mismatch analysis indicates different population histories in the two regions.

P–127
Intra- and inter- tooth variation in strontium isotope ratios from prehistoric seals by laser ablation (LA)-MC-ICP-MS

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Strontium isotope ratios (87Sr/86Sr) in marine environments are considered to be homogeneous averaging 0.7092. However, in the Baltic Sea there is major influx of freshwater, since more than 50 rivers discharging into the Baltic drain sedimentary rock-bearing areas of the Baltic Shield with different geological origin and thus different strontium isotope ratios. This results in mixing of sea water and continental drainage, leading to regional variations of strontium isotopic ratios. The aim of this pilot study was to explore if these regional variations of Sr can be detected in marine mammals from archaeological sites in the Baltic Sea. This was investigated by performing a sequential measurement of 87Sr/86Sr ratios in tooth enamel from three seal species by using laser ablation MC-ICP-MS. An inter-tooth 87Sr/86Sr variation can be detected in marine mammals that lived in the Baltic Sea, suggesting that different Sr ratios can be detected in different regions of the Baltic Sea. Furthermore, an intra-tooth variation suggests possible different geographic origin or seasonal movement of seals within different regions in the Baltic Sea through their life time. The data show clearly that we deal with a non-homogenous strontium isotope ratio in the Baltic Sea Basin. Archaeological implications are discussed.

Session • Pathogen genomics

P–128

De novo assembly of a second pandemic plague genome and the genomic evolution of *Yersinia pestis*

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Yersinia pestis (*Y. pestis*), the causative agent of plague, has caused at least three historic pandemics and has infected humans as early as the Late Neolithic/Early Bronze Age (LNBA). The study of *Y. pestis* evolution has largely focused on the study of virulence factors showing the gain of plasmids (pPCP and pMT) and genes (e.g. ymt) with the combination of gene loss (such as flagellar genes), has shaped the *Y. pestis* genome to become the highly virulent pathogen we know today. Despite the fact that the genus *Yersinia* is known for genomic plasticity, few studies have focused on *Y. pestis* structural genome evolution. In this study, we combine *de novo* assembly of an ancient genome with a phylogeny-wide comparative analysis to gain insight into the structural genome evolution of *Y. pestis*. *De novo* assembly of ancient genomes has proven to be challenging due to the intrinsic characteristics of ancient DNA, such as short fragment length and low genomic coverage. Technological advancements in ancient DNA research coupled with its use in elucidating key aspects of *Y. pestis* evolution during the historic pandemics, have led us to the recovery of an exceptionally well-preserved *Y. pestis* genome from London, dating from the second pandemic. We have performed a *de novo* genomic assembly of an ancient variety of this pathogen. Various assemblers and parameters were tested to obtain the improve the quality of the assembly. This *de novo* approach opens the door to explore the structural genome evolution of an ancient *Y. pestis* strain, such as rearrangements. Furthermore, we attempt to explore the hidden patterns of genetic insertions and deletions in the *Y. pestis* phylogeny, and the content of particular functional gene groups that could help inform on changes in virulence of *Y. pestis* through time and space. The time transects in both the LNBA and the second pandemic periods allow us to trace insertions and deletions along the evolution of complete lineages. By this we aim to utilize ancient DNA data in a new way for a better understanding of *Y. pestis* genome evolution as a whole.

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Retrospective genomic DNA analysis from formalin-fixed wet specimens

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Analysing ancient and historic pathogen genomes provides researchers with a wealth of information about infectious diseases in the past and therefore plays an important role in the study of pathogen evolutionary genetics, immunity, and host-pathogen interactions.

Although bone samples are often used for ancient DNA studies on past pathogens, wet specimens from medical and pathological museum collections are also suitable for investigations of human infectious diseases. Formalin is the most commonly used fixative for tissue preservation. However, its strong inhibiting properties cause cross-linking between nucleic acid and proteins, rendering DNA unavailable for downstream applications. Therefore, sequencing data obtained from formalin-fixed tissues are low in quality and quantity.

In this project we collected ten samples from the pathological collection in the Narrenturm at the Vienna Museum of Natural History. The samples originated from autopsy material collected between 1851 and 1936 and are associated with diagnoses of tuberculosis, leprosy, or anthrax.

In order to reverse the formaldehyde induced cross-linking, we tested 11 DNA extraction protocols, including commercially available kits and modified protocols with cross-link reversing chemicals such as CTAB, DTT and PTB and testing various pre- and post-digestion treatments. We produced shotgun high-throughput sequencing data on selected samples and evaluated all DNA extraction protocols based on several quality criteria at key steps of sequencing library preparation and data analysis pipelines.

Regardless of extraction protocol, formalin-induced inhibition of DNA amplification was still present and double stranded library preparation is not really effective, there was no general change in the library complexity. We are, however, able to make recommendations for future work on historic pathogens using formalin-fixed wet specimens and are currently testing single stranded library construction method which is based on single stranded DNA ligation with T4 DNA ligase and shows more efficient results with highly degraded DNA samples.

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The consequences of near-extinction in the black rhinoceros (*Diceros bicornis* L.)

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Numerous animal species have become extinct or undergone severe population size reductions in the last few centuries due to anthropogenic pressure. It is widely accepted that the Earth is experiencing a sixth mass extinction. For those species facing the abyss of extinction due to a population collapse, conservation efforts need to account for, among other things, the genetic consequences of the decline.

The black rhinoceros (*Diceros bicornis* L.) is one of these animal species that has been subjected to an enormous anthropogenic pressure for the past 200 years, and the severe and rapid reduction in their population size has put them through an extreme population bottlenecks. The small population size of this critically endangered African mammal justifies the concern that genetic threats, e.g. inbreeding depression, might jeopardise its viability. Nonetheless, comprehensive insight into the genomic consequences of this population size collapse is still lacking.

Our study aims at comparing the genomic status of pre- and post-bottleneck black rhinoceros populations to assess the eroding effects of the demographic collapse on their genomic status. For that purpose, whole-genome shotgun data has been generated from >50 museum specimens and 24 modern samples from across their entire natural geographic range.

With these datasets we attempt to assess the genome-wide diversity, population structure, gene flow, and effective population sizes of black rhinoceros populations at two different time points. This comparative workflow will help elucidate to what extent a population collapse affects genomic diversity, and how connectivity among black rhinoceros populations has changed over time. Moreover, such a dataset has the potential to prompt a revision of the taxonomic status of this species.

Given the delicate situation of black rhinoceros populations, and the need to optimize the resources allocated for their management, it is imperative to have reliable population genomics information available. The outcome of this work will clarify the population genomic dynamics of black rhinoceros over the past 200 years, and thus provide a powerful tool for designing effective conservation plans.

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Civilization and natural selection in Europe – changes in biological pathways during the last 6,000 years

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Civilization has changed not only the social history of humans but also their evolutionary history. Cultural practices have modified dramatically the relationship between the environment and the human organism. To answer the question of how civilization in Europe has shaped the human genome, we traced the microevolution of modern Europeans back to 6,000 years to their ancestors, carriers of the Late Neolithic and Bronze Age cultures. We made a direct comparison of the published whole-genome data of ancient and modern groups. Assuming that natural selection should act through phenotypes, we analyzed possible genetic changes at the level of biological pathways, where the influence of individual SNPs is aggregated into functional groups.

We did not find any significant difference in the distribution of synonymous SNPs between the ancient and the modern Europeans, which corresponds to the hypothesis of neutral evolution for this type of mutations. At the same time, analysis of non-synonymous SNPs revealed that a number of biological functions in the organisms of Europeans have undergone significant changes. For most of these functions, non-synonymous mutations have been accumulated over the 6,000 years separating the Bronze Age and the modern time. These include metabolic transformations, immune responses including protection against pathogens, alloimmune and autoimmune reactions, signal transduction, physical activity, and sensory perception. Accumulation of non-synonymous SNPs in these pathways can indicate signs of either positive or relaxed selection. At the same time, we found a decrease in non-synonymous SNPs in the pathways responsible for reproduction and cognitive functions, which might mean negative or, on the contrary, strong positive selection in these processes.

Based on our results, we suppose that the most important civilization events that have affected the genomes of Europeans are changes in diet and the pathogenic environment, the introduction of xenobiotics, modifications in lifestyle and in the information background. Our results show that even during a relatively short period of time, the human genome can be significantly shaped by selection if the selection is induced by mankind.

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Grape growing in the in ancient Nubia – DNA analysis of the grape pips from Qasr Ibrim, Egypt

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Qasr Ibrim is at the border of modern Egypt and Sudan. It was inhabited as a frontier outpost during the New Kingdom and had been continually occupied by a sequence of cultures spanned from Napatan, Roman, Meroitic, Christian to Islamic. until the 19th century. Qasr Ibrim is also out of the optimal climate zone of wine grape (*Vitis vinifera*). With the biological remains of excavated from distinct cultural stratum, we would like to further explore how an agriculturally important species adapt to the new environment with artificial introduction and manipulation.

In this study, we sequence and compare archaeological sequence of *V. vinifera* from different strata with its modern descendants. With this dataset, we aim to 1) verify if it"s domesticated form of grape. If it is domesticated grape, are they use for eating or wine-making.2) test the grape from different strata are inherited or was brought to the location during cultural shift, 3) find out the potential genomic regions under selection, and 4) whether they have anything to tell us about useful genetic variation in a drought stressed world.

This project would provide a glimpse of the cultural transition. It would also offer an objective insight into how different these cultures really were when it comes to alcohol production.

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Paleogenomics, its power and its caveats – a case study of the evolutionary history and population dynamics of bison in Europe and its adaptation to climatic fluctuation

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Paleogenomics was supposed to yield more robust data than paleogenetic analyses relying on PCR amplification of genetic regions of interest. While this assumption is correct to some extent, how robust and reliable are the data themselves and the conclusions that can be drawn? Data published in the last two years on the European bison using both paleogenomics of ancient bones and genomics of present-day animals have reached different conclusions. In an effort to integrate all data and to identify underlying causes for these discrepancies, we reanalyzed and integrated all genomic data produced in the last two years and combined them with morphometric analyses of a large corpus of metacarpal bones. These analyses yielded new insights in the evolution of bison during the Late Pleistocene and the Holocene and allowed us to explore various caveats of the paleogenomic approaches that can sometimes lead to erroneous misleading conclusions.

The largest European mammal that survived into the present, the bison or wisent *B. bonasus*, appears in the fossil record with the onset of the Holocene, but its origin was not known. The fossil finds in Upper Pleistocene Eurasia have been mainly attributed to the steppe bison, *B. priscus*. Using paleogenomic analyses of the maternally inherited mitogenome, we uncovered complex population expansion, contraction and successions of various lineages in different geographical places on the Eurasiatic continent from MIS5 to MIS1 involving ancestors of the present-day European and American bison. In contrast, nuclear genome analyses reveal that regular gene flow occurred between these distinct populations, presumably mediated by males as it was not reflected in the maternal lineages. In accordance with this homogenizing gene flow, morphometric analyses reveal the high similarity of the various lineages that could not be distinguished on morphological grounds.

We further observed that a clear evolutionary understanding of population dynamics requires a very large sample size with a diversity of sampling in both space and time. Our analyses thus yield not only a comprehensive view of bison evolution during the last 150,000 years, but also bring useful insights in the limits of the current methods and strength of the conclusions that can be drawn.

Ref: Massilani et al., BMC Biology, 2016, 14:93; Grange et al., 2018, submitted

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Large-scale mitogenomic analysis of the phylogeography of the Late Pleistocene cave bear

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Since 1994 numerous interdisciplinary ancient DNA (aDNA) studies examined the evolution, phylogeography and extinction of the Pleistocene cave bear *Ursus spelaeus* senu lato. Considered as the Late Quaternary mammal that gave rise to the largest fossil record in Europe, the cave bear is a predestinated model to study the causes of the extinction of a species, especially in the context of population dynamics, climate instability and changing human impact. Despite its substantial genetic diversity and distribution, the cave bear became extinct at the beginning or during the last Glacial Maximum (LGM) similar to numerous other Pleistocene megafauna species. However, the timing of its final extinction as well as the ultimate cause, with climate and subsequent vegetation change in the context of its vegetarian diet or human hunting impact commonly regarded as main potential factors of different extant, remain subject of controversial debates. To shed light upon the cave bear population dynamics and phylogeography during the Late Pleistocene, we collected more than 120 fossils representing populations from a Europe-wide transect. Using a silica-based extraction protocol in combination with aDNA library preparation and in-solution target enrichment we were able to reconstruct 57 complete mitochondrial genomes and compare it to 69 published Eurasian cave bear sequences ranging from Middle Pleistocene to the Lateglacial. Our phylogenetic reconstructions reveal a noticeably more complex biogeography of the European haplogroups during the last 50 ka years than previously assumed. Furthermore, calculations of the effective female population sizes (Ne) indicate that the start of the cave bear population decline leading to its extinction is located at around 40 ka BP at the onset of the Aurignacian, coinciding with the arrival of anatomical modern humans in Europe. Thus, our study highlights the potential role of human activity in the general extinction and local extirpation of the European cave bear and illuminates the fate of this iconic megafauna species.

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Hunting four thousand years of walrus genomes across the Atlantic Arctic

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Genetic effects on animals that arise from human hunting have generally been poorly understood, specifically their exact nature, duration and scale. Until recently, evidence for the impact from human-animal interactions was limited to historical documentation, anecdotal recollections and inference from modern populations. However, population wide, ancient genomic studies are now revealing the impact of human activities on the evolutionary and ecological histories of animals.
This study is a unique contribution to understanding human-animal interactions. It focuses on the genetic changes that have arisen within a single species of marine mammal, the Atlantic walrus (Odobenus rosmarus rosmarus), across the species" range and throughout the entire period of human Arctic occupancy.
The Atlantic walrus was chosen given its importance in human cultural histories throughout the Arctic, its threatened status and ongoing exploitation. The species has been hunted since pre-Dorset human cultures first arrived approximately four thousand years ago in northern Canada and Greenland, as well as by early maritime cultures in modern day Norway. Subsequently walruses survived throughout Norse (Viking) seasonal hunting trips focused on valuable ivory, and more recent commercial exploitation by European whalers and sealers, who often concentrated their efforts into large catches of several thousand animals. Despite acknowledgement that human hunting is likely to have impacted the distribution, behaviour and abundance of walruses, especially during the last few centuries, the details and evidence to support such claims has previously been limited.
This presentation outlines the results from over 180 archaeological walrus samples which have been shotgun sequenced to characterise historic and prehistoric walrus populations throughout the Atlantic Arctic. Mitochondrial genomes have been analysed to reveal the population structure, connectivity and levels of diversity in the Atlantic walrus and its subpopulations across millennia. The geographic and temporal context associated with each faunal remain reveals the timing and spatial distribution of population declines, movements and restructuring. This is the first study to investigate the genetic impact of human activities on marine mammal genomes across their distribution and throughout their history of interaction with humans, and offers a unique insight into an iconic Arctic species' evolution alongside humans.

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Reconstruction of genetic diversity from ancient DNA prior to recolonization of nearly extinct Alpine ibex (*Capra ibex*)

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As mankind spread across the world, drastic demographic changes in large variety of species occurred. Some species went extinct, others survived only in small and bottlenecked populations. Even though some of these species recovered from the edge of extinction due to intense conservation efforts, a substantially depleted genetic diversity often remained. Such a species is the Alpine ibex (***Capra ibex ibex***), which encountered a reduction in census size since the 15thcentury and resulted in a strong bottleneck in the 19thcentury. The Alpine ibex survived only in a small population in the Gran Paradiso National Park in Italy. Reintroduction led to a recovery of the species all over the Alpine ridge but recent populations show extreme low levels of genetic variability. However, genetic analysis in other species revealed a depleted genetic diversity even before human induced bottlenecks occurred. In this cases Pleistocene glaciation-interglaciation cycles or subsequent response to Holocene changes in habitat distribution were considered as cause. Using an ancient DNA approach, we investigated how the mitochondrial genetic diversity of the Alpine ibex changed over a time to determine the cause of the depletion in genetic variability. We were able to reconstruct Alpine ibex mitogenomes from six ancient samples (3300 BP to 8600 BP) and five historic samples (75 BP to 251 BP). We found a substantial reduction of Swiss haplotype diversity because only one out of eight recovered haplotypes survived the bottleneck in the 19thcentury. Furthermore, we discovered a strong difference in mitochondrial nucleotide diversity from ancient specimens in contrast to historic and modern Alpine ibex individuals. This findings indicate that the low genetic diversity in recent Alpine ibex populations is rather due to human influence during the last centuries than environmental changes in the past.

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Fig 1

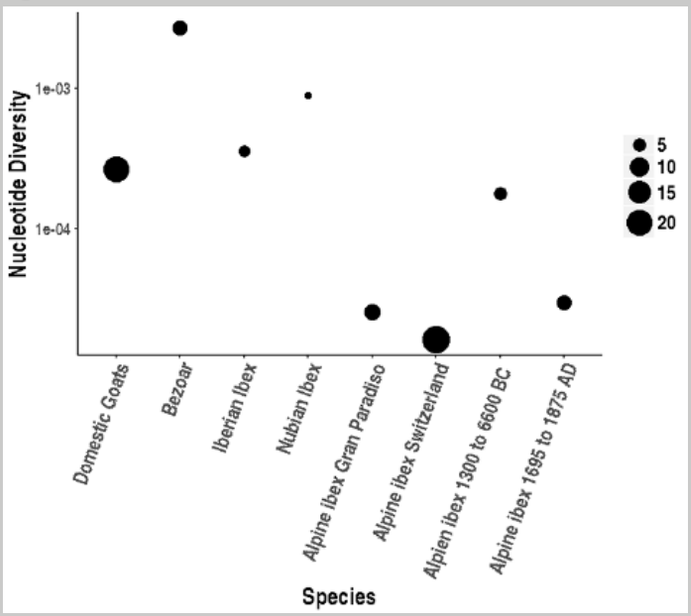
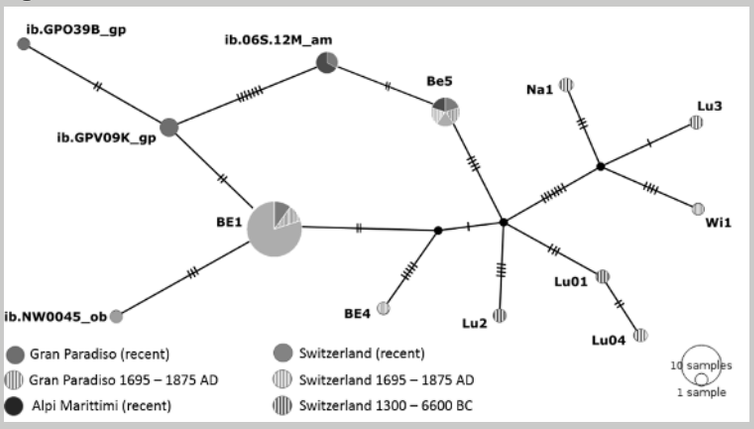


Fig 2



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Deified to extinction? – Conservation genomic and anthropological insights regarding royal Hawaiian featherwork

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Hawaiian featherwork, which predominantly exists in the form of capes and cloaks ('ahu'ula), constitutes a treasured element of Hawaiian cultural heritage. Feather artefacts curated in museums today date from the early 18th to the early 20th century and it is clear that their production required thousands of feathers from Hawaiian forest birds, which were craftfully attached to a netted backing of olonā fibre. These feathers were sourced from Hawaiian honeycreepers (Frigillidae:Drepanidinae) and Hawaiian honeyeaters (Mohoidae), birds that had sacred meaning to Native Hawaiians. In the present day, many of these bird species are either in decline or extinct. It is unclear to what extent featherwork manufacture contributed to their declines, given a backdrop of dramatic ecological impacts to their forest habitat associated with colonisation of the Hawaiian islands by Polynesians and then Europeans. We investigate this using both a non-invasive, museum collection-based approach (counts of feathers on 'ahu'ula, followed by extrapolation to total birds exploited) and genomic analyses (DNA extraction from individual feathers, followed by targeted capture and high-throughput sequencing). For the genomic work, we have made use of contemporary samples for the extant species, museum toepad specimens from the 19th and 20th centuries, as well as the unique source of DNA that are loose feathers from the 'ahu'ula themselves. We have created a population genomic framework within which data from cape feathers can be placed. Not only does this shed light on genomic diversity of the bird species at different historical time points, but it also provides clues regarding provenances of birds used in 'ahu'ula.

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Subsistence practices, past biodiversity, and anthropogenic impacts revealed by New Zealand-wide ancient DNA survey

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New Zealand"s geographic isolation, lack of native terrestrial mammals, and Gondwanan origins make it an ideal location to study evolutionary processes. However, since the archipelago was first settled by humans 750 years ago, its unique biodiversity has been under pressure, and today an estimated 49% of the terrestrial avifauna is extinct. Current efforts to conserve the remaining fauna rely on a better understanding of the composition of past ecosystems, as well as the causes and timing of past extinctions. The exact temporal and spatial dynamics of New Zealand"s extinct fauna, however, can be difficult to interpret, as only a small proportion of animals are preserved as morphologically identifiable fossils. Here, we conduct the first large-scale genetic survey of sub-fossil bone assemblages to elucidate the impact of humans on the environment in New Zealand. By genetically identifying over 5000 non-diagnostic bone fragments from archaeological and palaeontological sites, we reconstruct a rich faunal record of 110 species of birds, fish, reptiles, amphibians, and marine mammals. We report evidence of five whale species rarely reported from New Zealand archaeological middens, and characterize new extinct lineages of leiopelmatid frog (*Leiopelma* sp.) and kākāpō (*Strigops habroptilus*) haplotypes lost from the gene pool. Taken together, this molecular audit of New Zealand"s sub-fossil record not only contributes to our understanding of past biodiversity and pre-contact Māori subsistence practices, but also provides a more nuanced snapshot of anthropogenic impacts on native fauna following first human arrival.

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The complex history of human inflammation regulatory genes

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Humans live in extremely diverse environments, spanning extreme heat and cold, arid and humid conditions. In addition, the transition to farming and other cultural and demographic processes in the past exposed humans to novel diets and pathogens. These changes would have presented both challenges and opportunities, and set the stage for adaptations across the human genome. The skin and epithelial are the interface to the environment, and inflammation response is in the first line of defence against pathogens and foreign substances entering the body. In this talk I will focus on genes involved in skin inflammation response to illustrate how these genes, and how their expression is regulated, show a pattern of deep and complex evolution that has left a legacy in the genetic composition of modern populations around the world and may explain why some individuals are more susceptible to diseases linked to these genes (such as severe psoriasis) than others.

P–140
Reduced mtDNA diversity in Javan rhinoceros (Rhinoceros sondaicus)

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Javan rhinoceros (*Rhinoceros sondaicus*) is one of the five extant rhino species and is considered as one of the rarest large mammals on earth. Once widespread in all South-East Asia, *R. sondaicus* is currently on the verge of extinction with only one population (less than 100 individuals) in the wild on the island of Java, Indonesia. To assess the past genetic diversity of the female lineage of *R. sondaicus* we have collected bone samples from eight museum specimens dating back to the 19th century, i.e. before the range of the Javan rhinos were dramatically reduced. The samples were used for ancient DNA analysis and compared with the modern mtDNA sequences of *R. sondaicus* and other rhinos. Out of eight museum samples we succeeded in reconstructing five full and three partial ancient mtDNA sequences which more than doubles the number of published full mtDNA sequences of *R. sondaicus*. We used BEAST v1.8.4 to assess the phylogenetic relationship of the five extant rhino species and the ancient samples. The results showed that the oldest and most diverse mtDNA lineages of *R. sondaicus* were represented by only ancient samples indicating a significant reduction of mtDNA diversity of modern Javan rhinos.

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Punctuated evolution of the genus Homo: Evidence from mtDNA pseudogenes

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Whether evolution is a gradual or a punctuated process have been a subject of long-lasting debate. One way to address this issue is to ask whether mutations, i.e. the molecular basis of evolution, accumulate at a constant rate or accelerate at critical points in evolution. This is not an easy question, because usually the time of past mutational events is not known with any precision. Fortunately, exceptions from this rule do exist.
NUMTs , i.e., fragments of mtDNA have been inserting into the human nuclear genome over the entire evolutionary history of our species (as well as most other eukaryotic species). Formally, NUMTs are insertion mutations. However, because of their homology to mtDNA, sequences of NUMTs can be positioned as branches on the mtDNA phylogenic tree. mtDNA is a well behaved evolution clock, therefore branching points on mtDNA tree can be timed with considerable precision. This includes branching points of NUMT branches and therefore the NUMT insertions so can be timed with some precision. Using this principle we have determined the times of insertion of each pseudogene from a set of 18 human NUMTs that have been inserted within last 6 My and have passed our quality control criteria.

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We then asked whether these 18 NUMTs were inserted at a constant rate and in particular, whether NUMTs" insertion rate increased around 2.8Ma, which is a well documented period of speciation of the genius *Homo* from *Australopithecus* and a time of global climate change. Indeed NUMT insertion times appear to cluster around that interval (Figure 1). To determine whether appearance of this cluster around 2.8Ma is a statistically significant event, we performed a numerical simulation under null hypothesis of uniform insertion rate and demonstrated that the cluster is highly significant (p~0.001) and remains significant within a wide rnge of assumptions.

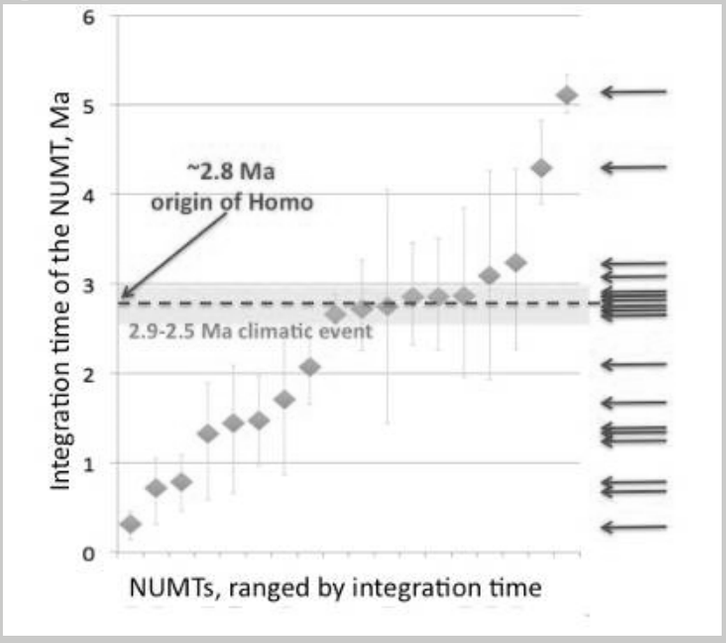
In conclusion, an uneven rate of insertion of NUMTs into human nuclear genome over the last 6 My corroborates the punctuation evolution or the "turnover pulse" hypothesis with respect to the evolution of the Genus *Homo*.

Reference: Such cluster of insertions constitutes and increase of insertion rates, in which corroborates the punctuated evolution hypothesis.

References:

Gunbin et al Mitochondrion (2017) https://doi.org/10.1016/j.mito.2016.12.001
Gunbin et al. Data in Brief (2017) https://doi.org/10.1016/j.dib.2017.05.024

Fig 1



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"mtDNA fossils" suggest distant interspecies interbreeding, mtDNA introgressions and "recombination" in our hominine ancestors

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Interspecies Hybridization. Evidence accumulates to support relatively recent genetic exchanges between *Homo* lineages (e.g. Humans, Neanderthals and Denisovans). Less is known about earlier exchanges involving more divergent lineages. Phylogenic analysis of nuclear pseudogenes of mtDNA (NUMTs) provides insight into such events. For example, copies of a NUMT residing on chromosome 5 in humans, chimps and gorillas (H,C,G) share a very long common stem, which appear to be comprised mostly of mitochondrial (*not* pseudogenic), highly synonymous, mutations worth ~4My of divergence (Figure 1A). This suggests that this NUMT has arisen in a now extinct hominine species that have separated from the ancestral HCG population about and have independently evolved for 4My at which point parts of its mitochondrial genome should have given rise to the NUMT on chromosome 5. Then individuals from this species must have interbred with the still not completely divided HCG population (Figure 1B) and in this way "delivered" this NUMT to Human, Chimpanzee and Gorilla. We show that phylogeny of this NUMT is unlikely a result of large effective population size or branch length artifacts. Reassuringly, interbreeding across comparable genetic distance has been shown in other primates, including baboons and colobines, so such a large genetic distance does not preclude such an event.

Traces mtDNA introgression and "recombination". The possibility of a distant interbreeding in the human lineage suggests an elegant explanation to "phylogenic mosaicism", an intriguing property of the great ape mtDNA. Interestingly, different regions of ape mtDNA appear to follow different phylogenies (Figure 2). In nuclear DNA, neighboring loci with highly divergent phylogenies are ordinary result of recombination. Although there is no standard recombination in mtDNA, there is ample data supporting the existence of repair-driven exchange of segments between mtDNA molecules. The difficulty of creating *observable* "recombinant" mtDNA (Figure 2A) is in bringing highly divergent mtDNA genomes into contact in the same cell. We hypothesize that such contact have happened during introgression of gorilla into the human/chimp ancestral population around the time of the H/C split. Rare paternal inheritance of mtDNA would have produced heteroplasmic individuals carrying both the G and the HC mtDNA types in whom a mosaic mtDNA precisely of the type observed in human and chimp (Fig 2A) would be created.

Reference:

Popadin et al. 2016 BioRxiv https://doi.org/10.1101/134502.

Session • Genetic adaptation and evolution, ecology and extinction

Fig 1

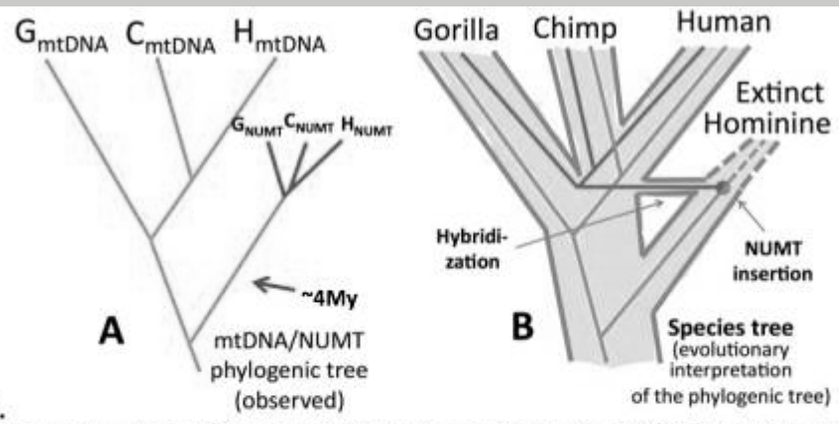


Figure 1.

A: Joint phylogeny of great ape mtDNA and a particular nuclear pseudogene of mtDNA (NUMT) located on chromosome 5. Note the disproportionally long (~4My) common stem of the NUMT subtree (red arrow). Note that this stem is painted green to reflect that it is "mitochondrial", i.e. mutations comprising this stem are highly synonymous, similar to other mitochondrial branches (green) and in contrast to highly non-synonymous mutations of the purely pseudogene branches (red). Pseudogene branches are short because mutational rates of mtDNA sequences after translocation to the safer nuclear decrease.

B: An interpretation of the phylogeny in *panel A*. Thick grey branches cartoonishly represent species and the entire sets of their genetic loci. We propose that the long mitochondrial stem of the NUMT subtree has evolved as a mitochondrial lineage in a now extinct hominine species, where it has been also inserted into nuclear DNA as a NUMT. The hominine species hybridized with the human/chimp/gorilla (HCG) ancestral population and brought the NUMT which them. Note that hybridization over 4My of separation has precedents in higher primates. We propose that positive selection of the NUMT (due to its effect on the expression of a nearby essential locus) helped it to get fixed in the HCG population.

Fig 2

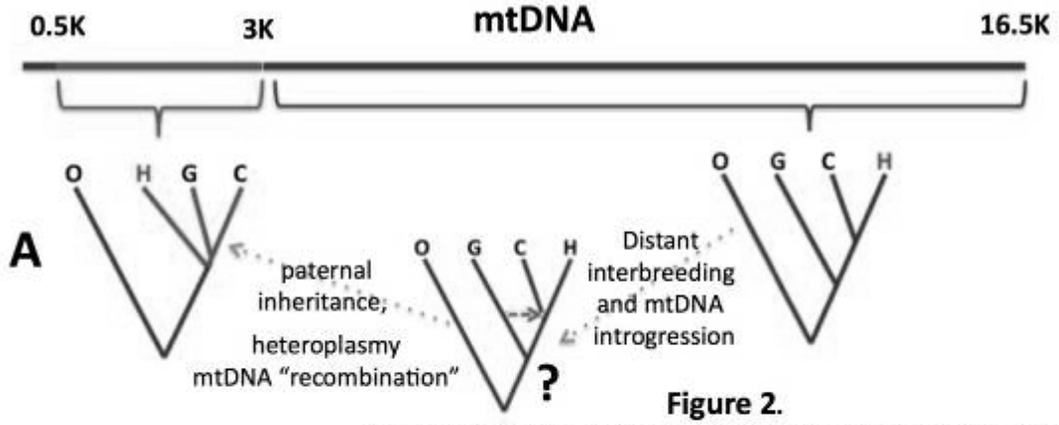
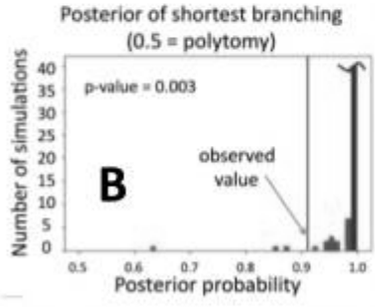


Figure 2.



A: A segment of mtDNA shows a unique phylogeny (i.e. *trifurcation*: same time separation of human , chimpanzee and gorilla (H, C, G) lineages. In contrast, the rest of the mitochondrial genome supports separation of gorilla 2-3 My prior to the H/C split. As a possible explanation we propose the Interbreeding/ introgression/recombination hypothesis. If gorilla introgressed and interbred with HC ancestors around the time of H/C split, the mtDNA brought by introgressors would follow the (H,C,G) trifurcation scenario, while mtDNA of the HC population would follow the G(H,C) phylogeny. Both types of mtDNA would be temporarily present in the population during introgression which, through rare male mtDNA inheritance would create heteroplasmy of the two types and allow their "recombination" (i.e. repair-driven exchange of mtDNA segments). This would result in the observed "phylogenetic mosaicism".

B. Reshuffling significance test. HCG MtDNA sequences were randomly reshuffled 1000 times trees were constructed on a 2.5K segment using Mr. Bayes. Phylogenic mosaicism was measured in each case (as the opposite of the posterior probability of the shortest branch). There were 3 cases that were more severe than the observed mosaicism.

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P–143

AmtDB – hand-curated database of ancient full mtDNA sequences and sample descriptors (amtdb.org)

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In recent years number of ancient DNA studies, amount, and quality of ancient DNA samples have been constantly rising. Thanks to advances in ancient DNA isolation and sequencing techniques, today we are able to access the population variability of many ancient populations. In most of the published studies the samples from Eurasia are being studied, with the focus on end of Pleistocene and beginning of Holocene. Today, autosomal SNPs and uniparental markers, Y chromosome or mitochondrial DNA, provide valuable insight into ancient population genetics. So far, the genotypes of few thousands of prehistoric samples have been published. For researchers, this provides a challenge, as the sequences and additional information about each sample are spread across many publications, in many different formats and places. That"s why we have created a database of ancient human full mitochondrial genomes, where researchers can find the mtDNA sequences and associated sample descriptors. AmtDB database is hand-curated and can be found at http://amtdb.org.

AmtDB has entered early access phase, v1.000, and contains 1107 ancient samples, out of that 887 with full mtDNA sequence. Ancient mtDNAs in FASTA format are ready to be downloaded, together with the metadata provided. The metadata descriptors include sample identifiers, country, continent of origin, latitude and longitude, region, archaeological site, culture, epoch, sex, mitochondrial haplogroup, Y haplogroup and haplotype, sample age (calibrated BCE or CE values, wherever possible), reference name + link, sequence data link.

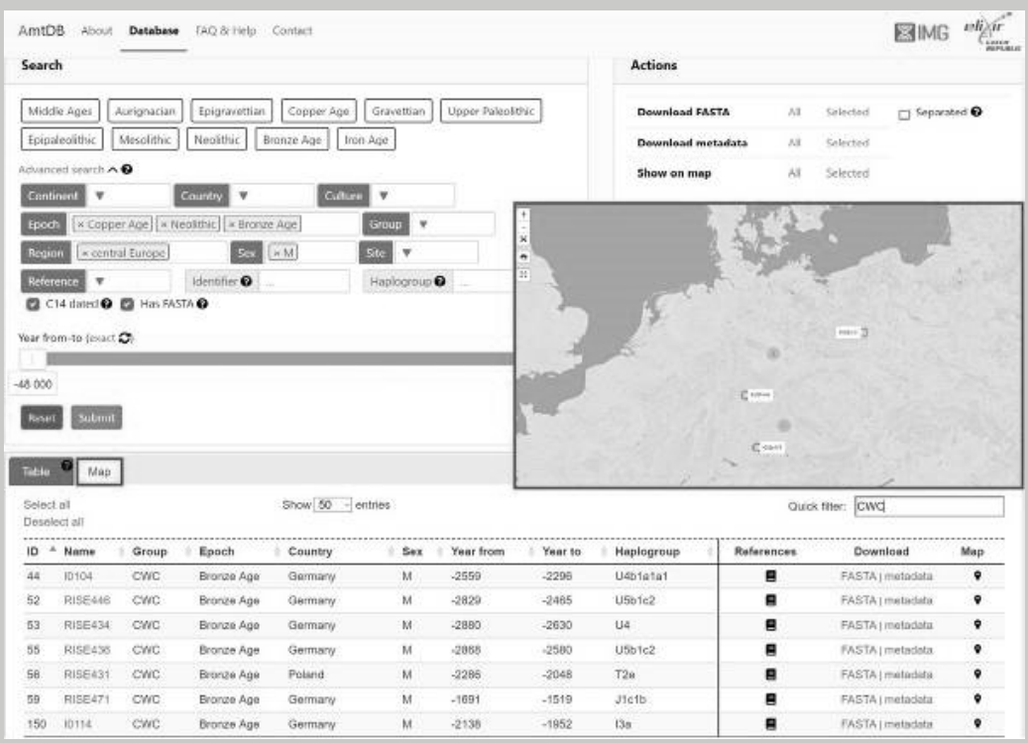
Following figure, Fig. 1, shows the main functionality of our search engine. We have filtered the database for Copper Age, Neolithic and Bronze Age samples from central Europe. We want only male samples, with 14C dating and full mtDNA in FASTA. From the 39 samples, we have further selected only Corded Ware associated sample with the "Quick filter" option. Location of the samples can be displayed on a map (preview in marked in red). Maps of selected samples (with several available overlays) can also be downloaded.

We hope the community of biomolecular archaeology researchers will find AmtDB useful, as currently there is not any comparable database in terms of usability and data content available.

This study was supported by ELIXIR CZ research infrastructure project (MEYS Grant No: LM2015047).

Fig. 1 – AmtDB (amtdb.org) advanced search screenshot.

Fig 1



Session • Deep human population prehistory

P–144
Population transformations in the 6000-2000 BC period of the Carpathian Basin

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Here we present the population versus cultural dynamics of Neolithization and later prehistoric times in the region of today"s Hungary. We use a high-resolution genome-wide ancient DNA dataset with over 100 samples from the Neolithic, Chalcolithic and Bronze Age periods (ca. 6000–2000 BC), carefully selecting from a series of succeeding archaeological cultures. We find that Neolithic genetic diversity was shaped predominantly by local processes, with slightly different sources and proportions of hunter-gatherer ancestry compared to other regions of Europe. The most probable scenario for a Neolithic population transformation in the Carpathian Basin was an initial (small-scale) admixture pulse between the farmer and hunter-gatherer populations that was followed by continuous gene flow over many centuries. The admixture between groups with different ancestry profiles was pervasive and resulted in observable population transformation across almost all cultural transitions. At the end of the Chalcolithic period new migration waves reached the Carpathian Basin from East (Yamnaya) and Northwest (Bell Beaker). The Early Bonze Age newcomer individuals lived in the Beaker culture complex began to admix with the descendant of the Neolithic farmers, and the new steppe type genetic ancestry reformed the genomic structure of the successor Bronze Age populations.
Our results published in Lipson & Szécsényi-Nagy et al. 2017 and Olalde et al. 2018 Nature papers demonstrate the potential of time-series-based sampling and modelling approaches that clarify multiple dimensions of historical population interactions.

P–145
Reconstructing the time scale of deep human population separations using modern and ancient genomes

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Analytical methods based on the sequentially Markovian coalescent, including PSMC and MSMC, can be used to infer effective size and separation histories of populations in deep time based on the distribution of coalescence times between small number of chromosomes. These methods have proved highly fruitful for studying the demographic histories of present-day human populations, but application to ancient genomes is challenging because such data typically have higher error rates at CpG dinucleotides, often are of lower coverage, and lack haplotype phase information. We explore ways in which to circumvent these issues. By calibrating a transversions-only mutation rate and ignoring transition mutations, we bypass the confounding effects of ancient DNA damage. Using modern genomes experimentally phased using linked-read technology, we avoid biases arising from poor haplotype phasing. We also make use of male X chromosomes, which are necessarily perfectly phased. Our results suggest that the deepest splits between present-day modern human populations occurred ~150-200 thousand years ago in Africa. Applying these methods to archaic human genomes, exploiting their low heterozygosity, we obtain split time estimates between these and modern humans, and recover signals of Neanderthal gene flow into non-Africans ~50 thousand years ago. We also compare our empirical results to simulations to explicitly test models on the timing of early human evolution.

Session • Diet and nutrition

P–146

Diets and physiological stresses of mummies (3800BP) at the Xiaohe site, Xinjiang by isotopic analyses of hair series

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Xinjiang is located in the heart of the Eurasia, connecting the East and the West. Since the Bronze Age, it had become a hotspot for crops and humans to move westwards or eastwards. Recent studies have showed the the eastern Xinjiang witnessed the eastward expansion of millet agriculture and Mongolian and that humans consumed substential millets in the early Bronze Age. However, the fluctuation of millet consumption and physiological stresses of those humans are still unknown. In this presentation, the searial sampling of human hair of 4 individuals at the Xiaohe Site, Xinjiang dated to c. 3800BP were undertaken for stable isotope analysis. the isotopic data indicated that the millet consumption was variable and played an important role before their death. On the other hand, the high-resolution isotopic variations suggested that humans had different physiological stresses during their lives. This pilot study will be quite helpful to understand the westward radiation of millets originated from China to Central Asia and Europe and the roles played in the Normadic lives better.

P–147

Bone collagen stable isotope analysis of a Bronze Age site of Liushugou in arid northwest China and its implication for subsistence strategy

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Liushugou consists of both semi-sedentary residential space and burial zone was a Bronze Age agropastoral community (3.5-2.9 cal ka BP). This study focused on bone carbon and nitrogen stable isotopic analysis of both human and faunal assemblage, by virtue of marcobotanical result, attempting to understand how these people responded to the harsh environment and thus source scarcity, and eventually overcame all and made a living in a valley for several centuries. The Liushugou population developed a mixed economy combined animal husbandry, sheep/goat herding, hunting as well as farming to adopt the circumstance. Stable isotopic results revealed that the inhabitants of this site have high animal protein in diet with mean δ13C value of -18.1 ± 0.4‰ and mean δ15N value of 13.1 ± 1.5‰ (n = 46). Sheep/goats served as their dominating livestock and also the primary food source which produce a mean δ13C value of -17.8 ± 1.2‰ and a mean δ15N value of 8.3 ± 1.7‰ (n = 37). Cattle was the second favorite in number output a mean δ13C value of -19 ± 0.6‰ and mean δ15N value of 8.9 ± 1.8‰ (n = 11). Wild animals like boars, deer, antelope, goral and hare were also explored as protein sources. Test flotation result demonstrated that if there was no other cereals, at least barley was grown there, implying they were no pure pastoralists. It is worth to mention that, one human first thoracic vertebrae sample was found on the floor of residential chamber 2, which is highly unusual and may suggest a violent past.

P–148

Diet reconstruction of Ancient population from Banlashan Cemetery, a Neolithic site of Hongshan Archaeological culture in Northeast China – evidences from Stable Isotopic and dental microwear analysis

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Hongshan culture is one of the most important Neolithic archaeological cultures in Northeast China. The diet of the late Hongshan population can be effectively reconstructed through integrating stable isotopic analysis with dental microwear analysis (DMA). The analysis of stable isotope shows that the δ13C value is between the range of -11.1‰~ -8.4‰, and the average value is -9.6±0.8‰, which means the diet structure of the Hongshan population should be subject to C4 plants or the animals feed on C4 plants. The mean value of δ15N was 9.1±0.3‰, indicating that the animal protein accounted for a high proportion. For dental microwear analysis, first or second permanent molars belong to 13 individuals of Banlashan population were analysed, the ratio between the length of the horizontal scratches and the length of the vertical scratches (LH/LV) is 87.14%, which is close to the ratio of that from Vedda and Andamanese population. It indicates that the population of the late Hongshan Culture in the Daling River basin not only planted crops and raised livestock, but also retained the tradition of hunting. The results of this study also show that the diet reconstruction of ancient population via a variety of methods is of great significance to the recovery of the economic structure and the status of social development.

Session • Diet and nutrition

P–149

Modeling the formation of growth layers in human teeth – toward more precise isotopic reconstructions of weaning ages by sequential sectioning of tooth dentin

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Stable isotope analysis of dentin serial sections of permanent human tooth has recently proposed as a powerful method to reconstruct chronological dietary change in infancy and childhood, especially for breastfeeding and weaning patterns. By sectioning dentin horizontally in approximately 1 mm thick and analyzing the sections sequentially, dietary change during the period of tooth formation can be reconstructed. The number of research that adopts this method increases. However, human tooth dentin grows like stacked cones, and the growth lines (i.e, Andersen lines) run obliquely compared to the sampling planes. Because these lines are cut horizontally in the existing common method, the derived isotope ratios of individual sections do not represent accurate dietary change but represent moving averages. In this study, obliqueness of dentin growth lines, changes in dentin secretion rate, and dentin outer shape are modeled mathematically, and its effects on stable isotopic reconstruction of weaning ages are discussed. The results of this study suggest that reconstructed weaning ages from the stable isotope ratios of sequentially sectioned tooth dentin deviate from the true weaning ages in a certain condition. Better sampling methods or mathematical models are needed to interpret the stable isotopic results of tooth dentin serial sections more precisely.

P–151

Carbon and nitrogen isotopic analysis of dentine serial sections from two Medieval sites (Prague, Czech Republic) with distinct demographic structure, adult dietary behavior and health status

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This study is focused on the early Medieval (9th-10th century AD) sites from the hinterland of Prague castle. Though these appeared similar from the archaeological point of view, striking differences between both sites were found during the bioarchaeological study. The Milady Horákové cemetery showed atypical demographic structure together with high incidence of skeletal pathologies and dental anomalies. None of these features was observed at Střešovice site. Also adult dietary behavior differed between both sites, especially in males. Thus the aim of this study was to explore if the early life experiences differed between these two sites.

First permanent molars of 12 individuals from Milady Horákové and 13 individuals Střešovice were sampled for carbon and nitrogen isotopic values of dentine serial sections. Their age-at-death varied from 4-5 to 40 years. Collagen was extracted using Method 2 described by Beaumont et al. (2013). The sampling strategy by Henderson et al. (2014) was then applied, sectioning the demineralised dentine into 10 horizontal strips (in case of fully developed teeth).

All the individuals show the increased $\delta^{15}N$ in the earliest dentine slices, attributable to the trophic level effect of breast-feeding. The corresponding rise in $\delta^{13}C$ is observed only in a part of the individuals, but the varying consumption of millet has to be taken into account as a confounding factor.

There is considerable variation in the magnitude and timing of decreases in $\delta^{15}N$, corresponding to weaning process, which will be discussed in relation to various factors, especially age-at-death.

The isotopic values from later forming tooth slices (reflecting the post-weaning period) show the same pattern as observed in adults: higher isotopic variation in terms of both carbon and nitrogen and at average lower $\delta^{13}C$ and $\delta^{15}N$ in Milady Horákové sample.

This study was supported by the Grant Agency of the Czech Republic (Grant number: 14-36938G) and Ministry of Culture of the Czech Republic (Grant number: P15/01IG-KA and DKRVO 2017/18 and 2018/17, National Museum, 00023272).

Session • Diet and nutrition

P–152
Sampling to preserve – isotopic studies of Finnish inland "Vikings"

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Introduction This contribution presents the first stable isotope study focusing on the Viking Age in Finland. We have studied a cemetery called Luistari in Eura. The past excavations have yielded over 100 Merovingian and almost 400 Viking Period graves, making Luistari a key site for the Finnish research. The fragmentary, but partly well-preserved skeletal tissues are rare, invaluable finds for bioarchaeological research. As such, they are subject to high research interest and sampling pressure, foreseen to increase in the future as new methodologies are developed.
Objectives Our aim was to depict the origin, climatic backdrop and nutritional habits of the Luistari people by utilizing multiple stable isotope analyses. Further, we wanted to heed the conflicting interests of exhaustive isotope analytics, and the need to preserve precious archaeological remains for posterity. To reach our objectives, we 1) analyzed the isotope composition of Luistari skeletal remains using conventional "bulk" methods, and 2) developed a new method to sequentially extract both the organic and mineral phases of a bone sample for stable isotope analysis.
Methods Depending on the preserved elements, we used isotopic analyses of $\delta^{13}C$, $\delta^{15}N$, $\delta 18O$, and $\delta^{34}S$ to study 75 humans buried in Luistari. Altogether ten Viking Period individuals, six women and four men, were further selected for dentine serial sampling. From 2 to 8 microsamples were taken from the permanent molars. A novel sequential sampling method was used to extract both organic (collagen) and mineral (bioapatite) phases for stable isotope analysis. The method allows the determination of C_{coll}-, N_{coll}- and O_{PO4}-isotope composition from a 2 mg subsample.
Results Our results reveal the use of high trophic-level protein sources during the childhood, likely the exploitation of fish. Intra-individual variation of up to 1.8‰ in $\delta^{13}C$ and up to 3.0 ‰ in $\delta^{15}N$, indicates probably both the weaning effect and dietary shift. Among the sampled humans there are individuals whose $\delta^{13}C$ values are high, up to -18.2 ‰, in comparison with the analyzed bulk data, with typical $\delta^{13}C$ values <-19.5 ‰. Likely this is due to consumption of marine fauna, but eating anadromous fish is also a noteworthy explanation.
Conclusion Despite the small sample population, our results show that individual diet development was not homogenous. The considerable isotopic variation implicates possible seasonality in diet and perhaps movement between inland and coast.

P–153
A late Mesolithic and early Neolithic isotopic baseline for southern Scandinavia

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The investigation of the Mesolithic-Neolithic transition (c. 4000 BC) in southern Scandinavia has advanced considerably since 1851, when the Mejlgård shell midden was excavated by the so-called first Kitchen Midden Commission. The Danish area offers tremendous potential to further this line of research, given its impressive archaeological record for the transition from hunting and gathering to agro-pastoralism. While several human remains from the late Mesolithic Ertebølle (5.400-4.000 BC) and early Neolithic Funnel Beaker (4.000-2.800 BC) cultures have undergone isotope analyses to investigate the radical change in the diet identified by Henrik Tauber in the early 1980s, the number of analysed animal bones is comparably low. As a result, our understanding of the specific contribution of different animal foodstuffs to human diets during the Mesolithic-Neolithic transition remains low. This paper discusses how we may improve the isotopic baseline to enable a better interpretation of the Ertebølle and Funnel Beaker diets using carbon and nitrogen isotope analysis on bone collagen. The work is ongoing, but so far 133 animal bones have been analysed along with 20 human remains. The sampling has targeted preferentially animal taxa for which little data are available (e.g. birds and cetaceans), but also seeks to improve the distribution of isotope values across present-day Denmark to account for regional or topographical variability. The improved isotope baseline produced by our project, will enable us to apply Bayesian mixing models for a more detailed interpretation of the carbon and nitrogen isotope record of the Ertebølle and Funnel Beaker cultures. This approach is aimed at reaching a better understanding of the dietary change that occurred at the Mesolithic-Neolithic transition and, specifically, to investigate the reliance on aquatic resources by early Neolithic people in southern Scandinavia.
Funding: This work is part of the Ph.D. research by R.M., which has been funded by the Aarhus University Research Foundation through a grant awarded to M.A.M. for the project (n. 21276) titled Danish and European Diets in Time.

Session • Analytical methods in population genetics

P–154

MITOMIX, an algorithm to reconstruct population admixture histories indicates Ancient European ancestry of Modern Hungarians

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Background: We present a primary report on a novel population genetic distance named Shared Haplogroup Distance (SHD) and a new algorithm (MITOMIX) to analyze admixture of populations. We provide comparison to F statistics (F_{ST}), the most widely used approach in population genetics which is based on idealized models (assuming isolated, stationary or equal sized populations). In contrary, the only premise in SHD calculation is that shared haplogroups have common origins, which link populations in an extent proportional to their shared haplogroups. SHD is a true mathematical distance that complies with all metric axioms, and enables global minimum optimization of hypothetical admixtures. Based on this approach, MITOMIX algorithm provides a hypothesis-independent search and admixture ratio for the best linear combination of populations without any preselection of potentially admixing partner-populations.

Results: In order to show that MITOMIX can reveal complex genetic relations, we carried out in-depth analysis of modern Hungarians (presenting 272 new full-length mtDNA genomes) and also present the admixture results for 87 (62 modern [12,261 samples] and 25 archaic [629 samples]) populations. MITOMIX analysis revealed that admixture is a general process between neighboring populations, but it was also able to indicate admixture between migrating populations.

Conclusion: SHD and MITOMIX analysis comply with known genetic data and shows that in case of closely related and/or admixing populations, SHD gives more realistic results and provides better resolution than F_{ST}. Our results suggest that the majority of modern Hungarian maternal lineages have Late Neolith/Bronze Age European origins partially shared with modern Danish, Belgian/Dutch and Basque populations, and a smaller fraction originates from surrounding populations. However only a minor genetic contribution (<3%) was identified from the IXth century Hungarian Conquerors whom are deemed to have brought Hungarians to the Carpathian Basin. Our analysis shows that SHD and MITOMIX can augment previous methods by providing novel insights into past population processes and offers an affordable substitute to the costly whole genome admixture analysis, especially for highly degraded archaic samples. Furthermore it could be also applied to the analysis of other non-recombinant haploid loci (Y chromosome, chloroplast DNA), which would be valuable in studying paternal lineages or plant population dynamics.

P–155

Ancient DNA phylogenomics using DNA capture and maximal information (super)trees

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Ancient DNA has long been used to resolve phylogenetic relationships between extant and extinct taxa. However, in the palaeogenomics era, phylogenomics has lagged behind other ancient DNA applications such as population genomics and palaeomicrobiology. Phylogenomic methodologies are sensitive to the high rates of missing data typically encountered in ancient DNA datasets and are computationally cumbersome. Hybridization capture technologies have alleviated, but not resolved, these issues. Supertree methods permit the circumvention of incomplete data matrices and can help resolve the computational limitations of these datasets. Here I describe the package *BaitsTools* – software developed to generate hybridization capture baits – and phylogenomic analysis of captured ancient DNA datasets using maximal information (super)trees.

Session • Analytical methods in population genetics

P–156

Y chromosome of ancient samples – NGS approach associated with target enrichment method

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The human Y-chromosome differs markedly from the other chromosomes in inheritance, size, genomic structure, content and evolutionary trajectory. The Y-chromosome is passed down from father to son and escapes the reshuffling effects of crossing-over with the exception of the two pseudo-autosomal regions (PAR) of XY sequence homology at the tips of the arms, which are required for proper chromosome segregation during meiosis. Due to its features, the Y-chromosome represents a powerful tool for analyzing the paternal ancestry of human populations and is a popular marker in population genetics. Methodological improvements and the advent of Next Generation Sequencing -NGS- technology have made possible also the nuclear DNA analysis in ancient samples, allowing to obtain enough molecules to permit whole genome analysis and minimizing artefacts owing to contamination and damage. To increase the fraction of sequenced molecules that align to subsets of the genome of interest, a standard tool in ancient DNA analysis has become target enrichment via hybridization capture that simultaneously allows to genotype hundreds of thousands of single nucleotide polymorphisms (SNPs). Therefore, in order to study paternal lineage in ancient DNA samples, approximately 30,000 phylogenetically informative markers located on Y chromosome were selected to develop approximately 40,000 RNA probes (Agilent Technologies) complementary to the euchromatic portions of the Y-chromosome that comprises the X-degenerate sequences. These innovative RNA probes were initially tested on modern and four ancient bone samples (three male individuals and one female) dated to the sixth century C.E. and previously successfully analyzed by shotgun approach. The hybridization protocol proposed by Agilent Technology was carried out and compared with that commonly used for ancient DNA samples. Our preliminary data showed that good coverage results of Y chromosome were obtained from both modern and ancient samples using both protocols. The preliminary comparative analysis between the two different protocols seems to suggest that the average coverage of ancient hybridization protocol is two times higher than the Agilent one for two out of three samples. Using this new set of probes comprising a huge number of SNPs it could be possible to improve the knowledge about Y chromosome variability in past and present-day human populations with important implications both in population genetics and forensics.

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Using artificial neural network classification and laser induced breakdown spectroscopy on archaeological bones and teeth

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The analysis of elemental compositions in human remains is problematic, because systematic and predictable theories about the main controls of elemental uptake are yet to be universally established. Physiological and locality specific factors cause large variations between individuals and prevent a straightforward approach like it is the case with stable carbon or nitrogen isotope analysis for gaining dietary information.

In our study, we do not aim to analyse elemental compositions in terms of dietary information or the individual's mobility throughout their life. Instead we make use of the variations between individuals and employ them to group and discriminate between remains from specific individuals based on their personal elemental signature. Using Artificial Neural Networks, we can build statistically valid elemental fingerprints and associate groups of bones and teeth that share an identical elemental composition.

The classification or grouping of modern bones and teeth using Artificial Neural Networks has been tested successfully on modern human remains, but we see a large potential for applications in archaeology as well. For instance, this information can be used to associate previously isolated bones or teeth with each other, which for instance were not excavated in direct proximity or were part of a deposit containing more than one individual.

This will enable us to target previously unassociated sample material for more sophisticated analyses (i.e. protein and DNA analysis) and generally increase sample sizes at sites with few finds or with finds of dubious relation.

Elemental analysis of Ca, Mg, Sr, Fe, Na, K, N, O is carried out using an automated Laser Induced Breakdown Spectroscopy (LIBS) system. LIBS is a fast and minimally destructive tool (~0.1µg) that does not require sample preparation or consumables. As such the analysis can be carried out inexpensively and on a substantial quantity of archaeological remains.

The Artificial Neural Network is trained and applied using the freely available software R and the neuralnet package.

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The over-representation of male horses in Viking-Age Icelandic horse burials

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Horses were the most common grave good in Icelandic Viking-Age graves, found in over a third of studied sites. Horse remains have traditionally been sexed using morphological characteristics including the presence of canine teeth and pelvis shape. Yet this method is problematic as canine teeth are found in over 30% of female horses and the pelvis is often too fragmented to be of use for sexing. We show how shotgun sequencing of aDNA retrieved from Viking-Age horse remains is now a cost-efficient and effective method through which to determine sex. Our results show that male horses were favoured for use in Viking-Age graves in Iceland.

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From higher-order organisms to microbes – a novel quantitative species identification method based on ancient DNA

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Genetic species identification of archaeological specimens is often difficult due to low DNA content and degradation. Yet specific and accurate identification of samples is essential not only for taxonomic identification, but also for elucidating community membership of ancient microbial metagenomic samples. Therefore, we created a method for identifying both higher-order organisms and microbes via aDNA, by investigating the presence of specific species in archaeological material, and quantifying the confidence of the performed identification. We present two case studies to highlight the utility of our pipeline in archaeological studies. Lively debate surrounds the introduction of non-indigenous domestic livestock to southern Africa, and it has been hypothesized that the frequency of domestic stock in the faunal assemblages has been overestimated by zooarchaeologists, with recent genetic studies discrediting previous taxonomic assignments. After analyzing samples from this area, and trying to quantify how well supported a genetic taxonomic identification was, it was suggested that more DNA data need to be generated from them, to confidently reject the morphological identifications. By using ancient dental calculus samples, we have attempted to robustly identify bacterial species within the sequences that have been generated from the substrate, and estimate how reliable a species assignment is. Thus far, we have detected a positive signature of *Corynebacterium diphtheriae*, the causative agent of diphtheria and a transient member of the oral biofilm. Our findings highlight the potential of ancient dental calculus to act as a reservoir for respiratory pathogens, and the value of screening this substrate for species of epidemiological interest.

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Human skeletal remains and biomolecular preservation at the Smithsonian Natural History Museum

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Uncertainty surrounding the preparation and early curation history of medical and other skeletal collections in museums pose challenges for biomolecular studies. Postmortem skeletonization (boiling, mummification, chemical treatment, etc.) and/or conservation processes (chemical pesticides, cabinet fumigants, heat treatments, etc.) can impact biomolecule preservation, but the extent of the damage caused by such treatments remains unclear. Because detecting and characterizing molecular damage patterns is an integral part of ancient biomolecule authentication, information on how samples were collected, washed, preserved, and maintained is valuable for generating and interpreting high throughput biomolecular data. Dental calculus has proven to be a rich reservoir of endogenous microbial, human, pathogen, and dietary biomolecules, enabling research on the evolution of the oral microbiome and reconstruction of individual life histories. Here, we discuss preliminary findings from the Smithsonian"s National Museum of Natural History"s Physical Anthropology collections on the prevalence of dental calculus within a large skeletal dataset (n=2793 individuals). Across the dataset, 54% of the individuals had associated teeth. Of the observable teeth, only 11% had notable amounts of dental calculus, which varied by collection. Approximately 27% of all individuals showed evidence of postmortem calculus loss, either through intentional cleaning or breakage during storage and handling. Factors like these are important to consider during study design for population level investigations because many collections may not contain sufficient dental calculus for analysis. Next, we compared DNA recovery from dental calculus in anatomical and archaeological collections. The amount of recoverable DNA in anatomical collections, known to have been subjected to heat and chemical maceration with boiling water and benzene vapors, was appreciably affected by these treatments. It has been previously shown that the normalized recovery of DNA from archaeological dental calculus frequently exceeds 40 ng DNA/mg of dental calculus; however, DNA recovery from the anatomical collection samples averaged 2ng DNA/mg. By assessing how biomolecules are affected by various chemicals and preservation methods, future studies can account for preservation changes to samples, allowing researchers to make better decisions when selecting samples for destructive analyses.

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Exploring biomolecules of Lobor (Croatia)

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During the archaeological research in 2011, five individual graves were revealed at younger burial phase, along with the east, outer part of the shrine of Our Lady of the Mountain. This special group shows the same or similar burial ritual in the contracted or semi-contracted position of the arms and legs in the burial pits, with orientation east-west. Similar rituals have not been previously recorded at that site, but generally, it is not an exceptional occurrence in the 10th or 11th century Pannonia. Datation of this group is from the first half of the 11th century to the 13th century. These graves were revealed in an unattractive part of the cemetery, positioned behind the front end or on the north side of the Medieval church. The primary anthropological identification, which includes sex, age at death and stature determination, together with the analysis of bone pathological conditions and the development of musculoskeletal attachments have given us an abundance of data. The multiple stable isotope analysis (13C,15N,18O) has given an insight in the personal migrations, the chemical description of the regions where our persons spent their early childhood, as well as of the regions which marked the last years of their lives. The skeletal and dental material from each grave was sampled for ancient DNA analysis, which was performed with Investigator 24plex QS Kit for human identification to gain information of possible kinship within a family group.

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Improving radiocarbon dating by pedigree-based Bayesian modelling

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The precision of calibrated ^{14}C dates is often limited by the shape of the calibration curve. This is one of the major obstacles for using in itself high-precision conventional ^{14}C data.
However, the interpretation respectively calibration of individual ^{14}C ages neglects the fact that known family relationships (provided by DNA analysis) can place additional constraints on the range of possible calendar dates in the calibration process.
Ancestors should generally show older calibrated ^{14}C dates than their descendants. That general assumption, however, becomes ambiguous when parents survive their children due to premature death of the children. Therefore, anthropological information are imperative for building reasonable models that can actually lead to much sharper date information.
We present this approach by using combined relationship and ^{14}C information of individuals from the Lech valley in southern Bavaria, Germany. DNA sequencing of a large number of individuals from rich burial sites revealed relationships between some individuals. Using those to chronologically sequence successive generations in combination with their respective ^{14}C dates, shows much improved calibrated ^{14}C dates and leads to much sharper information for archaeological interpretation.

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The comparison of DNA preservation across multiple skeletal elements from individuals recovered from the abandonded Medieval graveyard of Krakauer Berg, Germany

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Throughout the burgeoning history of ancient DNA (aDNA) studies several skeletal elements have been put forth as candidates for having the "best" aDNA retention, with the *pars petrosa* as the current favourite. As of yet, however, there has not been a systematic investigation comparing several skeletal elements across multiple individuals. Here we present a survey of endogenous aDNA in multiple skeletal elements from 11 Medieval individuals (12 skeletal elements each) using high-throughput, automated, single stranded library preparation and Illumina short read sequencing. The individuals in question were all excavated from a graveyard unearthed in the abandoned Medieval village of Krakauer Berg, Sachsen-Anhalt, Germany and represent individuals of both sexes ranging from the ages of ~10-45 years. The skeletal elements examined in this survey include multiple sampling sites sites from each of 10 bones stemming from both the appendicular and axial skeleton. Our analyses consider several aspects of aDNA preservation, including endogenous human DNA, contamination load, and library complexity of both target and off target species. The ranked listing of skeletal elements resulting from these analyses will provide investigators a better perspective on differential DNA preservation, which is of great importance for analytical procedures that rely on the destructive sampling of precious archaeological material.