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Welcome

Dear all,

Welcome to ISBA7, hosted this year by the PalaeoBARN at the University of Oxford.

We are delighted to have received so many abstracts for posters and talks from researchers at all stages of their careers and from all over the world.

Information about the programme, venue, abstracts and attendees is provided in rest of the handbook and we will have a manned helpdesk available at the Museum at all times for any queries that pop up during your stay.

Do feel free also to contact us with any questions using the isba7@arch.ox.ac.uk email address and remember to use the #ISBA7 twitter hashtag throughout the conference to stay in touch.

Thank you all for coming and we hope that you will have an enjoyable and stimulating time in Oxford. It's going to be a great three days!

The ISBA7 Organising Committee

Web: <http://palaeobarn.com/isba7>

Email: isba7@arch.ox.ac.uk<<mailto:isba7@arch.ox.ac.uk>>

Twitter: #isba7

Important: Please note that the default position is that we **do not** allow photography of slides or posters. Presenters are asked to specify if they are happy for the audience to tweet the content of their presentations and should do so at the start of their talk.

Our Sponsors

We are immensely grateful for the support of our lead conference sponsor, Biodiscovery LLC (dba MYcroarray), and of our two delegate sponsors, Novogene and Elsevier, without all of whom we would not have been able to award travel bursaries to students coming from overseas.

Biodiscovery LLC (dba MYcroarray)

Conference Sponsor

MYcroarray® is proud to sponsor the ISBA7 conference, and thank the presenters and attendees for their ongoing contributions to the field of biomolecular archaeology. We are a scientist-owned bioscience company specializing in custom microarrays, NGS sequence capture kits, synthetic biology products, and more. We design and manufacture the popular MYbaits® in-solution target enrichment kits for next-generation sequencing. We offer affordable custom and predesigned target capture kits for beginner and experienced users pursuing any genetic research project, such as mitochondrial, nuclear, or pathogen DNA. We also offer expert in-house services for all sample types, including ancient DNA.

Novogene

Sponsor of the prize for best student Oral Presentation

Novogene is a leading provider of genomic services and solutions with cutting edge NGS and bioinformatics expertise and one of the largest sequencing capacities in the world. Novogene utilizes scientific excellence, a commitment to customer service and unsurpassed data quality to help our clients realize their research goals in the rapidly evolving world of genomics.

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Elsevier is a world-leading provider of information solutions that enhance the performance of science, health, and technology professionals. Elsevier and the Journal of Human Evolution are proud supporters of ISBA7. The Journal of Human Evolution concentrates on publishing the highest quality papers covering all aspects of human evolution.

Visit <http://www.journals.elsevier.com/journal-of-human-evolution> to learn more.

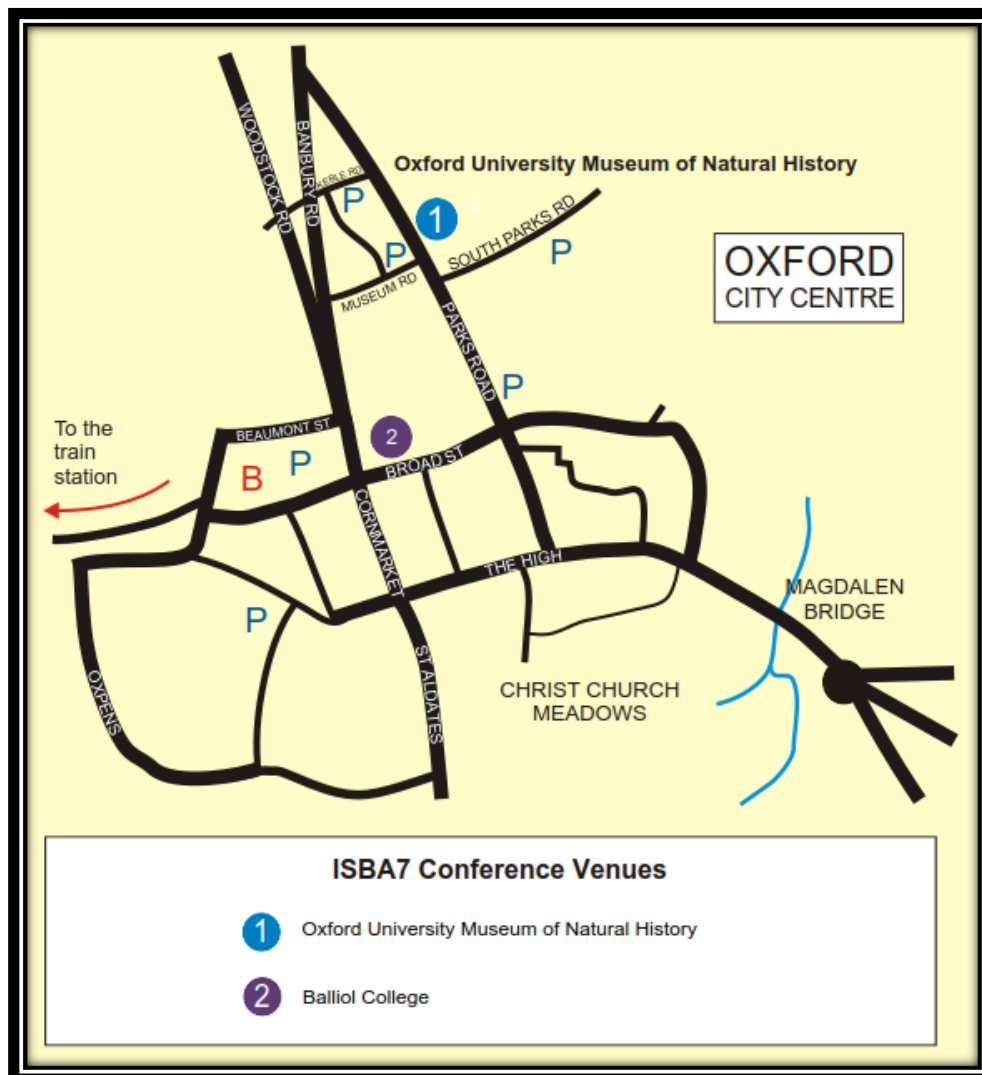
Useful information

Getting to Oxford

The University's website has a comprehensive description of how to reach the City of Oxford available here: <https://www.ox.ac.uk/visitors/visiting-oxford/how-get-oxford?wssl=1>

A detailed map of central Oxford and useful pages for visitors to the city can be found here: <http://www.oxfordcityguide.com/ee2/index.php?/Maps/MapOxford/>

The main conference venues and city centre map is detailed below. Roughly speaking, it will take about 5-10 minutes to walk between Balliol College and the Oxford University Museum of Natural History, and a 10 minute walk from the Railway Station to Balliol College



The Oxford University Museum of Natural History

Founded in 1860 as the centre for scientific study at the University of Oxford, the Museum of Natural History now holds the University's internationally significant collections of geological and zoological specimens. Housed in a stunning example of neo-Gothic architecture, the Museum's growing collections underpin a broad programme of natural environment research, teaching and public engagement. Among its most notable features (in addition to hosting ISBA7) are the Oxfordshire dinosaurs, the Dodo, and the swifts in the tower.

We will be using the Museum Lecture Theatre on the upper gallery level (see the Museum floorplan on the next page). The gallery extends around the full museum and will be available exclusively to the ISBA7 conference. This is also where the conference registration and help desk will be situated, where the posters will be displayed and where refreshments will be served. You are free to look around the rest of the museum exhibits during its opening times of 1000 to 1700.

*****Please note: no refreshments other than bottled water may be consumed in the lecture theatre*****

Wifi

Wifi is available at the museum. Connect to 'MNH public' and follow the instructions (entering an email address and agreeing to the fair use policy). Anyone with an Eduroam account will be able to use that.

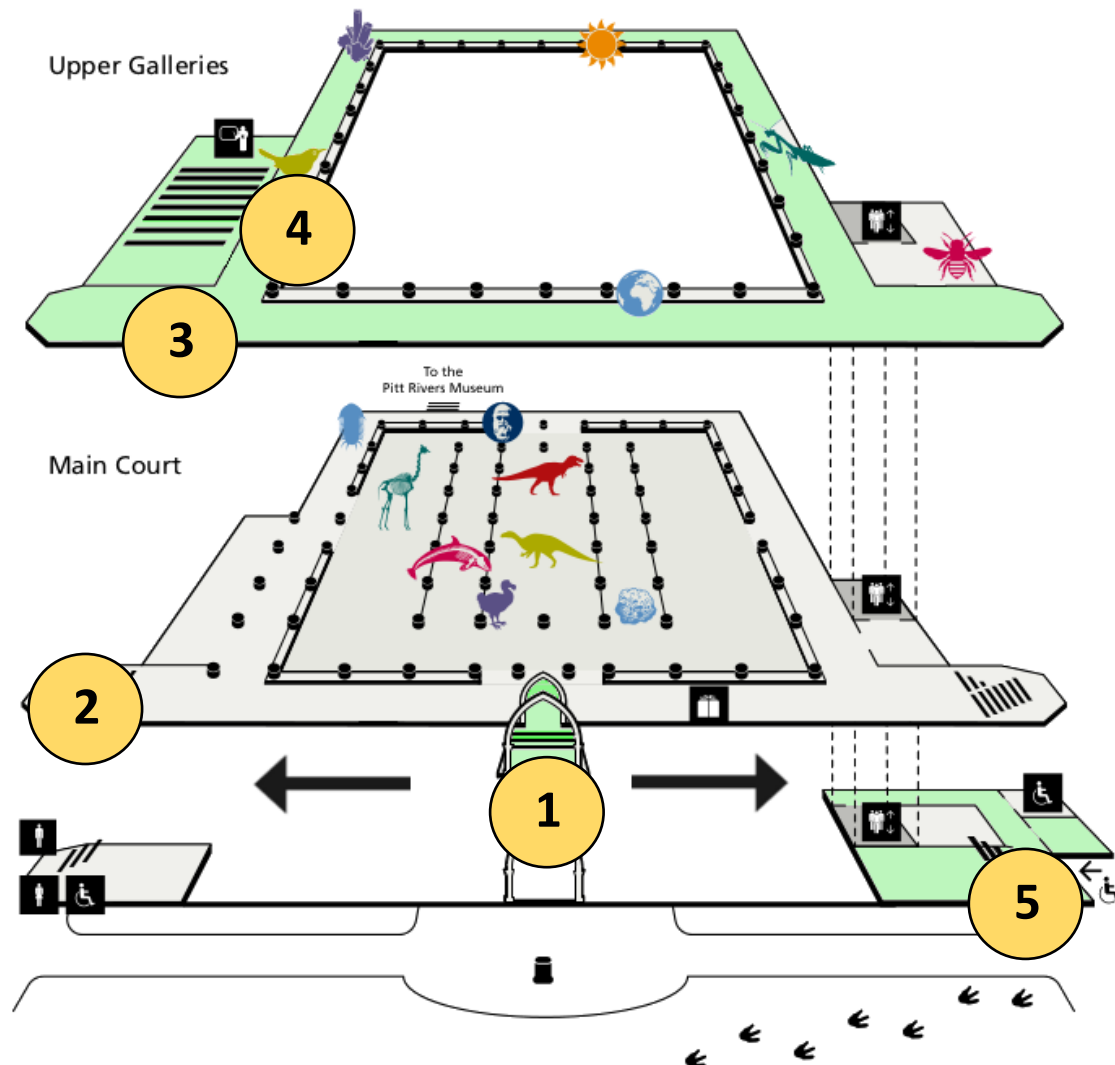
Health and Safety

First-aiders are present on site at all time and can be contacted via the Museum's main information desk at the entrance. There are no fire drills scheduled during the ISBA7 conference so if you hear the fire alarm it is for real. You should exit the building through the designated exits and the meeting point is in the centre of the grass area in front of the building.

Luggage and coats

Storage of luggage on arrival or departure day has been arranged in a room off the Annex area (see map) that will be locked or in use by the conference at all times. All luggage must be accounted for and will be assigned a ticket by our Event Staff. If the area is locked when you wish to collect your luggage, please speak to our Event Staff on the ISBA registration desk in order to retrieve it.

Floorplan – Oxford Museum of Natural History



- 1 - Main entrance to the museum.
- 2 - Stairs to Upper Gallery and/or down to toilets
- 3 - ISBA Registration/help desk
- 4 - Entrance to lecture theatre
- 5 - Entrance to Annex (for coats/parallel sessions)

Areas designated for ISBA7 conference are shaded in green

ISBA7 Programme summary

Wednesday – 14th September 2016

0930 – 1030	Arrival and registration
1030 – 1045	Welcome and opening talk – Greger Larson
1045 – 1200	Session 1 (Lecture Theatre) – Domestication
1200 – 1215	Tea and coffee
1215 – 1315	Session 2 (Lecture Theatre) – Domestication
1315 – 1415	Lunch
1415 – 1545	Session 3A – Isotopes and Populations (Lecture Theatre); and Session 3B – Ancient DNA Recovery (Annex)
1545 – 1630	Tea and coffee
1630 – 1800	Session 4A – Molecular Inference (Lecture Theatre); and Session 4B – Methods, Resolution and Effects (Annex)

Thursday – 15th September 2016

1000 – 1115	Session 1 (Lecture Theatre) – Isotopes and Crops
1115 – 1145	Tea and coffee
1145 – 1315	Session 2 (Lecture Theatre) – Palaeo Microbiomes and Pathogens
1315 – 1415	Lunch
1415 – 1545	Session 3A – Ancient Plants and Animals (Lecture Theatre); and Session 3B – Identification and Estimation (Annex)
1545 – 1630	Tea and coffee
1630 – 1800	Session 4A – Ancient Plants and Animals (Lecture Theatre); and Session 4B – Mobility, Trade and Material Culture (Annex)
1800 – 1900	Keynote – Matthew Collins – A talk 10 years in the Making

Friday – 16th September 2016

1000 – 1115	Session 1A – Old Tiny Critters (Lecture Theatre); and Session 1B – Ancient Individuals and Populations (Annex)
1115 – 1145	Tea and coffee
1145 – 1315	Session 2A – Old Tiny Critters (Lecture Theatre); and Session 2B – Isotopes and Behaviour (Annex)
1315 – 1415	Lunch
1415 – 1545	Session 3 – Ancient Humans (Lecture Theatre)
1545 – 1630	Tea and coffee
1630 – 1800	Session 4 – Ancient Humans (Lecture Theatre)
1915 – 2000	Pre-dinner drinks at Balliol College
2000 – 2200	Conference Dinner at Balliol College

Important information for presenters

Oral presentations:

We are running an extremely tight timetable and would be grateful for your assistance in all of the following to ensure we do not overrun. Please could we ask all presenters to do the following:

- Check that your presentation is working from your memory stick before giving it to us, and provide a copy of your talk (or bring your laptop if you are presenting directly from that) to the Event Staff in the room of your talk to test and load on the session computer *at the end of the session preceding the one in which you are speaking*.
- Take a seat close to the front of the stage during your session to ensure swift turn around (we will have reserved signs on seats at the front for session speakers)
- Be ready to take to the stage from the moment the previous speaker has finished their talk and is taking questions. One of our team will fit you with a lapel microphone (lecture theatre only) during this period (and help you remove it at the end)
- Advise the audience at the beginning of your talk whether you are happy or not for the content of your presentation to be tweeted
- Ensure your talk is no longer than 12 minutes. Our session chairs will assist if necessary!
- Answer any questions as concisely as possible, inviting further discussion over coffee/lunch as necessary in order that we can move the sessions on.

Poster presentations:

We will have numbered poster boards 1-24 arranged on the upper gallery and each poster has been assigned a board number and a day. Event Staff at the help desk will be available to help you with any questions or where to put posters and can supply poster fixings. Please also collect from them a label that must fix to your poster that clearly identifies you, your position and your session so that we know everyone is in the right place at the right time!

You are required to remove your poster at the end of the last session on the day that you are presenting. Any left over at 6.30pm will be removed by Event Staff and can be collected from the Help Desk.

Time		Title (Presenter)	
1030	Welcome (Greger Larson)		
Domestication			
1045	Lecture Theatre	177	Selection analysis applied to time series of ancient genotype data reveals how medieval religious reform shaped the genomes of modern chickens (Greger Larson)
1100		119	Genome sequence of a 5310-year-old maize cob provides insights into the early stages of maize domestication (Jazmín Ramos Madrigal)
1115		178	Seeing Beyond the Science: Multi-Strand Approaches to Human-Chicken Interactions (Julia Best)
1130		45	3,000 years of genome evolution in sorghum (Oliver Smith)
1145		128	Next-Generation-Sequencing of tetraploid wheat accessions and the origins of agriculture in the Near East (Hugo Oliveira)
1200		Coffee Break	
1215		5	Ancient viticulture uncorked: nuclear DNA from archaeological seeds sheds light on the history of grape varieties and berry color (Nathan Wales)
1230	176	Contemporary wolves trace their ancestry to an expansion from Beringia following the Last Glacial Maximum (Liisa Loog)	
1245	101	Genome sequences of 6000-year-old barley provide new insights into the history of crop domestication (Verena Schuenemann)	
1300	42	An ancient genomic perspective on the horse domestication process (Ludovic Orlando)	
1315	Lunch		
	Lecture Theatre	Isotopes and Populations	
1415		36	Using $\delta^{13}\text{C}$ and $\delta^{18}\text{O}$ time series from livestock teeth to reveal the seasonality of mobility, foddering, and stress during the Bronze and Iron Ages in eastern Kazakhstan (Taylor Hermes)
1430		15	Phosphate, carbonate, and Selected Ion Monitoring (SIM) oxygen isotope ratios in enamel apatite from Kromdraai Cave, South Africa: documenting diet, diagenesis and source water variation. (Linda Reynard)
1445		22	Resuming Resmo - sorting out mobility from diet using microsampling, multi-isotope analysis and modelling (Gunilla Eriksson)
1500		107	Stable isotope ($\delta^{13}\text{C}$, $\delta^{15}\text{N}$ and $\delta^{34}\text{S}$) and elemental analysis as markers for cultural heterogeneity and causes of death of a miner's population from Silbojokk in northern Fennoscandia during the 17th century (Markus Fjellström)
1515		66	Investigating early Neolithic vertical pastoralism movements of sheep in the Central Pyrenees by stable isotope analyses: data from a modern reference sample and archaeological specimens from Els Trocs (late VIth millennium cal BC; Spain) (C. Tornero)
1530		133	"Isoscapes" of tooth enamel phosphate oxygen isotopes ($\delta^{18}\text{O}_\text{p}$) help to identify human mobility in Early Bronze Age Britain (Maura Pellegrini)
	Annex	Ancient DNA Recovery	
		85	Improving The Recovery Of Ancient DNA Sequences From Highly Degraded Material (Isabelle Glocke)
		16	REALbaits capture on degraded DNA. Population genomics without a reference genome (Fátima Sánchez Barreiro)
		48	Identifying experimental conditions improving in solution target enrichment for ancient DNA (Antoine Fages)
		23	Relationship estimation from ancient DNA (Torsten Günther)
		135	Identify ancient microbial strains with < 100 palaeogenomic reads (Zhemín Zhou)
		52	Automated reconstructions of nucleosome and methylation maps with epiPALEOMIX (Kristian Hanghøj)
1545	Coffee Break		
	Lecture Theatre	Molecular Inference	
1630		136	Pasteurization, Processing, Palaeoenvironment – Applicability of modern dairy reference fats in archaeological lipid residue analysis using $\delta^{13}\text{C}$ of single fatty acids (Sarah Pederzani)
1645		111	Towards the identification of plant residues in prehistoric archaeological artefacts: integrating lipid and protein approaches (Andre Carlo Colonese)
1700		123	Compound-specific radiocarbon dating of food residues preserved in archaeological pottery vessels (Emmanuelle Casanova)
1715		150	Combining ancient DNA analysis and radiocarbon dating (Petra Korlevic)
1730		41	A new general model for ancient DNA decay based on paleogenomic meta-analysis (Logan Kistler)
1745		27	A comparison of methods for estimating evolutionary timescales using ancient DNA (Jun Tong)
	Annex	Methods, Resolution and Effects	
		50	Zonkey: a simple, accurate and sensitive method to identify first generation equid hybrids in archaeological assemblages (Charleen Gaunitz)
		46	LSD: a novel method to detect positive selection in tree time-slices (Pablo Librado)
	Annex	49	MALT: Fast alignment and analysis of metagenomic DNA sequence data applied to the Tyrolean Iceman (Alexander Herbig)
		17	20,000 bones and counting - Insights into zooarchaeology and Ancient DNA Preservation using Bulk-Bone Metabarcoding (Mike Bunce)
		109	A new methodological approach for the extraction and derivatization of absorbed lipid residues from very small and very old sample amounts of ceramic potsherds for molecular analysis by (GC-MS) and (GC-C-IRMS) (Vasiliki Papakosta)
		6	Effect of x-ray irradiation on ancient dna in sub-fossil bones – Guidelines for safe x-ray imaging (Alexander Immel)

Title	Presenter	Position
(2) Botanical and faunal stable isotope analysis at Baishui River valley (Shaanxi, China) to reconstruct crop management, climate change and palaeodietary during late Neolithic	Xin Wang	1
(7) Carbon and Nitrogen isotopic analysis on human and animal bones of Nanwa site, Henan Province, China	Guowen Zhang	2
(13) In-solution capture assay to screen for preservation and contamination of ancient human DNA	Marieke van de Loosdrecht	3
(18) The identity of the mysterious 'new glume wheat' of early European agriculture	Beata Czajkowska	4
(20) Full Mitochondrial Genomes of Central European Upper Palaeolithic Woolly Mammoths (<i>Mammuthus primigenius</i>)	James Fellows Yayas	5
(21) Osteometric and mtDNA analyses from the trading post of Empúries (north-east of the Iberian Peninsula) show first evidence of cattle trade during the Early Roman period	Lídia Colominas	6
(24) Genome Evolution of Trondheimers Through the Last 1000 Years	Inge Lundstrøm	7
(25) Burnt to a crisp? The high-throughput DNA sequencing of charred grains.	Jannine Forst	8
(31) Identifying <i>Mycobacterium tuberculosis</i> in ancient bone and dental calculus through DNA and protein analysis.	Aina Karlstrøm	9
(32) Story Hidden in the Cabinet? -Unveiling the Grape Evolution by Using Historical Herbarium Specimens	Hsiao-Lei Liu	10
(34) Nubian Barley evolution in a drought stress environment	William Nicholson	11
(40) The early agriculture and its impact in NW China	Xiaoqiang Li	12
(43) Genetics as a means of investigating cultural contact: The case of the Pitted Ware grave sites of the Island of Gotland in Scandinavia.	Alexandra Coutinho	13
(44) Whole mtDNA sequencing in Alpine populations and the genetic history of the Neolithic Tyrolean Iceman	Valentina Coia	14
(53) Characterization of cosmetic sticks at Xiaohu Cemetery in early Bronze Age Xinjiang, China	Yimin Yang	15
(55) Paleoproteomics for cultural heritage investigation, state of the art and perspectives.	Enrico Cappellini	16
(58) Multi-omics study of the Iceman's stomach content shows main components of a Copper Age meal: fat, wild meat and cereals.	Niall O'Sullivan	17
(59) Biosphere mapping- the next step.	Jane Evans	18
(61) Lipids absorbed in Epicardial pottery reveal large-group meat consumption in the oldest known domestic structure on the Barcelona plain.	Adrià Breu	19
(67) A comparative dataset of dentine and dental calculus from medieval Ireland	Susanna Sabin	20
(71) MALDI-FT-ICR-MS for archaeological lipid residue analysis	Ester Oras	21
(72) Screening for ancient tuberculosis DNA using MALT – a metagenomic approach	Åshild Vågene	22
(73) The First and Second Plague Pandemic in Bavaria, Germany - Preliminary Screening Results	Marcel Keller	23

Programme detail (talks) – Thursday 15th September

Time		Title (Presenter)				
Isotopes and Crops						
1000	Lecture Theatre	84	First molecular and isotopic evidence of millet processing in prehistoric pottery vessels (Carl Heron)			
1015		39	Wheat yields in ancient China: a study based on the carbon isotope discrimination of charred grains (Xinying Zhou)			
1030		92	The trials and tribulations of strontium isotope analysis of ancient charred grains (Amy Styring)			
1045		161	Gone to seed? Earliest direct evidence of plant processing in prehistoric Saharan pottery (Julie Dunne)			
1100		157	Nitrogen isotopic enrichment in the food chain: towards a metabolic explanation (Tamsin O'Connell)			
1115		Coffee Break				
1145		122	The effect of trophic level on individual amino acid $\delta^{15}\text{N}$ values in a terrestrial ruminant food chain (Iain Kendall)			
		Palaeo Microbiomes and Pathogens				
1200		38	Implications for mid Miocene Diet from Gomphotherium Phytoliths in Tooth Calculus (Yan Wu)			
1215		121	Digging deep into the ancient human oral microbiome: Metaproteomics challenges and perspectives for modern bioinformatics (David Lyon)			
1230	11	Proteomic evidence for dietary biomolecules entrapped in dental calculus (Camilla Speller)				
1245	3	Detecting ancient tuberculosis beyond the reach of ancient DNA with lipid biomarkers and characteristic bone lesions (David Minnikin)				
1300	54	Paleoproteomic analysis of early Pleistocene fossil remains (Enrico Cappellini)				
1315	Lunch					
	Lecture Theatre	Ancient Plants and Animals		Annex	Identification and Estimation	
1415		9	Origin of plant organic matter in permafrost revealed by ancient DNA and pollen analyses (Heike Zimmermann)		64	The painting technique of the giant Buddhas of Bāmiyān (Afghanistan) (Leila Birolo)
1430		171	Examining rabbit domestication: an historical, archaeological and genomic approach (Evan Irving-Pease)		113	The organic coating from a decorated human skull from the Neolithic site of Nahal Hemar (Israel): molecular evidence for the use of a vegetal substance (Blandine Courel)
1445		30	Ancient DNA from waterlogged oak wood provides a new baseline for evolutionary and archeological studies on temperate deciduous tree species (Stefanie Wagner)		56	Impact of modern cattle feeding practices on milk fatty acid stable carbon isotope compositions emphasise the need for caution in selecting reference animal tissues and products for archaeological investigations (Mélanie Roffet-Salque)
1500		33	Demonstrating mollusc seashells as new genetic archives of the past (Clio Der Sarkissian)		19	Tomb 7 at Monte Alban: Use, Antiquity and Importance (Noreen Tuross)
1515		79	The evolution of bison in Europe during the last 50,000 years (Diyendo Massilani)		1	Point count estimation of articulated husk phytoliths of foxtail millet and its prospective use in agricultural archaeology (Xue Shang)
1530		83	Degradation and recovery of DNA from 44,000 year-old rodent samples from Africa (Eva-Maria Geigl)		14	Identifying Scottish Soldiers from the Battle of Dunbar (1650) (Andrew Millard)
1545	Coffee Break					
	Lecture Theatre	Ancient Plants and Animals		Annex	Mobility, Trade and Material Culture	
1630		76	Genetic turnovers and northern survival during the last glacial maximum in European brown bears (Erik Ersmark)		35	Capture of ancient genomic DNA of individuals recovered from a Medieval Alemannic gravesite provides evidence for high mobility of fellowships during the 7th century CE (Niall O'Sullivan)
1645		162	Ancient DNA reveals differences in behaviour and sociality between brown bears and extinct cave bears (Gloria Gonzalez Fortes)		28	Trade and Empire in Ancient Bahrain: Bioarchaeological and Isotope Geochemical Perspectives (Damien Huffer)
1700		8	Population Genomics of Greenlandic polar wolves (Mikkel-Holger S. Sinding)		145	Paired radiocarbon dating on human samples and camelid textiles from Pica 8, northern Chile (Francisca Santana Sagredo)
1715		69	The genetic processes leading up to the woolly mammoth's extinction (Patrícia Pečnerová)		149	Illuminating the prehistory of northern Europe through lipid residue analysis of putative oil lamps (Harry Robson)
1730		129	Genomics of elephants and their extinct relatives (Eleftheria Palkopoulou)		60	Direct earliest evidence of dog domestication in East Asia (Yaowu Hu)
1745		80	Survival of eggshell peptides over millions of years in Africa is due to mineral binding (Beatrice Demarchi)		63	Drinking in the Andes: organic residue analyses of Inca aríbalo jars from Catamarca, Argentina (Irene Lantos)
1800	Keynote – “A talk 10 years in the making” (Matthew Collins)					

Title	Presenter	Position
(75) Investigating dietary habits by stable isotope analyses ($\delta^{13}\text{C}$ and $\delta^{15}\text{N}$) in bone collagen of cave bear (<i>Ursus spelaeus</i>) in southern latitudes of Europe during Late Pleistocene: the case of Toll Cave (MIS3; Spain)	Ivan Ramírez Pedraza	1
(77) Palaeolipidomics: developing a new lipid biomarker proxy to detect cereal processing in archaeological pottery	Simon Hammann	2
(82) Molecular markers in keratins from Mysticeti whales for species identification of baleen in museum and archaeological collections	Caroline Solazzo	3
(86) Genetic structure and geographic partitioning of <i>Lama guanicoe</i> sub-populations during the late Holocene	Cinthia Abbona	4
(87) Comparison of human and leprosy DNA content in petrous bones and teeth from St. Jorgen, Denmark (1270 - 1350 AD)	Lisa Boehme	5
(88) The Need for Resolution: Addressing the lack of multidisciplinary integration in Medieval plague research.	Meriam Guellil	6
(90) Expanding the oral microbiome reference set	Cody Parker	7
(91) Genetic Analysis of Neolithic individuals from Switzerland	Anja Furtwängler	8
(93) DNA quality in different types of archaeological plant materials	Maria Lundström	9
(95) Maternal Genetic Ancestry and Legacy of 10th Century AD Hungarians	A. Szecsenyi-Nagy	10
(96) DamageProfiler: Calculation of damage patterns in next generation sequencing data from ancient DNA	Judith Neukamm	11
(102) The efficacy of high-throughput sequencing and target enrichment on charred archaeobotanical remains.	Heidi Nistelberger	13
(103) Can the use of querns and millstones make a contribution of Sr to the human diet: An experiment in digestive Sr-isotope uptake.	Lucie Johnson	14
(104) Stable isotope evidence for diet and subsistence patterns of the prehistoric populations of south-eastern Uruguay	Patricia Mut	15
(106) The preservation of DNA from bone, dentin, and calculus from Gombe National Park and Pinnacle Point in Africa.	Anne Stone	16
(108) Ancient DNA from cats - a paleogenetics perspective into past distributions and patterns of dispersal of <i>Felis silvestris</i>	Claudio Ottoni	17
(110) Stable Isotope Analysis of the Blick Mead Dog: A proxy for dietary reconstruction of Mesolithic Hunter-Gatherers	Bryony Rogers	18
(114) Dietary practices in medieval Islamic Portugal: using stable isotopes to explore food consumption in 11-12th century Lisbon.	Alice Toso	19
(116) Finns in the light of ancient mitochondrial DNA	Kerttu Majander	20
(118) Mobility between the Aegean and the Levant in the Late Second Millennium BCE: inference from ancient DNA of pigs	Meirav Meiri	21
(120) Mitochondrial DNA analysis of first Neolithic farmers from Anatolia and Syria: implications for the Neolithisation of Europe	Luke Reynolds	22
(124) Identifying plague in 17th century London: a discussion of preliminary results	Elizabeth Nelson	23
(126) Investigating the possible brotherhood of two Egyptian mummies Nakht-Ankh and Khnum-Nakht via ancient DNA analysis	Konstantina Drosou	24

Programme detail (talks) – Friday 16th September

Time	Title (Presenter)	
	Old Tiny Critters	Ancient Individuals and Populations
1000	180 Ancient DNA and Gastrointestinal Parasites (Hannah Ryan)	74 A high-coverage <i>Yersinia pestis</i> Genome from a 6th century Justinianic Plague Victim (Michal Feldman)
1015	81 6380-year-old oral pathogens from hunter-gatherer remains found in Kiel bay: A metagenomic approach to ancient DNA (Sabin-Christin Kornell)	12 Geo-genetic population structure and gene flow in Eurasian barley populations (Mona Schreiber)
1030	70 Analysis of Ancient Dental Calculus Proteins from Northern European Viking Samples (Rosa Jersie-Christensen)	175 It's a dog's life! What can we tell from sequencing 1,000 ancient samples? (Anna Linderholm)
1045	115 Unappreciated ecosystem diversity of oral microbiota detected in ancient Britain (Andrew Farrer)	4 Bringing it all together: ancient DNA provides biological foundation for hypothesized population replacement in the California Channel Islands. (Christiana Scheib)
1100	170 Industrialization-associated changes in oral microbiome ecology (Irina Velsko)	78 Ancient DNA analysis of Scandinavian medieval drinking horns and the horn of the last aurochs bull (Maiken Hemme Bro-Jørgensen)
1115	Coffee Break	
	Old Tiny Critters	Isotopes and Behaviour
1145	97 Evolution history over millenia of sub-lineages of invasive <i>Salmonella enterica</i> (Mark Achtman)	143 Spatio-temporal mtDNA and isotope analyses of red deer (<i>Cervus elaphus</i>) in the Vosges: long-lasting co-existence of two "ecotypes" and low mtDNA diversity throughout millennia (José Granado)
1200	112 Metagenomic analysis of a permafrost-preserved woolly mammoth calf (Giada Ferrari)	156 Investigating dietary input across early iron age assemblages from Slovenia using stable isotopes (Hannah Koon)
1215	98 The 5,300-year-old <i>Helicobacter pylori</i> genome of the Iceman (Ben Krause-Kyora)	125 Seasonal reproductive patterns of buried sheep in the funeral Avellaner cave (Epicardial; Northeast Iberian Peninsula) by stable isotope sequences ($\delta^{18}O$) in bioapatite tooth enamel: funerary and sheep herding implications (Sheila Garcia Reig)
1230	172 Ancient Mitogenomes Shed Light on Population Affinity and Mortuary Practices in Southern Caucasus (L. Papac)	134 A Multi-Isotopic Investigation of a Large, Unusual Neolithic Assemblage (Sophy Charlton)
1245	57 A demographic history of plague revealed through historical <i>Y. pestis</i> genomes (Maria Spyrou)	89 Reconstructing the migratory behaviours of extinct fish populations using stable isotope analyses (Eric Guiry)
1300	62 B-Thalassemia cod39 mutation found in an individual from a Punic necropolis (VI century BC-II century AD) in Sardinia (Claudia Viganó)	
1315	Lunch	
	Ancient Humans	
1415	158 The Hole Story: Ancient DNA, stable isotope and radiocarbon analysis of human remains from the 'Mesolithic' cemetery at Aveline's Hole (Thomas Booth)	
1430	51 A stable story: insights in the development of a (post)medieval population in the east of the Netherlands (Eveline Altena)	
1445	47 Taxonomic and Tissue Specific Dietary Proteins in Pottery Residues (Jessica Hendy)	
1500	144 The Neolithic Transition at the Edge of Europe (Eppie Jones)	
1515	10 Pre-Neolithic mitogenomes suggest a single major dispersal of non-Africans and a Late Glacial population turnover in Europe (Cosimo Posth)	
1530	117 Tracing the origins of 19th century enslaved Africans from the island of Saint Helena (Marcela Sandoval Velasco)	
1545	Coffee Break	
1630	159 Population continuity in the time of admixture: exploring the Neolithic transition from Anatolia to Central Europe (David Diez del Molino)	
1645	147 Exploring the Migration of the World's first Farmers (Lucy van Dorp)	
1700	169 Testing continuity of ancient samples using SNP data (Joshua Schraiber)	
1715	99 Reconstructing population history in East Asia (Chuanhao Wang)	
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0001

Point count estimation of articulated husk phytoliths of foxtail millet and its prospective use in agricultural archaeology

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Many researchers have focused on the precise identification of phytoliths extracted from archaeological samples, and on the extraction methods of phytolith from all kinds of samples as well. Additionally, it is important to perfect the scientific method of phytolith quantification. Phytoliths, especially from the husk, are easily broken after being long-buried or during extraction treatment. These can result in uncertainties about quantification of grain numbers and varies under different conditions. Here we introduce a method of point count estimation of articulated millet husk phytoliths, and evaluate its accuracy. As a result, we successfully used the point count method into estimating the area of husk phytolith in unit weight of modern millet samples, which will broaden the available data in archaeobiological research. We suggest precise estimations can therefore be done with this method.

0002

Botanical and faunal stable isotope analysis at Baishui River valley (Shaanxi, China) to reconstruct crop management, climate change and palaeodietary during late Neolithic

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Here we present $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values of botanical and faunal remains, with nine radiocarbon dates to reconstruct crop management, climate change and palaeodietary at five sites in the Baishui River valley (Shaanxi, China) during the late Neolithic (5500-3500 BP). The foxtail millet ($n = 23$) $\delta^{13}\text{C}$ values range from -11.8‰ to -9.2‰ (mean $-9.8 \pm 0.7\text{‰}$) and the $\delta^{15}\text{N}$ values range from +3.9‰ to +6.9‰ (mean $+5.4 \pm 0.7\text{‰}$). The common millet ($n = 13$) $\delta^{13}\text{C}$ values range from -10.6‰ to -9.6‰ (mean $-10.1 \pm 0.3\text{‰}$) and the $\delta^{15}\text{N}$ values range from +3.3‰ to +6.6‰ (mean $+5.7 \pm 0.9\text{‰}$). Crop management is revealed in here: both foxtail millet and common millet grow under the similar conditions; manuring of cereal crops exists in this area at least 5000 BP, which is the first investigate of manuring in Neolithic China. Our results indicate diversity in climate effects on crops. The $\delta^{13}\text{C}$ values are elevated response to less water availability. Distinctively high $\delta^{13}\text{C}$ values of domestic pigs reflect intensive consumption of millets.

0003

Detecting ancient tuberculosis beyond the reach of ancient DNA with lipid biomarkers and characteristic bone lesions

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Elucidating the evolutionary interrelationships between ancient diseases, such as tuberculosis, and their animal hosts is a formidable challenge. In the past two decades, the analysis of ancient DNA data

has been refined to produce diagnostic information, but preservation is an ongoing limitation. Alternatively, *Mycobacterium tuberculosis* produces robust lipid biomarkers, particularly the long-chain lipid mycolic, mycolipenic and mycocerosic acids. Sensitive lipid biomarker profiles have supported DNA diagnoses, the oldest published examples being 9ka BP human tuberculosis from Atlit Yam in the Eastern Mediterranean [Hershkovitz *et al.* 2008 PLoS ONE 3:e3426] and a 17ka BP extinct *Bison antiquus* metacarpal from Natural Trap Cave, Wyoming [Lee *et al.* 2012 PLoS ONE 7:e41923]. In unpublished work, tuberculosis lipid biomarkers were found in a 40ka bison metacarpal from Kent's Cavern, Torquay and 12ka mastodon metapodials from Buffalo, NY. In Pleistocene megafauna, tuberculosis is indicated by metacarpal lesions "undermining the articular surface". Objective micro-CT scanning indicates clear lesions in bison metacarpals from Idaho (30ka), North Sea (37ka), Isleworth (50ka), Barrington (80ka), Wretton (80ka), Shropham (120ka), Joint Mitnor Cave (120ka) and Trimmingham (600ka). A coherent hypothesis is that tuberculosis evolved as a non-lethal zoonosis in a range of Pleistocene megafauna before becoming markedly virulent due to increased hydrophobicity and aerosol transmission [Minnikin *et al.* 2015 in: Ribón (Ed), Tuberculosis-Expanding Knowledge. InTech-Open Access, Rijeka, pp145-175]. Such a transformation might easily have contributed to the demise of megafauna in the late Pleistocene. In the Holocene, modern tuberculosis evolved in developing populations of *Homo sapiens* and other mammals.

0004

Bringing it all together: ancient DNA provides biological foundation for hypothesized population replacement in the California Channel Islands.

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In the direct path of any Pacific coastal migration into the Americas, there is evidence of human occupation of the California Channel Islands from 13k YBP. At the time of contact the southern islands were inhabited by Uto-Aztecan speaking peoples and the northern islands by Chumash speaking people. Patterns of change in the material record and in the morphology of human remains has led to speculation of an Uto-Aztecan expansion from the mainland between 1500-3000 YBP replacing earlier groups. Skeletal remains spanning the last 8,000 years were sampled from San Nicolas Island, San Clemente Island, Santa Catalina Island, San Miguel Island, Santa Cruz Island, Point Sal, Santa Barbara, Baja California, and the greater San Diego area. DNA was extracted and nuclear genomes were shotgun sequenced to an average coverage of 0.01 - 15X per sample. All ancient samples exhibit novel mitochondrial lineages within the known Native American haplogroups A, B, C, and D. All ancient male California samples belong to Y-chromosome haplogroup Q1-L53, the main lineage present in modern Native Americans. Principal Component analyses based on autosomal markers map all ancient Californian samples near modern Native American samples from Central and South America. At finer resolution, we detect in two distinct clusters that likely correspond to early and recent periods. We use statistical techniques to determine the extent of continuity between past and present populations and to examine the extent of admixture between the ancient populations in the region.

Ancient viticulture uncorked: nuclear DNA from archaeological seeds sheds light on the history of grape varieties and berry color

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The Eurasian grapevine (*Vitis vinifera*) is the world's most economically important fruit, with berries used as table grapes, raisins, and most commonly, in winemaking. Over the course of domestication, grapevines changed in a number of ways from their wild progenitors, including producing larger, sweeter berries in a range of colors and switching from dioecism to hermaphroditism. Grapevine domestication and improvement have been explored using modern samples, yet relatively little genetic work has been conducted on archaeological specimens. To provide a new perspective on past viticulture, we conducted a series of aDNA capture experiments on waterlogged seed excavated from French sites dating from before the Roman era to the medieval period. Testing endogenous DNA against well-characterized genes responsible for variation in anthocyanin content, we investigate the frequency of the derived white berries in the past. In addition, we explore how individual seeds can be affiliated with vegetatively propagated varieties. In these ways, we examine the history of different clonal lineages, and reach a new appreciation of the history of winemaking.

Effect of x-ray irradiation on ancient dna in sub-fossil bones – Guidelines for safe x-ray imaging.

Alexander Immel^{1,2}, Adeline Le Cabec^{3,4}, Marion Bonazzi⁵, Alexander Herbig¹, Heiko Temming³, Verena J. Schuenemann², Kirsten I. Bos¹, Frauke Langbein², Katerina Harvati⁶, Anne Bridault⁷, Gilbert Pion⁸, Marie-Anne Julien⁹, Oleksandra Krotova¹⁰, Nicholas J. Conard¹¹, Susanne C. Münzel¹², Dorothee G. Drucker¹, Bence Viola^{14,3}, Jean-Jacques Hublin³, Paul Tafforeau⁴, Johannes Krause^{1,2}

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Sub-fossilised remains may still contain highly degraded ancient DNA (aDNA) useful for palaeogenetic investigations. Whether X-ray computed [micro-] tomography ([μ]CT) imaging of these fossils may further damage aDNA remains debated. Although the effect of X-ray on DNA in living organisms is well documented, its impact on aDNA molecules is unexplored.

Here we investigate the effects of synchrotron X-ray irradiation on aDNA from Pleistocene bones. A clear correlation appears between decreasing aDNA quantities and accumulating X-ray dose-levels above 2000 Gray (Gy). We further find that strong X-ray irradiation reduces the amount of nucleotide misincorporations at the aDNA molecule ends. No representative effect can be detected for doses below 200 Gy. Dosimetry shows that conventional μCT usually does not reach the risky dose level,

while classical synchrotron imaging can degrade aDNA significantly. Optimised synchrotron protocols and simple rules introduced here are sufficient to ensure that fossils can be scanned without impairing future aDNA studies.

0007

Carbon and Nitrogen isotopic analysis on human and animal bones of Nanwa site, Henan Province, China

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The Nanwa site (1680BC-Song Dynasty; located in Dengfeng city, Henan Province, China) , as an important archaeological site in the Central Plains, provided a valuable opportunity for the Xia Dynasty and the Chinese civilization study. We could provide effective evidence for the food resources utilize pattern and agricultural economy development. Stable isotopic carbon, nitrogen analysis of 14 animals and 22 human bone collagen from the Nanwa site indicated that, wild animals (deer) (-19.9‰, 4.4‰, n=1) have a C3-based terrestrial diet. Domestication pigs (-7.6±0.6‰, 6.6±0.4‰, n=7) have a diet of predominated C4-based foods, as well as the sheep (-6.9‰, 6.2‰, n=1), cattle (-9.0‰, 7.8‰, n=1), dog (-6.6±0.5‰, 6.9±0.3‰, n=2), which likely obtain from the human feeding. The $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ value of the human from the Erlitou, Later Shang to Spring and Autumn period is -12.1±4.1‰, -11.6±1.3‰, -7.5±4.9‰ and 5.5±1.3‰, 6.8±0.3‰, 6.8±0.9‰, indicated that they mainly relied on C4 foods, probably the millet or few animals fed on C4 plants. Combined with the archaeological records and the isotopic analysis results, we also found that the Nanwa humans of the Erlitou to Late Shang Dynasty had consumed few C3 foods, indicated of a mixed agricultural economy, probably supplied by rice, bean and wheat. Compared to other archaeological culture people, the Nanwa humans had a different animal husbandry and agricultural economy pattern.

0008

Population Genomics of Greenlandic polar wolves

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For centuries wolves have been recorded in Greenland. Inuit mythology views the wolf as a supernatural creature intertwined in shamanism, and the historic polar explorers targeted wolves as precious specimens to add to their natural history collections. Although in the early twentieth century it is believed that wolves were likely exterminated from Greenland, the possibility exists that they may have survived in a refugium spanning the northernmost regions. In recent years - since the late twentieth century - wolves have begun to repopulate their former range, although the source population is uncertain (most like Northern Greenland or Canada). Overall therefore, despite two centuries of scientific research on the Biology of the Greenlandic fauna, remarkably little is known about the wolf – something we are currently rectifying. Specifically, we generated both mitochondrial genomes and low coverage nuclear genomes (from 0.1 to 10x coverage) from museum specimens and modern Canadian and Greenlandic wolves to explore their genetic affiliations. Our data demonstrates that both historic and modern day Ellesmere Island and Greenland host one population of wolves that are significantly different to other populations South of Ellesmere Island.

Origin of plant organic matter in permafrost revealed by ancient DNA and pollen analyses

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Ice-rich permafrost deposits store large quantities of plant organic matter and are highly sensitive to climate warming. With rising ground temperatures they will increasingly act as a substrate for microbial turnover to greenhouse gases, which can further enhance climate warming. To assess the future fate of the Arctic region, a better characterisation of plant organic matter is thus necessary. We applied ancient DNA-metabarcoding and pollen analyses at high resolution on an 18.9 m long permafrost core from the Buor Khaya peninsula (North-Eastern Siberia). Our aim was to reconstruct past local to regional flora to assess the taxonomic origin of plant organic matter and the environmental conditions during the time of accumulation. The core consists of two segments, which are divided by an ice-wedge: (1) Yedoma deposits (51-44 kyr BP, fine-grained, ice-rich permafrost with average total organic carbon contents (TOC) of 2.7 wt. %) and (2) a Late Glacial to Early Holocene cover (11-10 kyr BP, average TOC of 3.5 wt. %). With DNA metabarcoding we detected 112 terrestrial and 21 swamp and aquatic plant taxa, of which 81 % are identified to genus or species level. The taxonomic composition of Yedoma suggests an accumulation of organic matter in shallow water within a low-centred ice-wedge polygon. The pollen analyses support these findings but imply relatively arid environmental conditions on a regional scale. During the Late Glacial to Early Holocene transition the compositions recorded by both proxies indicate shrub tundra with more humid environmental conditions on a local to regional scale.

Pre-Neolithic mitogenomes suggest a single major dispersal of non-Africans and a Late Glacial population turnover in Europe

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The genetic diversity of the first modern humans who spread into Europe during the Upper Palaeolithic and the impact of subsequent climatic events on their demography before the Neolithic are largely unknown. Here we analyze an extended dataset of complete human mitochondrial genomes (mtDNA) from around 70 hunter-gatherers spanning ~35,000 years of European prehistory. We unexpectedly find mtDNA lineage M in individuals prior to the Last Glacial Maximum (LGM). This lineage is absent in contemporary Europeans, while found at high frequency in modern Asians, Australasians, and Native Americans. Dating the most recent common ancestor of each of the modern non-African mtDNA clades reveals their single, late and rapid dispersal less than 55,000 years ago. Demographic modelling indicates not only an LGM genetic bottleneck but also provides surprising evidence of a major population turnover in Europe around 14,500 years ago during the Late Glacial, a period of climatic instability towards the end of the Upper Palaeolithic.

Proteomic evidence for dietary biomolecules entrapped in dental calculus

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Archaeological dental calculus has emerged as a rich source of ancient biomolecules. During life, as dental plaque mineralises to form calculus, it entombs and preserves biomolecules associated with oral microbiota, the host, as well as inhaled and/or ingested microdebris, including food particles. Previous proteomic analysis of ancient dental calculus revealed the presence of β -Lactoglobulin (BLG), a protein found in the whey fraction of milk, providing direct evidence of dairy consumption in the archaeological record. However, the potential for calculus to preserve other food-related proteins has not been systematically explored. We analysed shotgun metaproteomic data from over 60 British archaeological skeletons ranging from the Iron Age to the Post-Medieval period, as well as modern individuals, to characterise dietary evidence preserved within dental calculus. In addition to BLG, we detected the presence of other milk proteins, as well as proteins from meat sources, cereals, and vegetable products. Although the overall quantity of dietary proteins recovered was generally low, the data provided new evidence for the consumption of certain food products which are generally poorly preserved within the archaeological record.

Geo-genetic population structure and gene flow in Eurasian barley populations

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The Neolithic transition describes the shift of nomadic hunter-gatherers to farming and sedentism. This transition is mainly characterised by the process of domestication, which presumably began in Southwest Asia more than 10,000 years ago. Archaeobotanical remains show the use of wild plants in late Palaeolithic times and suggest the “Fertile Crescent” as the centre of origin for domestication.

Barley (*Hordeum vulgare* L.) is considered to be a founder crop, one of the first domesticated cereal species together with emmer and einkorn. *Hordeum vulgare* ssp. *spontaneum*, the putative wild ancestor of barley, is most abundant in the Fertile Crescent as well as further east in Central Asia.

The process of domestication left its traces in the genomes of the domesticated species and can give evidence to reconstruct the past and to get a better understanding of this momentous change in our history.

Here, we present a population genetic analysis of genome-wide sequence data for 91 wild barley and 137 domesticated Eurasian barley accessions divided into nine and eleven groups, respectively, based on a geo-genetic structuring approach using TESS3, and applied D statistics to establish patterns of gene flow.

We were able to detect gene flow from Central Asian wild barley into domesticated populations from Eastern Europe and Russia compared to Southwest Asia. Furthermore, our results show evidence for gene flow from wild populations in the Fertile Crescent into modern domesticated populations in Central Asia, which supports existing hypotheses about connections between these groups.

In-solution capture assay to screen for preservation and contamination of ancient human DNA

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DNA quantity and quality in ancient human remains varies notoriously between bone types, archaeological sites and (thermal) age^{1,2}. An effective screening method to assess DNA preservation and contamination in a given sample can greatly improve time- and cost-efficiency in ancient DNA research.

We developed in-solution capture probes for target enrichment via DNA/DNA hybridization and subsequent sequencing on Illumina platforms. Our probes include the entire human mitochondrial genome and select diagnostic SNP positions for basal Y-chromosome haplotyping, autosomal phenotypic traits and a mixture of rare ($0.001 > \text{MAF} < 0.01$) and common ($0.3 > \text{MAF} < 0.5$) X-chromosomal variants. By using SNPs on both sex-chromosomes and the autosomes, differences in SNP coverage can provide an initial indication of the genetic sex of the individual, and provide estimates for library complexity as well as human contamination. Due to the low number of SNP positions used, both probe costs and bioinformatic analysis time are kept to a minimum.

Here we provide the rationale and methods for the computational design of such an efficient sample-screening probe set.

Identifying Scottish Soldiers from the Battle of Dunbar (1650)

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In November 2013 construction work for a new café on Palace Green, Durham uncovered human remains. We have identified them as Scottish Soldiers captured by Oliver Cromwell at the Battle of Dunbar in 1650. Historical evidence shows that prisoners were marched to Durham and 3000 imprisoned in the disused Cathedral and Castle. Over 1600 died of dysentery and other diseases.

Osteological examination yielded an MNI of 17 though 28 were numbered during excavation. All adults were male and most individuals were aged between 13 and 25, consistent with a military grave. Two individuals displayed pipe facets, thus dating them after the arrival of cheap tobacco in 1613. Bayesian analysis of radiocarbon dates yielded a most probable date of AD 1625-1660.

Initial analysis of strontium and oxygen isotopes in the enamel of second molars showed a very wide range of values. We concluded that five individuals had values compatible with being from Scotland or Northern England. Another five were compatible with Scotland but not Northern England. The other three analysed were likely to be immigrants to the British Isles. Lead isotopes also favour a Scottish origin for some men, and lead levels suggest many of them were not exposed to anthropogenic lead.

These very broad estimates of places of origin can now be refined, drawing on further isotopic analysis and investigation of historical records about the recruiting areas of the regiments involved.

Phosphate, carbonate, and Selected Ion Monitoring (SIM) oxygen isotope ratios in enamel apatite from Kromdraai Cave, South Africa: documenting diet, diagenesis and source water variation.

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We report $\delta^{18}\text{O}_{\text{PO}_4}$ and $\delta^{18}\text{O}_{\text{CO}_3}$ from 1-2 Ma fossil enamel from Kromdraai Cave, South Africa, that is located in the Cradle of Humankind World Heritage Site. In addition, selected ion monitoring (SIM) mass spectrometry of $\delta^{18}\text{O}$ was utilized to examine the distribution of oxygen isotopes in a subset of enamel samples from the Kromdraai B location. Diagenetic alteration of oxygen isotope ratios in fossil enamel is documented with significant departures from the 1:1 carbonate ($\delta^{18}\text{O}_{\text{CO}_3}$) to phosphate ($\delta^{18}\text{O}_{\text{PO}_4}$) line defined by modern enamel (Iacumin et al., 1996, Zazzo et al., 2004; Martin et al., 2008, but see caution expressed by Pellegrini et al., 2011). A large fraction of the samples from Kromdraai depart from the modern reference line. Higher $\delta^{18}\text{O}_{\text{PO}_4}$ in primates over other fauna suggest alteration of the carbonate apatite $\delta^{18}\text{O}$ which shows smaller magnitude differences than $\delta^{18}\text{O}_{\text{PO}_4}$ among the taxa. Higher $\delta^{18}\text{O}_{\text{PO}_4}$ in the primates is also consistent with frugivory. The $\delta^{18}\text{O}$ from SIM analysis documents the separation of wildebeest and primate oxygen isotopes observed in the $\delta^{18}\text{O}_{\text{PO}_4}$, the possible seasonal input of the oxygen from water, and the diagenetic alteration in the samples.

Compilation of the published literature and construction of prediction intervals suggests that diagenetic alteration, most plausibly of $\delta^{18}\text{O}_{\text{CO}_3}$, is increasingly common in samples older than the Palaeolithic. We conclude that in older fossil enamel, both $\delta^{18}\text{O}_{\text{PO}_4}$ and selected ion monitoring mass spectrometry can be used together to obtain a much fuller and more accurate interpretation of dietary choices, seasonality, and diagenesis.

REALbaits capture on degraded DNA. Population genomics without a reference genome

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For non-model species, population genomics analyses pose methodological challenges due to the lack of good quality genomic references. Reduced representation library (RRL) methodologies, which often rely on digestion of genomic DNA by restriction enzymes, seem to overcome many of those challenges. However, because high molecular weight DNA is a prerequisite, RRL methods are generally unsuitable for samples with degraded DNA, such as ancient and historic samples. Given that these specimens can provide key temporal perspectives to evolutionary questions, we explored how custom-designed RNA probes could enrich for RRL loci (Restriction Enzyme-Associated Loci baits, or REALbaits).

Starting with Genotyping-by-Sequencing (GBS) data generated on modern common ragweed (*Ambrosia artemisiifolia* L.) specimens, we designed 20,000 RNA probes to target well-characterized genomic loci in herbarium voucher specimens of *A. artemisiifolia* dating from 1835-1913. We observed an enrichment of the targeted loci at 20-117-fold compared to shotgun sequencing. Additionally, we found that a 10-fold dilution of the capture bait could yield enough genomic for downstream analyses, and that ~7.5M reads per sample was the optimal sequencing depth. When expanding the REALbaits capture pipeline to a dataset of 78 herbarium samples (1835-1939), we discovered >40,000 SNPs, which provided sufficient genomic resolution to distinguish geographic populations across the native

range of *Ambrosia artemisiifolia* in different time windows. Our findings can help researchers design capture experiments for RRL loci, and also demonstrate that population genomics analyses with a historic perspective are feasible, can be streamlined and do not require a reference genome.

0017

20,000 bones and counting - Insights into zooarchaeology and Ancient DNA Preservation using Bulk-Bone Metabarcoding.

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Fossil bones provide a unique window into the past but they are often difficult to interpret. Only a small proportion of animals are preserved as fossils – an even smaller fraction are then recovered and able to be identified morphologically. We have developed a globally applicable next generation DNA sequencing method that offers a genetic perspective on fossil assemblages with the aim of rapidly overlaying genotype data over more traditional methods of study. Our approach is called bulk-bone metabarcoding (BBM). BBM involves the conversion of largely non-diagnostic bone fragments into powder which is then genetically indexed, amplified and sequenced on NGS platforms.

This presentation will showcase some BBM data from a variety of sites across Australia, New Zealand, Hawaii, USA, Madagascar and Armenia. The data generated using BBM provides some key insights into past biodiversity and faunal turnover. Moreover the approach is an efficient way to assess DNA preservation both within and between fossil sites. Taken together, bulk-bone metabarcoding provides a powerful and cost-effective way to study past biodiversity with tangible benefits in conservation science, paleobiology and archaeology.

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The identity of the mysterious 'new glume wheat' of early European agriculture

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"New glume wheat", NGW is unidentified, extinct today *Triticum* species, formerly classified as 'aberrant' or 'slender emmer'. Its close relationship to modern tetraploid *Timopheevii* wheats has been proposed with respect to spikelet bases and the grains. In prehistoric times NGW could have been a widespread crop with archaeobotanical records ranging from Anatolia to Western Germany, from various cultures from the Early Neolithic to the Iron Age. Domesticated *T. timopheevii* is not a common species; being restricted to localized regions of Georgia. The aim of the project is to establish the identity of the NGW - to distinguish if archaeological tetraploid NGW is related to *araraticum-timopheevii* (A_tA_uGG) or to *dicoccoides-dicoccum* (A_uA_uBB) group. Archaeobotanical study is not sufficient in diagnosing definite taxonomic identification of the NGW. However, there are unambiguous differences at the molecular level: *Timopheevii* Wheat possesses the G and A_t genomes; whereas emmer's genomic composition is B and A_u . The specific objective of the project is therefore to use ancient DNA (aDNA) sequencing to determine if the NGW contains a B or G genome. Plant material consists of 41 *T. timopheevii* accessions, 12 *T. araraticum* and charred NGW grains from Assiros Toumba, Greece. We will *de novo* sequence variable regions of at least 50kb of the G genome in order to identify diagnostic polymorphisms, apply target enrichment and then sequence targeted aDNA from charred cereal grains. Prevalence of major plasmon haplotypes can also determine *Triticum* species so we will confirm species identity via chloroplast and mitochondrial marker identification.

Tomb 7 at Monte Alban: Use, Antiquity and Importance

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In 1932, Alfonso Caso (Caso, 1968) opened a small tomb (Tomb 7) at the monument site of Monte Alban in Oaxaca, Mexico and discovered one of the richest archaeological finds in the Americas. Among the offerings of gold, turquoise, alabaster, jade and coral, human skeletal elements were scattered throughout the tomb (Rubín de la Borbolla, 1968). Both the style and manufacture of the offerings are associated with the Mixtec peoples, while the tomb's architectural style is found in Zapotec buildings. We have obtained 43 radiocarbon dates from skeletal elements in Tomb 7. Two human bone pieces date to the time of the tomb construction in the range of the postclassic, and the remaining dates cluster between approximately 1200 and 1400 AD. This suggests that the materials left by Zapotec peoples in initial use of the tomb were not removed, at least not completely. Furthermore, a combination of stable isotopic analyses (carbon, nitrogen and oxygen of bone collagen) demonstrates that the later Mixtec skeletal elements came from a wide geographic range throughout Oaxaca, and that Tomb 7 was likely a place of honor for the final repose of isolated skeletal elements by the Mixtec peoples. The use of oxygen isotopes from bone collagen requires a unique preparation that involves exposure to light and heavy water, but offers an opportunity to measure long-term adult residence locations. Finally, antiquity and likely origin of the famous turquoise skull from Tomb 7 will be reported in the context of the other tomb materials.

Full Mitochondrial Genomes of Central European Upper Palaeolithic Woolly Mammoths (*Mammuthus primigenius*)

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A recently identified 'European' clade (clade III) of woolly mammoth has been suggested to have become extinct around 34 ky cal BP, and replaced by a migrating North American clade from the east around 32 ky cal BP. However, this was based on a small number of short HVR sequences. Here we present 15 complete mitochondrial genomes (>10x coverage, and 75% of the genome covered) from central European woolly mammoth specimens, produced using an in-solution capture method without the need of *in silico* design of DNA probes. We have recovered complete European clade III mitochondrial genomes ($n = 11$) and mitochondrial genomes of clade I from central Europe ($n = 4$). We show members of clade III were still present in Europe after 34 ky cal BP. In addition, we identify and describe challenges in resolving the topology of a phylogenetic tree of woolly mammoth populations. We find that the supposed replacement event occurred around the time of high climatic variability and just after the modern human transition to the Gravettian culture, but the event was not as abrupt as previously proposed.

Osteometric and mtDNA analyses from the trading post of Empúries (north-east of the Iberian Peninsula) show first evidence of cattle trade during the Early Roman period

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Written sources show that livestock were traded during the Roman period. However, there is scarce information available to characterise this trade because of its invisibility in the archaeological record. In this poster, we shed light on this issue by applying both osteometric and genetic analyses on cattle remains from the Roman trading post of Empúries (north-east of the Iberian Peninsula) to determine how livestock contributed to Roman trade and, thus, to the economy of the Empire.

Osteometric analysis of 26 cattle metacarpals from Empúries has allowed us to document the presence of three different cattle morphotypes in this city during its Early Roman occupation: very large robust specimens; smaller more gracile specimens; and variably shaped but very small individuals, similar to Iron Age local stock. MtDNA analysis of the same 26 cattle metacarpals has allowed us to document that nine individuals grouped within the T3 or the T/T3 haplogroup and two individuals belonged to haplogroup T1. All the metacarpals belonging to the T3 or T/T3 haplogroup were from the very large robust or smaller more gracile specimens. Conversely, the two T1 metacarpals belonged to the very small individuals.

These morphological and genetic differences, plus the large genetic diversity seen in Empúries cattle, can be explained through trade of different specialised cattle varieties. Taking into account the morphological characteristics of the new morphotypes, we suggest that cattle were traded mainly for milk production and traction, and they were used to improve the local stock, which were more suitable for meat production.

Resuming Resmo - sorting out mobility from diet using microsampling, multi-isotope analysis and modelling

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A megalithic tomb on the island of Öland in the Baltic Sea, excavated in the early 20th century, has been subjected to analysis at the Archaeological Research Laboratory for a number of years. The human remains were disarticulated and commingled, so 30 mandibles and one infant femur were individually radiocarbon dated, demonstrating deposition in the tomb during three distinct chronological phases during the Neolithic and the Bronze Age. Where present, dentine from the cervix of the first, second and third molars from each individual, along with bone, were subjected to analysis of $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ in collagen, demonstrating a diet derived from a mixture of marine mammal and terrestrial herbivore protein - with an estimated marine protein input ranging between 10% and 55%. In order to study mobility, the material has also been analysed with regard to dentine and bone collagen $\delta^{34}\text{S}$. For a subsample of the material, dental enamel $^{87}\text{Sr}/^{86}\text{Sr}$ analysis was also performed - both solution measurements (TIMS) and incremental laser ablation measurements (LA MC-ICPMS). One of the challenges is the fact that the level of marine dietary input affects both the sulphur and strontium isotope values, which means that the terrestrial isotopic signal - used for identifying mobility - may be obscured by a marine signal. A multi-isotopic approach, combined with microsampling and modelling has been used to resolve this issue.

Relationship estimation from ancient DNA

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Archaeogenomic research has proven to be a valuable tool to trace migrations of historic and prehistoric groups. We have learned a lot about genetic similarities and dissimilarities between several ancient populations, while relationships within a group or burial site were rarely studied so far. Knowing the genetic kinship of archaeological samples would give important insights into social structures and burial practices of different cultures. Most archaeogenetic research concerning kinship has been restricted to uniparental markers (Y chromosomes and mitochondrial haplogroups), while studies using genome-wide information were mainly focused on comparisons between populations. Applications which infer the degree of relationship used with modern DNA require diploid SNP data or a number of high-quality microsatellite markers. Low concentration of authentic DNA, fragmentation and other post-mortem damage to ancient DNA makes the application of such tools infeasible for most archaeological samples. To infer family relationships for degraded samples, we developed the software READ (Relationship Estimation from Ancient DNA). By down-sampling and pseudo-haploidizing modern sequence data from individuals with known relationship, we show that READ can successfully infer up to second degree of relationship with as little as 0.1x shotgun coverage per ancient genome. READ is then applied to aDNA data from a number of cultures where we detect and discuss previously unknown relationships between several individuals.

Genome Evolution of Trondheimers Through the Last 1000 Years

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In Trondheim has human skeletal remains of approximately 2000 individuals been excavated from a cemetery complex, and are now contained at NTNU Museum of Science, Trondheim. This collection of individuals is an exceptionally unique record of human presence, as not only is the collection osteologically described, well-dated and well-preserved, but coming from a single location they thus provide a valuable temporal series of human samples spanning the last ~1000 years in time; from the Viking Age to the Industrial Revolution. Preliminary testing has recovered 5-50 % endogenous DNA with whole genome shotgun sequencing. Subjecting the genomic data to temporal analyses for directly observing what parts of the genome are under selection, which parts are under drift, and correlate the result with both demographic and historical events, will offer the potential to characterize micro evolutionary change in a single human “population” at high resolution, throughout a period of significant human societal change.

Burnt to a crisp? The high-throughput DNA sequencing of charred grains.

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The genetics behind the spread of agriculture is important to determining not only how and when it occurred but also its sustainability in our changing climate. Most studies using archaeological grains to answer the many questions about the origins and spread of agriculture use desiccated or water-logged grains because of their better DNA preservation. The work presented here builds on studies using charred archaeological grains, a generally under-utilised resource due to the many problems associated with the extraction and characterisation of DNA from charred material. To evaluate the amount and nature of DNA degradation caused by charring, along with potential damage patterns,

both PCR and NGS were applied to artificially charred emmer grains. These modern grains were also exposed to 210°C for different time periods to investigate the effect of charring time on DNA preservation. The results from the modern emmer grains were then compared to sequences obtained from the NGS of archaeological charred barley from the late Bronze/early Iron Age site of Assiros Toumba (from Phase 9, 1395-1343 BC) in Greece. This was done to evaluate if the data from modern charred grains could be used to determine if sequences from archaeological samples originated from endogenous ancient DNA or contaminating environmental DNA, the results of which are presented here.

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A comparison of methods for estimating evolutionary timescales using ancient DNA

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Phylogenetic analysis of DNA from modern and ancient organisms allows the reconstruction of important processes such as domestication and migration, as well as the past changes in population size. Recently, the combination of better DNA sequencing techniques and new statistical methods promises to enhance the power of phylogenetics to complement archaeology and palaeontology. These new innovations present new challenges to the field. Here, I will explain the sources of error that afflict molecular dating. I will also outline and compare the performance of three molecular-clock methods: root-to-tip regressions, least-squares dating, and Bayesian inference. Reliable estimations of evolutionary rates and timescales from time-structured DNA sequences, such as those recovered from ancient samples, are contingent upon the validity of various statistical assumptions in clock models.

0028

Trade and Empire in Ancient Bahrain: Bioarchaeological and Isotope Geochemical Perspectives

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During the Bronze Age (c. late third-early second millennium BCE), Bahrain was the centre of the Dilmun Empire, with mercantile connections to Mesopotamia, Arabia, and South Asia. The island's role as a trading hub continued during the Early Islamic Period (c. 14th-16th century AD), when the Portuguese built fortifications on top of earlier Dilmun centres to control spice trade traffic in the Persian Gulf. However, questions remain regarding the extent to which community structure and genetic diversity differed within the unique milieu of the Dilmun or Early Islamic Period trade network. The assemblages from the burial mound fields of Saar (n=15) and Hamad Town (n=24) together represent a substantial Bronze Age sample recovered from salvage excavations during the 1980s. The assemblage from the Portuguese occupation-era Islamic cemetery from Qal'at-al-Bahrain (n=25) represents one of the few Spice Trade era cemeteries from the Arabian Peninsula region. This paper will use bioarchaeological and isotopic data to investigate the real extent of foreign-local interactions on Bahrain itself during each time period, allowing another means to assess the extent to which these trade networks depended on the movement of people, material goods or both. New morphological (age and sex estimates, intra-population genetic relatedness via non-metric trait analysis) and strontium and oxygen isotope data for each assemblage will be presented, contextualized against new isotopic baselines, the secondary literature, and new isomaps to assess meteoric drinking water variation.

Ancient DNA from waterlogged oak wood provides a new baseline for evolutionary and archeological studies on temperate deciduous tree species

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Long-lived tree species build up global forest ecosystems and have been exploited by humans for thousands of years. They are presently of particular concern as their long generation times may limit their adaptability to fast-changing environments. Temporal-series from ancient tree populations can provide a unique perspective on tree evolutionary and forest use history, that may not be detected by studies relying exclusively on extant populations. This information, and a better knowledge of the interplay between forest tree species, humans and climate will likely be paramount for anticipating the potential consequences of ongoing environmental changes. In this study, we took European white oaks (*Quercus robur* and *Q. petraea*) as a tree model species group with the aim to use ancient DNA to track past population dynamics and selective trajectories in the face of major environmental changes. Since ancient DNA studies on trees, in particular in temperate regions, are still in their infancy, we first investigated subfossil and archeological wooden remains from different taphonomical and temporal contexts to define conditions that optimize access to authentic ancient DNA. Following optimized aDNA extraction methods and shotgun sequencing, we succeeded in authenticating genetic data retrieved from 128 ancient oak DNA samples aged between 700 and 9,500 years. We will present the first analyses on this extensive dataset, focusing on key drivers of endogenous oak aDNA content and the novel insights on the expansion dynamics from glacial refuges.

Identifying *Mycobacterium tuberculosis* in ancient bone and dental calculus through DNA and protein analysis.

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The possibility of detecting *Mycobacterium tuberculosis* in archaeological material through proteomic analysis has recently been challenged by Hendy et al. (2016). By combining ancient DNA analysis with proteomics, this study attempts to prove presence or absence of *M. tuberculosis* in archaeological bone using modified protocols specific to ancient samples. Ancient DNA was extracted from various skeletal material including rib, femur, lumbar, pleural tissue, tooth root and dental calculus, while protein extraction was conducted on dental calculus. The objective is to investigate whether a combination of the two biomolecular approaches can aid in the detection of pathogenic *M. tuberculosis* in humans, and whether the source of skeletal material is of relevance to this potential detection. Through shotgun proteomics, we will address the challenge of identifying proteins that are unique to *M. tuberculosis*, while shotgun sequencing will hopefully further support the presence or absence of the ancient pathogen.

Story Hidden in the Cabinet? -Unveiling the Grape Evolution by Historical Herbarium Specimens and the Newly Developed SNP Capture

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Wine grape (*V. vinifera* var. *vinifera*) were domesticated more than thousands of years yet little is known about how distinct varieties came from and its genomic change from time to time. Here, we use the newly developed GrapeReSeq SNP capture technique test three different specimens collected from major herbaria in Europe.

The results suggested that even using relatively low quality of DNA, the GrapeReSeq SNP capture successfully assigned the variety consistent to morphological characters, and the geographic information also congruent with specimens' annotation. This finding present the potential of this newly developed technique, and illuminates the crucial role of the museum and herbarium collection on the domestication and evolutionary research. The further understanding of the genetic changes through time will provide us more insight about how grape has been shaped by the demands and limitation from the society and the artificial environment.

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Demonstrating mollusc seashells as new genetic archives of the past

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Mollusc seashells enclose a wealth of information on coastal marine organisms and their environment. Their life history traits as well as (paleo-) environmental conditions, including temperature, food availability, salinity, and pollution, can be traced through the analysis of the shell internal structure and geo- and biochemical composition. Adding to this list the DNA entrapped in shell carbonate biominerals could offer a novel and complementary proxy for reconstructing paleo-environments and tracking mollusc evolutionary trajectories. We assess this potential by applying DNA extraction, high-throughput shotgun sequencing and metagenomic analyses to 34 mollusc seashells covering the last 6,000 years. We report successful DNA extraction from seashells, including ancient specimens, and show that DNA recovery is dependent on their biomineral structure, carbonate layer preservation, and disease state. We demonstrate positive taxonomic identification of mollusc species using a combination of mtDNA barcodes and complete mitogenomes, nuclear genomic data, and metagenomic approaches. We find seashell biominerals to contain a diversity of microbial DNA from the marine environment. Finally, we reconstructed the complete genome sequences of the *Vibrio tapetis* bacteria from Manila clam shells diagnosed with infection by this pathogen. Our results reveal mollusc seashells as genetic archives of the past and open new perspectives in ancient DNA research, with the potential to reconstruct the evolutionary history of molluscs, microbiomes, and pathogens in the face of environmental changes. Other future applications include conservation of endangered mollusc species and aquaculture management.

Nubian Barley evolution in a drought stress environment

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Archaeobotanical samples of barley found at Qasr Ibrim display a two-row phenotype that is unique to the region of archaeological sites upriver of the first cataract of the Nile, characterised by the development of distinctive lateral bracts. The phenotype occurs throughout all strata at Qasr Ibrim, which range from 3000 to a few hundred years in age. Previous work by the group, showed a discord between the genotype and phenotype with regard to the *Vrs1* gene, responsible for row number in extant barley - indicating a six-row ancestry for the Qasr Ibrim barley, followed by a reassertion of the two-row condition. SNPs and indels called from sequence data of captured DNA was phased using novel technologies for a number of different genes. Subsequent analysis of the phased data - including analysis with ChromoPainter, FineSTRUCTURE and inferences concerning loss of gene function - give insight into whether the curious phenotype of this barley is reflected in a more widespread pattern of adaptation across the genome.

Capture of ancient genomic DNA of individuals recovered from a Medieval Alemannic gravesite provides evidence for high mobility of fellowships during the 7th century CE.

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Whether the historic spread of cultural/language groups such as the Alemanni were migrations or local adoption of culture is still unresolved in archaeology. The Alemanni were a confederation of tribes that inhabited an area, from the third to the 10th century CE, which approximately overlaps with the modern distribution of Alemannic German dialect in Swabia. We present the genomic and isotopic data of eight individuals excavated from a gravesite in Niederstotzingen, Germany of supposed Alemannic origin dated to the 7th century CE. There were two multiple burials at the site suggesting either kinship or fellowship between the individuals. The tombs in the gravesite contained cultural artefacts and weapons indicating close contact of the Alemanni with Longobards and Byzantines. We investigated the genetic affinity of these individuals between each other and to modern West Eurasians. The genetic analysis utilised the targeted enrichment and sequencing of over 1.2 million genetic markers that have known ascertainment. From these data, we found no familial relationship among the individuals in the multiple graves, thus supporting a burial practice based rather on fellowship. All individuals were genetically male. The genetic affinities of the individuals, based on modern genetic distributions, were five Eastern Europeans, two Germans/Austrians and one Southern European. Isotopic data supports that only the Southern European individual was certainly born outside this region. The genetic data appear to correlate with the provenance of the burial artefacts, showing that westward movements and interactions among cultural groups likely occurred in this region during the 7th century CE.

Using $\delta^{13}\text{C}$ and $\delta^{18}\text{O}$ time series from livestock teeth to reveal the seasonality of mobility, foddering, and stress during the Bronze and Iron Ages in eastern Kazakhstan

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Seasonal variations of stable isotopes in herbivore teeth can be used to infer particular animal management practices and the timing of life history events. This paper focuses on carbon and oxygen isotopes incrementally sampled from mandibular molars of domesticated cattle and caprines from pastoralists sites in eastern Kazakhstan with Bronze and Iron Age occupations. The intra-tooth patterning of $\delta^{13}\text{C}$ and $\delta^{18}\text{O}$ values are used to characterize access to high-elevation pasturage, foddering with millets, and the seasonality of physiological stress marked by tooth enamel hypoplasias. Results indicate that vertical transhumance is less common than previously argued, despite the sites being located 15-20 km from rich mountain pastures available in the summer. During the winter, some animals were consuming large proportions of C4 plants, presumed to be millets, as early as 2400 cal BC. Variation in diverting this resource to animals, if at all, is observed across sites and into the Iron Age. We find that hypoplasias in livestock teeth exclusively formed during the winter, likely due to harsh conditions that impeded access to sufficient nutrition; a greater disease burden cannot be ruled out. Our data suggest that ancient animal management practices included discretionary strategies of vertical mobility and foddering with agricultural product in order to support pastoral activities in the highly seasonal environment of Inner Asia.

Contextualizing the Tianyuan genome within present and ancient human genomic diversity

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Recently, many studies have produced an unprecedented number of ancient human genomes, providing insight on human dynamics in many regions, particularly West Eurasia and the Americas. Here, we present genome-wide data from the Tianyuan specimen, dating to ~40,000 years ago. Unlike other ancient genomes studied to date, the Tianyuan genome is the first ancient Upper Paleolithic sample analyzed to have contributed greatly to the East Eurasian ancestral lineage. We compare Tianyuan to several ancient and present day human genomes to better understand both the genetic diversity in the Upper Paleolithic and the similarities and differences between Tianyuan and present day populations. Overall, the addition of genome-wide Tianyuan data provides greater insight into the population history in Eurasia over the last 40,000 years.

Implications for mid Miocene Diet from *Gomphotherium* Phytoliths in Tooth Calculus

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The coevolution of plants and animals has long been proposed. Calculus removed from the teeth of four samples from two *Gomphotherium* contained phytoliths which reflect mid Miocene dietary components. Four samples contained abundant grass phytoliths (ca. 82% of total), with long cells and bilobate short cells dominant (ca. 19 and 25%, respectively). *Gomphotherium* are traditionally considered browsers. However, grass phytolith assemblages in two individual *Gomphotherium* suggest that presence versus absence of grass phytoliths may distinguish mixed feeders and grazers from browsers. It indicated that these grasses were a significant part of the diet. Abundant Panicoid

phytoliths and sponge spicules indicate that these *Gomphotherium* grazed in a warm, moist mid Miocene environment, possibly near water.

0039

Wheat yields in ancient China: a study based on the carbon isotope discrimination of charred grains

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Wheat is now the third most cultivated crop worldwide. The evaluation of wheat yield under different climate condition is therefore crucial for making predictions of future food security. Wheat grain carbon isotope discrimination has been believed as an important index for estimating the ancient grain yield. In this study, $\delta^{13}\text{C}$ values of charred wheat grains from 26 archaeological sites in Northern China were measured. The relationship between the grain carbon isotope discrimination value and yield in modern wheat was assessed and used to calculate ancient grain yields at each archaeological site. Direct dating by AMS ^{14}C measurement of wheat grains produced ages spanning from 3952 ± 66 to 389 ± 73 cal a BP. Estimated yields based on ancient grain isotope measurements compare well with historical records of crop yield, and thus verify the value of the method. Long-term trends in ancient wheat yield are apparent yield estimates show a decrease in wheat production since the mid-Holocene of more than 50%. This decrease is likely to be linked to millennium-scale climate cycles. Ultimately, the observed decrease in wheat yield may have played a role in the decline of Bronze Age cultures in Hexi corridor, which were cultivating wheat as the primary food crop since about 3500 cal a BP.

0040

The early agriculture and its impact in NW China

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The agriculture appeared in the early Holocene and developed rapidly. The NW China lies between the heartlands of wheat, rice and rain-fed agriculture and is also crossed by the famous ‘Silk Road’. Wheat was added as a new crop to the existing millet based agricultural systems around 4100 cal BP. Land use and fire activity by early farmers affected the vegetation and environment greatly during Neolithic. When the forest were destroyed, it was hard to be rebuilt. When farmlands were abandoned, vegetation recovered with shrub and grasslands in semi-arid area. The intensity and scale of the early agriculture impact were much greater than previously thought during the Neolithic in NW China.

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A new general model for ancient DNA decay based on paleogenomic meta-analysis

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The dynamics of DNA degradation over archaeological and paleontological timespans are still poorly understood, but important for establishing practical limits of DNA survival and authentication criteria in paleogenomic datasets. To better understand the decay kinetics of DNA degradation and the environmental predictors of ancient DNA survival, we analyze 149 diverse shotgun paleogenomics datasets using established and newly developed metrics of DNA degradation. We find that a simple thermal age model describes only some aspects of degradation, such as cytosine deamination. Surprisingly, however, we find no correlation between DNA fragmentation and age—or thermal age—over long timespans. We observe that libraries of highly fragmented DNA from warm or thermally fluctuating environments are disproportionately depleted of low-energy and low-complexity DNA

motifs. We hypothesize that thermal and hydraulic stress drives histone unspooling and local denaturation in these genomic regions, exposing vulnerabilities for rapid cleavage to an asymptotic saturation point of fragmentation. Previous studies have shown links between age and recoverable endogenous DNA content in subfossil remains, suggesting theoretical limits to DNA preservation. We suggest that the primary responsible mechanism for this depletion is bulk organic displacement, and that continual DNA fragmentation is not the major limiting variable to ancient DNA recoverability with increasing age. In a closed system and a steady environment, we propose that DNA preservation over multimillion year timespans should be possible. However, environmental dynamics and organic tissue types result in open systems imposing practical age limits.

0042

An ancient genomic perspective on the horse domestication process

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The domestication of the horse in the Pontic-Caspian steppes some 6,000 years ago represents one major turning point in human history. With horses, humans could travel for the first time well above their own speed and carry their germs, culture and genes across vast geographic areas. The development of horse-drawn chariots and cavalry also radically changed the history of warfare and was instrumental to the emergence of transcontinental empires. Additionally, beyond the battlefield, farm horses have massively impacted agricultural productivity. The biological changes that accompanied the process of horse domestication are, however, difficult to reconstruct from current patterns of genetic diversity both due to the development of intensively selected and extremely influential breeds during the last two centuries, and the almost extinction of wild horses. Recent developments in ancient DNA research have opened for the characterization of complete genomes, epigenomes and microbiota over long time series. We have applied such approaches to a large panel of horse remains spread across Eurasia and dated to 44,000-200 years ago. This started revealing the genetic structure of horse populations prior to and during early domestication stages as well as the history of genetic changes that accompanied their further transformation in a range of cultural contexts. I will present our latest progress made on an extensive dataset of ancient horse genomes spanning the whole domestication temporal and geographical range.

0043

Genetics as a means of investigating cultural contact: The case of the Pitted Ware grave sites of the Island of Gotland in Scandinavia.

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The interplay of contacts between different cultures in archaeological history has been of much interest to archaeologists studying cultures throughout the world. This is the case where the Neolithization of Europe is concerned. Scandinavia is unique in that it is one of the only regions of the world where a hunter gathering society coexisted with a farming society for a thousand years before both disappeared from the archaeological record. The Pitted Ware Culture (PWC) were the last hunter gatherer group during the Middle Neolithic in Scandinavia. In the later stages of their existence, a regional variant of the Corded Ware Culture called the Battle Axe Culture (BAC) coexisted with the PWC before both cultures disappeared from the archaeological record around 2300 BC. Gotland boasts many Pitted Ware Culture burial sites where evidence of this coexistence may be apparent. Most individuals from these sites are buried in a supine position typical of PWC burials. However, a

smaller group of burials display individuals buried in a hocker position which is typical of the BAC. The aim of my project is to sequence individuals from both groups to determine whether they are genetically similar and belong to one population, or are genetically different and so are part of two populations. In so doing I assess whether coexistence between the PWC and BAC cultures involved only cultural influence of one upon the other, or whether there was some physical migration involved between the two cultural groups. Presented here are my initial genetic results

0044

Whole mtDNA sequencing in Alpine populations and the genetic history of the Neolithic Tyrolean Iceman

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The Tyrolean Iceman (also known as Ötzi or Similaun Man) is a very well-preserved natural mummy, that lived south of the Alpine ridge ~5,200 years before present (ybp), during the Copper Age. Scientific interest is further increased by the preservation of parts of his clothes and equipment (such as loincloth, shoes, leggings, axe, bow). Although the mummy has been extensively characterized genetically, the relation of the Iceman's maternal lineage with present-day mitochondrial variation remains unclear. Studies of the Iceman have shown that his mitochondrial DNA (mtDNA) belongs to a novel lineage of haplogroup K1 (K1f) not found in extant populations. We analyzed the complete mtDNA sequences of 42 haplogroup K bearing individuals from populations of the Eastern Italian Alps - putatively in genetic continuity with the Tyrolean Iceman- and compared his mitogenome with a large dataset of worldwide K1 sequences (> 1070). Our results allow a re-definition of the K1 phylogeny, and shows that the K1f haplogroup is absent or very rare ($\leq 0.3\%$) in present-day populations. We suggest that mtDNA Iceman's lineage could have disappeared during demographic events starting in Europe from ~5,000 ybp. At last, we compared our results with published data on mtDNA and Y-chromosome from modern and ancient DNA studies. We propose a scenario that could explain the apparent contrast between the phylogeographic features of maternal and paternal lineages of the Tyrolean Iceman within the context of the demographic dynamics happening in Europe from 8,000 ybp.

0045

3,000 years of genome evolution in sorghum

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Sorghum bicolor is the 5th most important cereal crop globally and a staple food source in Africa, largely due to its tolerance to environmental stress. Its relatively small genome size makes it an ideal archaeobotanical candidate for a genomic-scale investigation of domestication history.

We have sequenced the nuclear genomes of 13 modern and 11 archaeological Sorghum samples, including domesticates, semi-domesticates, wild and hybrid varieties to track the evolution of this species under domestication. The archaeological sorghums form a 3-millennium time series, giving us a time window that spans close to the origin of the crop 4000 years ago. High levels of genomic diversity are apparent between extant crop domesticates and their wild relatives, suggesting

introgression between these wild types and early cultivars; pertinently, 80% of the diversity typically found in wild sorghum can be seen in modern domesticates. We observe large differences between the archaeological genomes and modern genomes, indicating that we are observing some of the significant introgression events over time that may have been responsible for the evolution of this species to an increasingly hardy crop.

Here we show our tracking of the complex genomic changes through time, which will help to explain how this crop became so well suited to the arid latitudes it dominates today.

0046

LSD: a novel method to detect positive selection in tree time-slices

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Recent advances in ancient DNA research have considerably helped revisit the demographic history of human populations, as well as the evolutionary trajectories of other species, including the spatial and temporal origins of domesticated animals, such as dogs, dromedaries, cattle and horses. Until very recently, however, the challenges associated with ancient DNA sequencing mostly precluded the genome-wide characterisation of multiple individuals from the same ancient population. This has dramatically limited our ability to understand the role of adaptation in driving or facilitating major demographic changes. Here, we present LSD, a new methodological framework to perform genome-wide selection scans, which aims at pinpointing loci that underwent episodes of positive selection along a phylogenetic tree. LSD thus allows to time slice the past and follow the adaptive genetic changes that accompanied the emergence of species, populations and/or breeds. Unlike current methods, LSD can simultaneously operate on multiple ancient and modern-day populations, even in the presence of samples sequenced at low-to-moderate coverage. Forward simulations revealed excellent LSD performance and robustness under a wide range of demographic scenarios. Through the comparison to an extensive panel of horse genomes, we illustrate how LSD can be advantageously used to reveal the genetic changes at the foundation of the domesticated horse lineage.

0047

Taxonomic and Tissue Specific Dietary Proteins in Pottery Residues

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Organic residue analysis has been widely applied to determine the use of ceramic vessels and elucidating past economies and culinary practices, with approaches typically focussing on the recovery of lipids. Here we present a novel method for extracting dietary proteins from pottery residues and report the detection of tissue-specific dietary proteins down to the species level using LC-MS/MS.

Using this approach, we were able to extract proteins from limescale deposits on sherds from Early Chalcolithic Çatalhöyük West in Anatolia and identify peptides from milk products, cereal grains and peas at high confidence. These results demonstrate the versatility of shotgun proteomics for detecting different foodstuffs within the same analysis, often with a high degree of tissue and species specificity.

0048

Identifying experimental conditions improving in solution target enrichment for ancient DNA

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The advent of Next Generation Sequencing has deeply expanded the field of ancient DNA, making it possible to generate extensive genetic data and even whole genomes from historical and ancient samples. However the classical shotgun approach can be very costly when dealing with samples with poor preservation, associated with low endogenous levels and environmental contamination. Instead, DNA capture-enrichment methods have proven to be more cost-effective and thus better-suited for samples with low endogenous content. We have investigated different experimental parameters that could impact the effectiveness of MYbaits in-solution capture assays of ~5,000 nuclear loci or the whole genome. We found that the quantity of template DNA and molecular probes did not significantly influence the capture assay. However, the tiling of the probes, the hybridization temperature, and the proportion of endogenous DNA all heavily affected the efficacy of the assay. Besides, the GC content, the number of CpG dinucleotides, the sequence complexity and entropy, and self-annealing properties represent critical features for capture assay. Overall, we hope that our study will help improve the recovery of endogenous DNA from ancient and degraded material.

0049

MALT: Fast alignment and analysis of metagenomic DNA sequence data applied to the Tyrolean Iceman

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Modern sequencing technologies allow for the production of vast amounts of DNA sequence data in large-scale metagenomic studies revealing the complexity of microbial communities in unprecedented detail. These analyses require high-throughput computational methods for a fast processing of sequencing data while retaining a high level of sensitivity and precision.

Here we present MALT (**M**egan **A**lignment **T**ool) a program for fast alignment of DNA sequencing reads to large reference databases. MALT processes hundreds of millions of reads within only a few hours. Furthermore, MALT implements a taxonomic binning algorithm that is able to assign reads to specific bacterial species. Its tight integration with the interactive metagenomic analysis software MEGAN allows for further analysis and visualization of results. These analyses can be performed in a comparative manner for studying the dynamics of microbial communities over time, or from different habitats or hosts. In particular the human microbiome is of major interest as it is comprised not only of a large number of commensals, but potentially also pathogens that have evolved with their human host. To gain insights into these evolutionary relationships, the field of paleogenetics aims to study ancient metagenomes based on DNA extracted from archaeological remains.

We demonstrate MALT by its application to the analysis of two ancient microbiomes from the 5,300-year-old Tyrolean Iceman based on oral cavity and lung samples. Despite a strong environmental background, MALT is able to detect the weak signal of the endogenous microbiomes and identifies multiple species that are typical representatives of the respective host environment.

0050

Zonkey: a simple, accurate and sensitive method to identify first generation equid hybrids in archaeological assemblages

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The members of the Equidae family, including horses, asses and zebras, can develop first-generation (F1-) hybrids, despite their striking karyotypic and phenotypic differences. Such F1 hybrids are mostly infertile, but often present characters of considerable interests for breeders. For instance, mules have stronger working capacities, longer life spans, and are more resistant to disease than horses. They were, thus, extremely valued in antiquity, especially for trade, transport and the military applications, and relatively commonly represented in art and on coinage. Surprisingly, hybrids show a relatively limited appearance in archaeological faunal assemblages. This is mostly because taxonomic identification using only morphological traits and/or morphometrical data is extremely difficult. In this study, we developed a methodological framework that exploits high-throughput sequencing data retrieved from archaeological material to identify F1-equine hybrids. Our computational methodology is distributed in the open-source Zonkey pipeline, and shows high sensitivity and specificity, even following limited sequencing efforts.

A stable story: insights in the development of a (post)medieval population in the east of the Netherlands.

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We applied a combination of different bioarchaeological methods to 200 individuals. This enabled us to create a detailed picture of the population of Oldenzaal and surroundings and its development over time between the early middle ages and early 19th century. Recently excavations took place on the historic cemetery of this eastern Dutch town and 200 of the, in total 2750, excavated skeletons were selected for detailed analysis.

Research questions concerned the themes demography, socio-economic position, health, diet and migration and mobility, with a focus on diachronic changes. The following methods were applied on all 200 skeletons: physical anthropology, palaeopathology, DNA analysis (autosomal and Y-chromosomal STR's and mitochondrial and Y-chromosomal haplogroups) and isotope analysis (strontium, oxygen and carbon and nitrogen).

Overall we see proof of a stable population. There are no significant changes over time in the level and type of genetic diversity or amount of migrants and diet based on isotopes. Although several migrants from outside of the Netherlands could be identified, the results of the DNA and isotope analysis indicate that this population was not so much influenced by large distance migration, but rather by mobility on a regional level. The temporal changes that are observed are mainly related to changes in life conditions and daily activities over time.

Automated reconstructions of nucleosome and methylation maps with epiPALEOMIX

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Pioneering studies in the Saqqaq Palaeo-Eskimo individual and archaic hominins have shown that genome-wide ancient epigenome maps can be reconstructed from High-Throughput DNA Sequencing (HTS) data. The evidence is, however, hitherto limited to only three samples. The extent to which ancient genome-wide epigenetic landscapes can be reconstructed thus remains contentious. We developed *epiPALEOMIX*, a pipeline aimed at reconstructing genome-wide methylomes and nucleosome maps in ancient individuals, by exploiting natural post-mortem DNA degradation patterns present in HTS datasets. *epiPALEOMIX* is fast, accurate and available as an open source package, with extensive documentation. We apply *epiPALEOMIX* to the HTS data underlying 35 ancient samples including ancient anatomically modern humans, archaic hominins, equids and aurochs. We find that genuine cross-tissue and tissue-specific methylation signatures can be obtained in a range of tissues, including bone, hair and tooth. Additionally, nucleosome-positioning patterns can be reconstructed as a result of the protection of the DNA associated with nucleosomes dyads for a large subset of the analyzed samples. Finally, we identify computational parameters and sample-dependent features such as DNA damage levels, sequencing depth and cell death processes that limit the preservation of epigenetic signatures in ancient samples. This work, and the framework developed within

epiPALEOMIX opens for further investigations of ancient epigenomes through time especially aimed at investigating epigenetic changes during major evolutionary, environmental, socio-economic, and cultural transitions.

0053

Characterization of cosmetic sticks at Xiaohe Cemetery in early Bronze Age Xinjiang, China

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Cosmetics have been studied for a long time in the society and culture research, and its consumption is regarded as a cultural symbol of human society. This paper focuses on the analysis of the red cosmetic sticks, found in Xiaohe Cemetery (1980-1450BC), Xinjiang, China. The structure of the red cosmetic sticks was disclosed by SR- μ CT scanning (Synchrotron Radiation Micro-computed Tomography), while the chemical components were characterized by FTIR (Fourier Transform Infrared Spectroscopy), Raman Spectroscopy and Proteomics. The results suggested that the cosmetic sticks were made from the cattle heart and covered with a layer of hematite powders as the pigment. Given the numerous red painted relics in Xiaohe Cemetery, this kind of cosmetic sticks might be used as a primitive form of crayon for makeup and painting. The usage of cattle hearts as cosmetic sticks is firstly reported up to our knowledge, which not only reveals the varied utilizations of cattle in Xiaohe Cemetery but also shows the distinctive religious function. Furthermore, these red cosmetic sticks were usually buried with women, implying that the woman may be the painter and play a special role in religious activities.

0054

Paleoproteomic analysis of early Pleistocene fossil remains

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Ancient DNA sequencing liberated geneticists from accessing present-day genomic information only. Recovering ancient genetic information has enabled reconstruction of molecular phylogenies for extinct species and major breakthroughs in phylogeography and population genetics. Nevertheless, despite technological and methodological improvements in recovering and sequencing small amounts of damaged DNA, the oldest genomes reconstructed so far date to less than 1Ma even in high latitudes.

Sequencing of ancient protein residues using mass spectrometry represents an alternative solution to extend biomolecular investigation further back in time. Ancient protein residues persist in fossil samples much longer than DNA. We will present preliminary data demonstrating feasibility of retrieving ancient proteomes, extracted from fossil remains dated to approximately 2 million years ago (Mya) and originating from temperate geographic areas. These results, obtained from a previously neglected fossil material: dental enamel, allows molecular-based phylogenetic reconstruction of early Pleistocene remains.

Paleoproteomics for cultural heritage investigation, state of the art and perspectives.

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Cultural heritage, serves as a basis for communication of common values. European cultural heritage is one of the world's most diverse and rich patrimonies, attracting millions of visitors each year. It represents an important component of individual and collective identity, contributing to the cohesion of the EU and playing a fundamental role in European cultural integration.

Most of the cultural heritage objects produced using biogenic materials are rich in protein residues. They have been utilised for clothing, artistic expression, construction, tool assemblage and even for writing support. Ancient proteins are found almost everywhere in cultural heritage.

Only very recently the introduction of analytical approaches, most notably high-throughput mass spectrometry (MS)-based protein sequencing, allowed confident sequencing of ancient proteins. This approach, we call paleoproteomics, already demonstrated it can provide innovative results in the study, diagnostics, and protection of cultural heritage collections. Today, many of the major Natural History Museums have ancient DNA laboratories and protocols in place. It is very probable that in the near future, ancient protein research units will equally be embedded in major art and archaeology museums.

Examples of successful application of paleoproteomics analysis to cultural heritage materials will be discussed, as well as factors limiting a broader application of this approach to museum collections. The recent activation of "TEMPERA", a EU-supported Marie Skłodowska Curie European Training Network will be presented as an initiative to create an environment to train young specialists operating at the interface between proteomics and cultural heritage preservation.

Impact of modern cattle feeding practices on milk fatty acid stable carbon isotope compositions emphasise the need for caution in selecting reference animal tissues and products for archaeological investigations

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Degraded animal fats, characterized by the presence of palmitic (C_{16:0}) and stearic (C_{18:0}) fatty acids and related glycerolipids are the most common class of preserved lipids in organic residues trapped in the porous clay matrix of archaeological ceramic vessels. The ubiquitous presence of fatty acids in animal fats and plant oils precludes identification of fat types by the solely molecular composition of residues. Hence, animal fats are identified by determining their fatty acyl lipid distributions and stable carbon ($\delta^{13}\text{C}$) values allowing distinctions to be drawn between non-ruminant and ruminant, and dairy and adipose fats. The $\Delta^{13}\text{C}$ proxy ($= \delta^{13}\text{C}_{18:0} - \delta^{13}\text{C}_{16:0}$) originally proposed in the 1990s by Evershed and co-workers was based on modern reference fats sampled from animals raised in Britain on C₃ plant diets. Further analyses on adipose and dairy fats from ruminants grazing in a wide range of isoscapes have shown that the $\Delta^{13}\text{C}$ proxy can be applied in mixed C₃/C₄ environments, such as in Africa. Here we show, however, through the investigation of milk fats, how the $\Delta^{13}\text{C}$ proxy can be perturbed when animals are reared on modern diets, specifically maize silage. It is thus shown that extreme care has to be taken when choosing modern reference fats for archaeological studies, and especially that insecurely-sourced animal fats should be precluded from such databases.

A demographic history of plague revealed through historical *Y. pestis* genomes

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The second plague pandemic began with the Black Death (1347-1353) and continued with sporadic outbreaks until the 18th century in Europe. Its causative agent, the *Yersinia pestis* bacillus, is considered as one of the deadliest bacterial pathogens with an almost worldwide distribution today. Although plague is not currently considered as a pandemic threat, the reconstruction of its genetic history may potentially be utilized as a model for infectious disease epidemiology and surveillance. In recent years, the sequencing of ancient *Y. pestis* genomes has revealed the involvement of the Black Death in giving rise to most of the strain diversity present around the world today. In addition, recent climatic and ancient DNA studies have attempted to explore the relationship between the Black Death and the later European outbreaks of the second pandemic, although a clear consensus is still yet to be reached. Here, we present three historical *Y. pestis* genomes from the second plague pandemic in Spain, Russia and Germany. Our results provide support for low genetic diversity in the plague bacterium during the Black Death and an eastward travel shortly thereafter that reveals a relationship between the medieval and modern worldwide epidemics. In addition, our data from 16th century Germany suggests the presence of a European plague reservoir between the 14th and 18th centuries.

Multi-omics study of the Iceman's stomach content shows main components of a Copper Age meal: fat, wild meat and cereals.

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Human evolution is closely linked to dietary changes and food processing. This is clearly observed with the transition from hunter-gatherer lifestyle to agriculture, which gave rise to cultivation of crops, animal husbandry and permanent settlements. The more stable availability of food boosted ancient population growth. However, changes in diet had drawbacks for health such as increased rates of caries. Added to this, congregating in permanent large settlements with the adoption of agriculture promoted the spread of density-dependent infectious diseases. This study aims to reconstruct the dietary choices of ancient populations and the consequences these may have had for their health. The detection of the Iceman’s stomach content provided the unique opportunity to fully reconstruct the main components of a Copper Age meal. Initial macro- and microscopic analysis revealed that the material is extraordinarily well preserved and contains large amounts of fat residues. By using a combined multi-omics approach targeting biomolecules (ancient DNA, proteins, metabolites, and lipids), we obtained a molecular “fingerprint” of the Iceman’s diet preceding his death. The molecular data we present shows the presence of four components in the Iceman’s last meal: ibex and red deer meat supplemented with cereals and traces of bracken. In addition, the distribution of triglycerides and their constituting fatty acids is consistent with the consumption of animal muscle and adipose tissue. Our multi-omics study provides important insights into the general life and nutritional habits of a Copper Age individual in the Alpine area.

0059

Biosphere mapping- the next step.

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The current strontium isotope biosphere variation map of Britain has been well used (122 citations since publication in 2010) however it has limitations. These include: inconsistent data coverage; variable sample types; no assessment of the robustness of the data distribution and boundaries; limited accommodation for superficial deposits such as glacial moraines; no estimate of how gradational the boundaries are and finally the map is difficult to update when new data are generated. Furthermore the “measure and match” approach, used in all the currently published Sr biosphere maps, makes understanding the inherent uncertainty in creating the isotope domains difficult to communicate.

In order to address these issues NERC Isotope Geosciences Laboratory is collaborating with the British Geological Survey GeoAnalysis and Data Modelling directorate to develop a model for isotope biosphere variation based on the interaction of geological, climate and geographic contributions.

The overall aim of this project is to develop a multi-layer, multi-purpose resource that can be interrogated for archaeological, environmental, food security and ecological studies by linking geographically distributed isotope variation with environmental data. This presentation will describe how this is being produced and what the final map will look like and how it will operate.

Direct earliest evidence of dog domestication in East Asia

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As one of human best friends and pets, domestic dogs play many roles in human society. However, how, where and when it was domesticated are still controversial. Especially, the dog domestication in East Asia has not well understood in the zooarchaeological assemblages. In this presentation, the canid remains at the Shuangta Site, Jilin, China dated to the 11000 years ago were carefully studied to differentiate the domesticated dogs from the wolves by the methods of biometric measurements. In addition, stable isotope(C, N) analysis of the animals and human bones were undertaken. Quite large isotopic variations were found in the canid population, indicating some canids might have been controlled intentionally by humans. Therefore, our study provides the direct earliest evidence of dog domestication in East Asia.

0061

Lipids absorbed in Epicardial pottery reveal large-group meat consumption in the oldest known domestic structure on the Barcelona plain.

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Recent excavations beneath modern Barcelona have revealed up to 283 structures dating from the Neolithic. One of these (E-III at Reina Amàlia Street) preserves the diagnostic features of a built domestic structure. Radiocarbon dates (4700-4500 cal BC) situate it in the Ancient Epicardial Neolithic, making it the oldest known dwelling on the Barcelona plain. In consequence, the site provides an excellent opportunity to detect the range of pottery practices the first Mediterranean farmers developed during its consolidation stage. With that goal, 52 pottery samples from the structure's lower stratigraphic layers were sampled and analysed for organic residue analysis by acidified methanol extraction, GC-MS and GC-C-IRMS.

The pottery analysed has higher abundances of degraded free fatty acids in the samples located closer to the structure's hearth and the presence of ruminant fat and C18 ω -(o-alkylphenyl)alkanoic acids, which would have been thermally produced at temperatures higher than 270°C, have been revealed through biomarker analysis. The rim diameter and the sherd width, when used as a proxy for vessel dimension, suggest that significantly large quantities of meat were repeatedly cooked in the site. Such practices are consistent with isotopic analyses from human bone, bone butchery marks and hearth architecture data in the north-eastern Iberian Neolithic. Therefore, organic residue analysis has been able to provide the first direct evidence of large-group communal consumption of meat in the prehistoric Barcelona plain.

B-Thalassemia cod39 mutation found in an individual from a Punic necropolis (VI century BC-II century AD) in Sardinia

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The Mediterranean island of Sardinia has been infected by malaria since VI century BC when, according to historical records, the Punics brought it from Northern Africa. Nowadays the island has the highest frequencies of malaria genetic adaptations in Europe, with 10.7% of the population heterozygous for B-Thalassemia. In more than 95% of cases, it is caused by a single point mutation in cod39 of the beta-globin gene. However, it is still debated whether the high frequency of cod39 mutation in Sardinia, and its presence in the Western Mediterranean, reflects the colonization of the Mediterranean by the Punics or a later migration of people out of Sardinia. Here we developed a PCR based method to analyse 19 Sardinian samples collected in Punic and Roman necropolis. The Cod39 mutation was found in an individual from the Punic period. In order to better understand the origin of this individual, mitochondrial and Y chromosome haplotypes were also investigated. The mitochondrial haplotype is U5a1, which is common in both Sardinian and Punic population. Y-chromosome haplogroup is I and is present in 40.7% of the Sardinian population and in less than 2% within the populations in the areas where the Punics originated. Further analysis to investigate the Y-chromosome haplogroup's subclades may give more information about the provenance of the individual and therefore about the origin of cod39 mutation.

Drinking in the Andes: organic residue analyses of Inca *aríbalos* jars from Catamarca, Argentina.

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Festive events were part of the Inca domination strategy and fermented drinks were salient elements of the liturgy. Hospitality banquets were the setting for negotiations with annexed populations, who had an active participation in the production of beverages.

We studied organic residues from nine ceramic jars (*aríbalos*) to explore their use as containers for beverages. Samples came from Inca sites in Catamarca, Argentina (San Francisco, Las Coladas, Fuerte Quemado Intihuatana). We recovered lipid, carbohydrate and protein residues from the ceramic matrixes. We also studied native maize, mesquite and llama for comparative purposes. Samples were studied by GC-MS, EA-IRMS, HPLC-ESI and MALDI-TOF-MS.

Results from GC-MS indicated mixtures of plant and animal lipids. Plant residues result from storage of fermented drinks. Animal fats were possibly used to seal inner surfaces to hold liquids. Biomarkers for ruminant animals suggest South American camelids as probable sources. Jars show no signs of sooting from cooking. Isotopic analyses indicated some *aríbalos* with $\delta^{13}\text{C}$ values similar to *aloja*, a local beer made from mesquite (C_3 plant). Other *aríbalos* exhibited $\delta^{13}\text{C}$ values similar to *chicha* made from

maize (C₄ plant). Initial results from HPLC-ESI showed that lipids were partially found as intact triacylglycerides, indicating exceptional preservation. Acylglyceride characterization is being currently carried out to find biomarkers for native plants and animals. Results from MALDI-TOF-MS of carbohydrates were consistent with oligosaccharides from black mesquite. Optimization of peptide extraction is currently in process.

This evidence indicates that both chicha and aloja were integrated into the political commensalism sponsored by the Incas.

0064

THE PAINTING TECHNIQUE OF THE GIANT BUDDHAS OF BĀMIYĀN (AFGHANISTAN)

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A chemical investigation of the organic paint binders of the Giant Buddhas of Bāmiyān was performed using an analytical approach based on advanced proteomics methodologies and traditional gas chromatography/mass spectrometry protocols. The research was carried out on a selection of rescued fragments. The data revealed the use of egg proteins as the paint binders of the original layers, in accordance with the traditional use of this proteinaceous medium in antiquity, spanning from the Mediterranean basin to the Far East, and already in the Bronze Age. Egg tempera was thus known to artists of the region in the first centuries AD, probably also due to the position of the Bāmiyān valley, which was connected to the Silk Road. Milk was found in the overpaintings that were applied in the following centuries. The proteomics approach allowed us to identify the source of the milk proteins present in the restoration layers, despite their age and degradation. In particular cow's and goat's milk were both found, in agreement with the documented presence of rich pastures in the Bāmiyān valley when the historical restorations were carried out.

Investigating the materials of the Giant Buddhas not only enabled us to obtain isolated data on these invaluable works of art, which are now lost, but contributes in understanding the big “puzzle” of our past and the development of our culture, by implementing and supporting written sources, stylistic and anthropological studies with molecular data.

0066

Investigating early Neolithic vertical pastoralism movements of sheep in the Central Pyrenees by stable isotope analyses: data from a modern reference sample and archaeological specimens from Els Trocs (late VIth millennium cal BC; Spain)

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Early Neolithic vertical pastoralism movements of sheep from the Ebro valley to the Central Pyrenees are investigated by stable isotope analyses in modern and archaeological samples. Sheep specimens of one of the last flocks that still perform this activity in this region were analyzed by sequential analyses ($\delta^{13}\text{C}$ and $\delta^{18}\text{O}$) in bioapatite of tooth enamel. Tooth series were interpreted on a seasonal basis according to the data obtained in rainfall distribution, seasonal patterns in sampled $\delta^{18}\text{O}$ of meteoric water, vegetation changes and $\delta^{13}\text{C}$ values in sampled pastures along the altitudinal gradient in the area. The results obtained define a new analytical and conceptual framework for the interpretation of archaeological samples in this region that we follow to analyze sheep remains recovered in the high-altitude Neolithic site of Els Trocs located in Central Pyrenees (Bisaurri, Spain; 1600 m.a.s.l.). This analytical approach allows recognition of vertical seasonal movements by a similar relationship with the sequential carbon and oxygen series observed in tooth molars of modern specimens. In sum, data suggest that altitudinal pastoralism of sheep following seasonal environmental conditions in this region was already practiced since the early steps of the Neolithisation in the Iberian Peninsula.

0067

A comparative dataset of dentine and dental calculus from medieval Ireland

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Dental calculus has been used for decades in bioarchaeological contexts to study diet through microfossils, but the material has gained recent popularity in paleogenetics as an excellent preservation environment for DNA. Dental calculus can form above or below the gum-line during life, as calcium phosphates precipitate through biofilm which has formed on the surface of the tooth or root. This calcification captures constituents of the individual's oral microbiome at the time of its formation, providing paleogeneticists with a wealth of ancient genetic data. This reveals information on diet, oral or general health, and on a broader scale, changes in the human oral microbiome over time. However, the breadth of preservation and full interpretive potential of ancient dental calculus remains unexplored in a large comparative framework with other known materials, while our own ability to characterize ancient microbial communities in an unbiased and accurate way is still nascent.

The medieval Irish burial ground at Kiltasheen provides a suitable comparative framework to explore these matters. A dataset is presented that compares the bacterial content and human DNA preservation of ancient dentine and dental calculus sampled from the same tooth for nearly forty samples. These data shed light on taphonomic differences between the materials in terms of invasion by exogenous species and endogenous DNA preservation in general. Dentine, a material well-known and often-used in paleogenetics, acts as a qualitative baseline from which to judge the advantages and limitations of dental calculus as a source material for ancient DNA.

The genetic processes leading up to the woolly mammoth's extinction

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The woolly mammoth was one of the most common and widespread Pleistocene megafaunal species, with a range stretching from the British Isles across Eurasia and into North America. The process of its extinction likely started with a complex series of climatic and environmental changes, as well as hunting by expanding human populations. After becoming extinct throughout most of its range at the Pleistocene-Holocene boundary, the woolly mammoth survived in small isolated populations on islands off the coasts of Siberia and Alaska. Wrangel Island was the terminal refugium where mammoths became extinct approximately 6 thousand years after separation from the Siberian mainland. Because of its evolutionary history and long-term isolation on a small island, the woolly mammoth is an excellent model system for testing basic population genetic principles related to the effects of small population size, such as the effects of genetic drift and inbreeding. Here, we study temporal changes in neutral and adaptive genetic diversity preceding the woolly mammoth's extinction. The observed loss of genetic diversity suggests that the last population of the woolly mammoth was affected by the initial bottleneck and ensuing long-term reduction in population size associated with the isolation on Wrangel Island.

Analysis of Ancient Dental Calculus Proteins from Northern European Viking Samples

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Ancient dental calculus has been proven as a valuable and high-quality reservoir of ancient biomolecules, including DNA and proteins. Through examining dental calculus from archaeological sites, we can now gain a better understanding of the oral microbiomes of past individuals. The human oral microbiome consists of a very complex mixture of bacteria, fungi and archaea. The composition of these microbiomes alters with disease states or dietary changes, which can be reflected in these archaeological samples. With the use of high-resolution mass spectrometry we aim to reveal and analyse the protein profiles for different Northern European calculus samples dating from the Viking period. In the preliminary data we find that the most abundant species are *Actinomyces dentalis*, *Lautropia mirabilis*, *Propionibacterium propionicum* and *Homo sapiens*. Gene Ontology analysis of the human proteins shows that they are enriched in extracellular proteins and are known to be involved in different immune responses. In terms of paleopathological information, we also identify proteins in several samples from the bacterial species belonging to 'the red complex' comprised of *Porphyromonas gingivalis*, *Tannerella forsythia* and *Treponema denticola*. This complex of oral bacteria is associated with severe periodontitis. Samples with different geographical origin are compared for any variations in diet and health which might be related to different lifestyles and food sources. Besides host and microbiota derived proteins we also identify proteins from dietary sources including the milk consumption marker, bovidae beta-lactoglobulin, which we found in several samples.

MALDI-FT-ICR-MS for archaeological lipid residue analysis

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Archaeological lipid residue analysis has shown rapid development in recent decades with gas chromatography-mass spectrometry (GC-MS) in combination with isotope ratio mass spectrometries (GC-C-IRMS and EA-IRMS) becoming routine laboratory methods for studying past cuisine, technology and economy. However, there is still a search for other promising methods for identifying ancient biomolecules. One of those is mass spectrometry with the so-called soft ionisation methods covering, among others, the matrix assisted laser desorption/ionization mass spectrometry (MALDI MS).

We present the results of ancient lipid identification with matrix assisted laser desorption/ionization - Fourier transform - ion cyclotron resonance - mass spectrometer (MALDI-FT-ICR-MS). This is a high-resolution and sensitive method with low limits of detection allowing reliable identification of small to medium molecular weight compounds. Due to its principles the results can be obtained with very little or no sample preparation and from samples with variable rates of preservation. The paper discusses sample preparation protocols, selection of suitable solvents and matrix solutions, briefly also sample droplet methods and instrument settings. The results obtained from experimental as well as archaeological pottery are presented

Screening for ancient tuberculosis DNA using MALT – a metagenomic approach

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The *Mycobacterium tuberculosis* complex (MTBC) evolved from soil dwelling mycobacteria to become a major human pathogen encompassing strains that are adapted to a range of animal hosts. The zoonotic potential for one of these strains was demonstrated by the recent study of three pre-contact era coastal Peruvian humans. These individuals harboured MTBC strains closely related to those circulating in seals and other marine mammals, which rarely infect humans today. European settlers likely introduced a human-adapted MTBC lineage that replaced pre-existing strains and now dominates in the New World. Pre- and post-contact era samples are currently being genotyped to broaden our overview of ancient MTBC diversity and investigate whether the ancient Peruvian MTBC strain was present in non-coastal populations, which would support the notion that it was human-adapted in the past. Eleven putatively positive MTBC samples were identified based on PCR and gene-capture approaches. In addition, the bioinformatics tool MALT (MEGAN ALignment Tool) was applied to shotgun-sequenced data to generate a metagenomic profile of the bacterial DNA content in these samples. MALT rapidly aligns sequences to a reference database and assigns reads to their taxonomic category of best fit. The bacterial profiles demonstrate varying levels of mycobacterial background amongst samples, likely originating from environmental sources. This approach identifies endogenous MTBC reads and allows the user to evaluate the level of contaminant sequences closely resembling MTBC target organisms in ancient samples, thus providing an indication as to which samples may perform better than others for genome-wide hybridization capture.

The First and Second Plague Pandemic in Bavaria, Germany - Preliminary Screening Results

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Placed in the heartland of Central Europe, Bavaria was not only ravaged by the second pandemic of plague starting with the Black Death in 1348-1352 CE, but also experienced the first pandemic, the so-called Justinianic Plague (541-750 CE). DNA analyses of skeletal material from Aschheim and Altenerding in Bavaria have provided the first solid evidence that *Yersinia pestis*, the causative agent of plague, was implicated in the first pandemic.

The aim of this study was to systematically investigate deviant and multiple burials from Bavaria for the presence of *Y. pestis* to learn more about the fine-scale spatial and temporal distribution of the two pandemics.

In total, we screened 100 individuals from 21 sites for the presence the high copy number plasmid pPCP1 via qPCR.

Based on preliminary screening results that reveal seventeen potentially positive individuals from eight different sites, we find plague to have been a widespread phenomenon in the Early Medieval period, even in the absence of historical records. Moreover, our results indicate that the Justinianic Plague seems to persist in Bavaria until at least the end of the 7th century. Additionally, we were able to identify plague victims from the 14th century, probable victims of the Black Death 1348-1352 CE, and from a subsequent plague outbreak in the 15th century. By contrast, we were unable to detect presence of *Y. pestis* in skeletal material from the supposedly plague-free eras before the Justinianic Plague (300-541 CE) and between it and the Black Death (750-1348 CE).

A high-coverage *Yersinia pestis* Genome from a 6th century Justinianic Plague Victim

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The Justinianic Plague, which started in the 6th century and lasted to the mid 8th century, is thought to be the first of at least three historically documented plague pandemics. It was suggested to be one of the main factors that contributed to the decline of the Eastern Roman Empire and marks the transition from Antiquity to the Middle Ages. Historical accounts and molecular data suggest the bacterium *Yersinia pestis* as the etiological agent for this devastating pandemic. Here we present a high coverage *Y. pestis* genome, obtained from a 6th century skeleton recovered from a Southern German burial site close to Munich. The reconstructed genome is characterized by substitutions that are unique to this

lineage, and structural differences in regions of the genome that have been previously suggested as virulence factors. These results may be influential for functional investigations that could explore the role of these newly discovered genomic characteristics in terms of physiology, virulence and adaptation. We confirm *Y. pestis* was circulating in mainland Europe during the Justinianic pandemic and that this lineage is likely to have become extinct. Comparative analysis to a previously published lower coverage *Y. pestis* genome from the same time period and region suggests low genetic diversity of the plague bacteria during the 6th century in rural Southern Germany.

0075

Investigating dietary habits by stable isotope analyses ($\delta^{13}\text{C}$ and $\delta^{15}\text{N}$) in bone collagen of cave bear (*Ursus spelaeus*) in southern latitudes of Europe during Late Pleistocene: the case of Toll Cave (MIS3; Spain)

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Dietary habits of the extinct *Ursus spelaeus* have been always a controversial topic in paleontological studies. Previous studies measuring bone collagen carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) isotope values of Late Pleistocene European cave bears during MIS3 show usually lower positions in the trophic chain, similar or lower to those of pure herbivores. That suggests an unusual physiology conditions related to hibernation or a pure non-protein herbivorous diet, although a major number samples is desirable. In this work we investigate carbon and nitrogen values in collagen of *Ursus spelaeus* recovered in Level 4 (dated to 57.9 and 69.8 ka BP) from the Toll Cave (Moià, Catalonia, NE Iberian Peninsula). A total of 12 cave bear specimens were analyzed together with a representation of the whole contemporaneous fauna spectrum recovered in the same level. Specimens were individualized considering taxonomical identification by osteological criteria, bilateral symmetry and osteometric measures. Preservation and quality of extracted collagen was checked ensuring reliability of isotopic measures. Preliminary results show lower values ($\delta^{13}\text{C}$ & $\delta^{15}\text{N}$) in cave bear than in pure herbivores (i.e. *Cervus elaphus*), all recovered from same levels of Toll Cave. This data is discussed in the frame of work of all available data in Europe and add new information about dietary habits of this species at southern latitudes of Europe during late Pleistocene periods.

0076

Genetic turnovers and northern survival during the last glacial maximum in European brown bears

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The current phylogeographic pattern of European brown bears (*Ursus arctos*) has commonly been explained by postglacial re-colonization out of geographically distinct refugia in southern Europe, a pattern well in accordance with the Expansion/Contraction model. Studies of ancient DNA from brown

bear remains have questioned this pattern, but have failed to explain the glacial distribution of mitochondrial brown bear clades and their subsequent expansion over the European continent. We here present new mitochondrial sequences generated from remains with a wide temporal and geographical range, showing a high Late Pleistocene diversity across the continent and rejecting the confinement of bears to traditional southern refugia during the LGM. The mitochondrial data further suggests a genetic turnover just before this time, as well as a steep demographic decline starting in the mid-Holocene. Levels of stable nitrogen isotopes from the remains confirm a previously proposed shift towards increasing herbivory around the LGM in Europe. Overall, these results suggest that anthropogenic impact and inter-specific competition, rather than climate, may have had more important effects on the brown bear's ecology, demography and genetic structure than previously thought.

0077

Palaeolipidomics: developing a new lipid biomarker proxy to detect cereal processing in archaeological pottery

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The domestication of cereals and thus the development of farming is one of the most significant events in human history. However, data on the timing and the intensity of early farming in individual regions in Europe is sparse and considerable controversies exist regarding these important questions. Here we present details of a new NERC-funded project which aims to target key questions surrounding the early establishment of cereals in European prehistory. These questions will be approached through the development of a novel, lipidomics-based methodology. This poster will outline the experimental stages that will be undertaken in this project. Initially, the lipidome of historic varieties of key cereals will be assessed using non-targeted gas chromatography-quadrupole time-of-flight mass spectrometry (GC-qTOFMS). With the aid of statistical analysis, the most promising biomarker proxies will be determined. The selective and sensitive GC-qTOFMS technique will then also be used to target biomarkers surviving within the fabric of cooking vessels used to prepare cereals. Further experiments will be performed to quantify the transfer lipids into the vessel wall during cooking and to assess the effects of degradation, leaching and mobility in the soil. By analysing pottery sherds from sites with high evidence for cereal consumption and processing we want to verify the results from these experiments. Finally, we will outline the project's ultimate application to tackle overarching questions concerning the nature of early agriculture in northern and northwestern Europe.

0078

Ancient DNA analysis of Scandinavian medieval drinking horns and the horn of the last aurochs bull

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The now-extinct aurochs is the ancestor of modern domestic cattle, which were domesticated ca. 8500 BC. Genetic studies show that interbreeding between introduced domestic cattle and local aurochs probably occurred during their coexistence in Europe. The last known aurochs lived in Poland, and was killed in 1627. The timeline and extent of admixture that occurred between wild aurochs and cattle remain largely unexplored. To help investigate this, we extracted and shotgun sequenced DNA from six Scandinavian medieval drinking horns as well as the horn of the last aurochs bull. We successfully reconstructed the mitochondrial genome from five of the drinking horns, and the last aurochs bull. The mitochondrial phylogeny shows that two of the drinking horns and the horn of the last aurochs bull belong to the T3 haplotype characteristic of domestic taurine cattle, while the remaining three drinking horns exhibit European aurochs mitochondrial haplotype P. Since haplotype P is today found

only in rare cases among domestic cattle, the drinking horns with this haplotype most likely represent some of the last aurochs in Europe. Our results demonstrate that drinking horns are an excellent potential source for investigating the genetics of the last European aurochs, and further suggest that hunting of aurochs to make drinking horns contributed to their extermination. Lastly, the observation that the last aurochs bull carries a domestic cattle haplotype demonstrates how introgression from domestic cattle left a signal in the last population of aurochs.

0079

The evolution of bison in Europe during the last 50,000 years

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Climatic and environmental fluctuations as well as anthropogenic pressure have led to the extinction of much of Europe's megafauna. Here we show that the emblematic European bison has experienced several waves of population expansion, contraction and extinction during the last 50,000 years in Europe, culminating in a major reduction of genetic diversity during the Holocene. Fifty-seven complete and partial ancient mitogenomes from throughout Europe, the Caucasus and Siberia reveal that three populations of wisent (*Bison bonasus*) and steppe bison (*B. priscus*) alternated in Western Europe correlating with climate-induced environmental changes. The Late Pleistocene European steppe bison originated from northern Eurasia whereas the modern wisent population emerged from a refuge in the southern Caucasus after the last glacial maximum. This last population went extinct in the Middle Ages in France, while a related population with reduced genetic diversity survived into the 20th century in Eastern Europe. A population overlap in a transition period is reflected in ca. 36,000 year-old paintings in the French Chauvet cave. Bayesian phylogenetic analyses of these complete ancient mitogenomes yielded new dates of the various branching events during the evolution of Bison and its radiation with *Bos* that lead us to propose that the genetic affiliation between the wisent and cattle mitogenomes result from incomplete lineage sorting rather than post-speciation gene flow.

0080

Survival of eggshell peptides over millions of years in Africa is due to mineral binding

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Protein sequences can complement ancient DNA in reconstructing evolution and phylogeny, and extend the reach of biomolecular studies into deep time. It is a universal truth that proteins survive better than DNA, but for how long can they really withstand the combined effect of time and temperature? Claims of intact dinosaur protein sequences are in sharp contrast with the extent of degradation consistently found in closed-system biominerals and predicted by kinetic models. Indeed, the very mechanisms for exceptional survival have not yet been clarified. Here we use an unprecedented combination of rigorous, multi-analytical testing of the authenticity of ancient protein sequences and computational modelling of protein-mineral interactions. We target ostrich eggshell from sites spanning the last 4 million years in Tanzania and South Africa and we unequivocally demonstrate the survival of peptide sequences in palaeontological eggshell which has endured the combined effect of temperature and time for the equivalent of ~ 16 million years at 10°C (thermal age). The peptide sequence surviving consistently in the oldest eggshells is chemically unstable but calculations of the binding energy show that it is strongly bound to the mineral surface. The effect of binding is loss of entropy at the mineral surface, lowering the effective temperature of the local environment, so that the peptides are "frozen" to the surface. Biomineralising proteins from eggshell, shell and other organic-inorganic biomaterials have the best potential for preservation in the fossil record over geological timescales and can therefore help to answer fundamental questions about the past.

0081

6380-year-old oral pathogens from hunter-gatherer remains found in Kiel bay: A metagenomic approach to ancient DNA

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Dental calculus is an excellent source for well-preserved ancient DNA - even in several thousand years old remains. Dental plaque is fossilized during lifetime into dental calculus, which can be defined as a calcified bacterial biofilm. This dental calculus preserves bacterial DNA, and allows investigation of the ancient oral microbiome. Potentially, it is possible to understand the evolutionary history of the human diet as well as causes and evolution of specific oral diseases. Well preserved teeth with dental calculus from an underwater site in Kiel bay, Germany were discovered. Radiocarbon dating of the bones dates the individual in the Ertebølle culture (6380±35 BP). This late Mesolithic period is characterized by non-sedentary, hunter-fisher-gatherer societies, with no excess e.g. to starch or sugar rich food resources. DNA was extracted from dental calculus, next generation libraries were built, shotgun sequencing applied and different bioinformatic tools were used to interfere the metagenome. We were able to identify several oral pathogens, including different strains involved in the pathogenesis of periodontal disease. Amongst them, *Tannerella forsythia*, *Porphyromonas gingivalis* and *Treponema denticola*, which are all members of the so called "red complex bacteria". This is a group of bacteria associated with a severe form of periodontal disease.

These findings are very surprising due to the fact that Mesolithic remains infrequently possess dental calculus. The presence of dental calculus and oral pathogens in our case could be seen as a first hint for an imbalance in the oral bacterial community, which has been verified with our metagenome analyses.

Molecular markers in keratins from Mysticeti whales for species identification of baleen in museum and archaeological collections

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Baleen, or whalebone, has long been harvested by indigenous people as a raw material for tools, utensils, cordage, and cultural objects, and at a larger scale, collected by commercial whalers for its high value as a tough, flexible material before the advent of plastics. Applications of baleen in modern times are as diverse as they are abundant, yet the material itself has been little studied and is often ignored or overlooked in museum collections. Baleen constitutes a rich source of biomolecular information that is yet unexploited; baleen in museum collections or recovered from prehistoric or modern artefacts have the potential to contribute to studies of conservation, genetic diversity and generally the exploitation of Mysticeti whales in past and recent times. Baleen is mostly made of proteins (keratins), the same type that makes up hair or fingernails, but these proteins have not yet been sequenced in Mysticeti whales, with the exception of the minke whale. Using a methodology used for the characterization of peptidic markers in tissues such as bone and hair (peptide mass fingerprinting), we examined baleen from ten different species of whales and determined molecular markers that allow identification of all species tested. In some cases (such as in Bryde's whales) differences between specimens suggest the possibility of distinct species or sub-species. Finally the methodology was tested to identify unknown baleen and baleen scraps from an archaeological assemblage from Labrador (Canada) that span up to 1500 years of aboriginal whaling.

Degradation and recovery of DNA from 44,000 year-old rodent samples from Africa

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Rodents are important paleoenvironmental indicators and their investigation has the potential to deliver a large amount of information for the interpretation of archeological sites and past environments. Data from paleogenetic and paleogenomic analyses of this important resource could contribute substantially to these interpretations. Most rodent remains, however, originate from accumulations through predators, such as pellets of raptors. We performed taphonomic studies of DNA preservation to explore the feasibility of recovering genetic information from ancient rodent samples. In modern pellets, we could show that the passage of rodents through the digestive tract heavily damages DNA in their bones and teeth but that a minute portion of DNA can be rather well preserved. The extent of DNA damage seems to depend on the location of the skeletal parts in the stomach of the predator and the duration they are subject to the attack of the gastric juices. It is likely that the minority portion of DNA that is preserved is prone to long-term preservation. Indeed, we could show DNA to be preserved in rodent remains from a cave in Morocco in levels dated to ca. 6,000 and 44,000 years. This was possible due to the development of an optimized, sensitive and economical high-throughput genotyping assay, aMPlex Torrent, which is suitable for the screening of a large number of archeological samples containing only traces of highly degraded DNA.

First molecular and isotopic evidence of millet processing in prehistoric pottery vessels

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Analysis of organic residues in pottery vessels has been successful in detecting a range of animal and plant products as indicators of food preparation and consumption in the past. However, the identification of grain crops in pottery, has not been established as a routine approach. Extending the spectrum is highly desirable, not only to strengthen our understanding of the dispersal of crops from centres of domestication but also to determine modes of food processing, artefact function and the culinary significance of the crop. Here, we propose a new approach to identify millet in pottery vessels, a crop that spread throughout much of Eurasia during prehistory following its domestication, most likely in northern China. We report the successful identification of miliacin (olean-18-en-3 β -ol methyl ether), a pentacyclic triterpene methyl ether that is enriched in grains of common/broomcorn millet (*Panicum miliaceum*), in Bronze Age pottery vessels from the Korean Peninsula and northern Europe. The presence of millet is supported by enriched carbon stable isotope values of bulk charred organic matter and *n*-alkanoic acids, consistent with a C₄ plant origin. These data represent the first molecular and isotope identification of millet in archaeological ceramic vessels, providing a means to track the introduction, spread and consumption of this important crop.

Improving The Recovery Of Ancient DNA Sequences From Highly Degraded Material

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It is long known that ancient DNA survival is inversely correlated with fragment size. However, current sample preparation techniques are not fully suited to recover DNA sequences from fragments shorter than approximately 35 bp. Recent genetic analyses of the Middle Pleistocene remains from Sima de los Huesos in Northern Spain have shown that the recovery of such short fragments can prove critical for successful retrieval of sequence information from particularly strongly degraded ancient biological material (Dabney et al., 2013; Meyer et al. 2014). Here we show that the loss of short molecules predominantly occurs during DNA extraction and that it can be minimized when adjusting the binding buffer composition in silica-based DNA extraction. Our new extraction method not only enables efficient recovery of molecules as short as 25 bp, but also doubles the yield of sequences from longer DNA fragments compared to a previous extraction method (Dabney et al., 2013). Analyses of damage-induced substitutions as well as the base composition in sequences generated with this method indicate that this effect may be partly due to a more efficient recovery of molecules with single-strand breaks, which are easily lost under non-optimal conditions. The optimized DNA extraction in combination with single-stranded library preparation and new computational approaches for the analysis of very short DNA sequences could help to access extremely ancient or highly degraded specimens for genetic analysis that failed to produce positive results with previous methods.

Genetic structure and geographic partitioning of *Lama guanicoe* sub-populations during the late Holocene

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Archaeological studies in southern Mendoza, Argentina, have suggested a growing increase in hunting pressures on populations of *Lama guanicoe* due to an increased human population density. This would have affected the effective size of *L. guanicoe* populations potentially causing a bottleneck around 2000 years before present. This hypothesis also implies a partition of populations of *L. guanicoe* by the interruption of gene flow, especially between the mountains to Piedemonte and Payunia (lowlands).

New archaeofaunal and stable isotope studies cast doubt on previous ideas, questioning the representativeness of the data and the ambiguity of the results. But the controversy still persists, since both subsistence and mobility strategies of human groups underwent profound changes during the late Holocene, which could be explained by differences in the availability of *L. guanicoe*. For this reason, independent evidence is sought through aDNA analysis from *L. guanicoe* remains from different archaeological sites. Our research aims to determine whether the genetic structure and geographic partitioning of the populations of *L. guanicoe* changed between the beginning of the late Holocene (4000-2000 years BP) and end of the late Holocene (post-2000 BP). We will thus test the following two hypotheses:

Hypothesis 1: The size population declined drastically throughout the late Holocene. Therefore, a significant drop will be seen in genetic variability (i.e. bottleneck effect).

Hypothesis 2: Monte, Patagonia and Altoandino subpopulations maintained contact and gene flow. Therefore, haplotype and nucleotide diversity, and unique haplotypes composition are similar over time and space between subpopulations.

0087

Comparison of human and leprosy DNA content in petrous bones and teeth from St. Jorgen, Denmark (1270 - 1350 AD)

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In order to overcome the problem of low yield in ancient DNA, the petrous bone has been introduced to the field. The high density of the skulls' petrous portion causes reduced bacterial post-mortem decay. Recent studies show higher human DNA yields in pars petrosa compared to other bones. Since our research focuses on the rise and fall of leprosy in the medieval ages, it was necessary to evaluate this bone for leprosy DNA content. The pathogenesis of the disease allows hypothesizing the bacterial DNA being present at higher amounts in parts of the body that are well circulated, such as teeth, compared to dense bones.

Samples were gathered from 17 individuals buried in the St. Jorgen leprosarium cemetery in Odense, Denmark (in use from 1270 - 1350 AD). We evaluated the petrous bone for leprosy as well as human DNA content and compared the results to that of a tooth from the same individual.

Results show significantly higher human DNA content in the petrous bone compared to a tooth. Leprosy reads were more present in all teeth compared to petrous bone, except for one. We suggest that starting material needs to be evaluated for the pathogen of interest in order to generate reliable screening results. Bacterial infections take diverse pathways in the human body and we assume that there is no universal human bone that can be used for general pathogen research, metagenomics and host genetics combined. More likely, for each infection, suitable parts of the skeletal should be evaluated.

0088

The Need for Resolution: Addressing the lack of multidisciplinary integration in Medieval plague research.

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The study of the plague pathogen *Yersinia pestis* has led to a number of published ancient strains in the last years. These few assemblies have been under scrutiny to address questions relating to the spread, distribution and evolution of *Y. pestis* within and outside of Europe. How was plague introduced to Europe? When and how many times? Was there an established host reservoir within Europe during the Second Plague Pandemic? These are some of the most pressing questions research is currently trying to answer. The ancient branches of *Y. pestis*' phylogenetic tree are slowly "multiplying" but the achieved resolution is not sufficient to address any of these questions with certainty and no ancient data from Asia or ancient data from other known modern plague reservoirs are available for comparisons. Additionally, the available data itself relies solely on chromosomal data and not at all on *Y. pestis*' plasmids, which have been shown to be heavily associated with the pathogens virulence and are expected to show more variability than chromosomal DNA. Here we will discuss the importance of a good integration of the available genetic data with our current knowledge in ecology, history and archaeology, which has sadly often been disregarded. We will demonstrate that at this stage the use of genetic data alone is not sufficient to answer the questions raised by the literature. To illustrate this we will show examples from the Second Plague Pandemic whose origin has been heavily debated in the last few years.

0089

Reconstructing the migratory behaviours of extinct fish populations using stable isotope analyses

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Some of the world's most enigmatic animal populations were extirpated or became extinct prior to scientific study, leaving conservation biologists with little to go on when designing ecosystem rehabilitation and species reintroduction programs. Stable isotope analyses of archaeological and historical faunal remains have untapped potential to provide vital baseline information about the behaviours and other life characteristics of past animal populations. We examine the case of the unique Atlantic salmon (*Salmo salar*) population in the Lake Ontario watershed, which supported an immense freshwater fishery before it became extinct during the late nineteenth century. We use stable carbon, nitrogen, and sulphur isotope analyses of salmon collagen from archaeological bones and historical skin mount scales to address fundamental questions about the migratory behaviour of this species, which was such an important part of the subsistence system of indigenous peoples and is currently the subject of reintroduction efforts. We hope that this research will provide an example

of how zooarchaeological isotopic data can provide new insights into key issues for the conservation and management of contemporary ecosystems.

0090

Expanding the oral microbiome reference set

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Many of the cells in the human body are not of human origin. This fraction is comprised of microbes collectively referred to as the human microbiome. These microbes are responsible for a variety of physiological processes (i.e. digestion and disease resistance) and as such, must co-evolve with their hosts. Tracking the evolution of the human microbiome through time has proven difficult. Ancient samples of the soft tissues in which the majority of these microbes reside are often difficult to obtain and/or are too highly degraded for molecular characterisation. The oral microbiome is an exception, as dental calculus (calcified plaque) has been shown to contain highly preserved DNA from a diverse range of oral flora. The oral microbiome is thought to be comprised of ~700 prokaryote species, of which ~225 are described only as uncultivated phylotypes (groupings of isolated diagnostic sequences; Dewhirst, et al 2010). Research of the ancient oral microbiome is, therefore, not hindered by a lack of sample material, but rather by a lack of adequate reference datasets. Here we aim to create a more complete oral microbiome reference set. We will use a metagenomic pipeline incorporating programs such as MetaVelvet (Afiahayati, Sato, and Sakakibara 2015) to extend current assemblies and compile new genomes and MALT (Herbig, et al 2016) to characterize whole bacterial content using data obtained via high-throughput sequencing of 21 modern human calculus samples obtained from the Danube Private University.

0091

Genetic Analysis of Neolithic individuals from Switzerland

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The beginning of the Neolithic period in Central Europe as well as the transition to the Bronze Age was most probably marked by a genetic turnover of the population as shown recently by genetic studies. The transition from foraging and hunting to agriculture and livestock farming in the 6th millennium followed a migration wave from the Near East which split in two major routes: the Balkan/Danube route in the Southeast and the Mediterranean/Rhone route in the Southwest. A second Neolithic migration from the Pontic steppes into Central Europe is postulated for the early 3rd millennium and possibly linked to the spread of the Corded Ware Culture. Both migrations spread westwards starting from the East and then spread across Europe. Due to its geographical location the Swiss Plateau is located in between of the dispersals of these population movements and therefore might have undergone a different development than Central Europe. An excellent opportunity to investigate population dynamics in this area in the late Neolithic are the dolmen burial of Oberbipp discovered in 2012 and dated to 5500 years BP as well as the multiple burial of Spreitenbach which is approximately 4500 years old. The two sites give the possibility to compare for this region, Neolithic farmers to a population from the end of the Neolithic assigned to the Corded Ware Culture. The reconstruction of complete mitochondrial genomes using Next-Generation-Sequencing and the determination of the haplogroups shows that typical haplogroups for Neolithic farmers and Early Bronze Age populations are present in both groups.

The trials and tribulations of strontium isotope analysis of ancient charred grains

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The $^{87}\text{Sr}/^{86}\text{Sr}$ composition of charred cereal grains from archaeological sites is increasingly cited as a potential means of identifying the movement and trade of crops in the past. Given the potential for contamination of charred cereal grains with strontium (Sr) from the burial environment, thorough investigation of the preservation of biogenic $^{87}\text{Sr}/^{86}\text{Sr}$ signatures in grains buried in a range of soil types is required. A study by Heier et al. (2009) showed that it was possible to remove diagenetic Sr contamination from charred grains buried in calcareous soils. Here, we present the results of 3-9 month-long burial experiments of both cereal grains and their rachis in peaty gley soils with high silicate content. We also compare three leaching methods and assess their potential for removing diagenetic Sr contamination. Having encountered difficulties in digesting archaeological charred cereal grains, we also share methods that have allowed us to extract enough Sr for isotopic analysis and yield reproducible results.

DNA quality in different types of archaeological plant materials

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Analyzing DNA from plant specimen from museums or archaeological excavations can improve our understanding of the history of our crop plants. DNA in dead plant materials is in a state of degradation, but under favorable conditions small amounts can survive for hundreds, sometimes thousands, of years. Desiccated grain tend to contain more DNA than waterlogged and charred specimen. The latter two are, however, more common at archaeological sites, and finding affordable methods to identify the useful samples and analyze them would greatly expand the available pool of samples for genetic analysis. With this in mind we have started looking into available methods for analyzing aDNA from plant remains and evaluating the materials themselves for suitability for DNA analyses. So far we have tested a few different genotyping methods. The desiccated materials are the most probable to permit PCR amplification, but we have also successfully amplified and sequenced part of the trnL region in waterlogged 17th century Swedish barley. In addition a set of waterlogged and charred materials were genotyped using KASP (Kompetitive Allele Specific PCR). Some of the waterlogged samples, but none of the charred, produced a few reliable genotypes although both age and absolute DNA concentrations were similar for waterlogged and charred samples. The charring process itself has been shown to damage the DNA, but also generates metabolites that act as PCR inhibitors, which may explain the lack of results for charred specimen.

Maternal Genetic Ancestry and Legacy of 10th Century AD Hungarians

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The ancient Hungarians originated from the Ural region in today's central Russia and migrated across the Eastern European steppe, according to historical sources. The Hungarians conquered the Carpathian Basin 895-907 AD, and admixed with the indigenous communities. Here we present mitochondrial DNA results from three datasets: one from the Avar period (7th-9th centuries) of the Carpathian Basin (n = 31); one from the Hungarian conquest-period (n=76); and a completion of the published 10th-12th century Hungarian-Slavic contact zone dataset by four samples. We compare these mitochondrial DNA hypervariable segment sequences and haplogroup results with published ancient and modern Eurasian data. Whereas the analyzed Avars represents a certain group of the Avar society that shows East and South European genetic characteristics, the Hungarian conquerors' maternal gene pool is a mixture of West Eurasian and Central and North Eurasian elements. Comprehensively analyzing the results, both the linguistically recorded Finno-Ugric roots and historically documented Turkic and Central Asian influxes had possible genetic imprints in the conquerors' genetic composition. Our data allows a complex series of historic and population genetic events before the formation of the medieval population of the Carpathian Basin, and the maternal genetic continuity between 10th -12th century and modern Hungarians.

DamageProfiler: Calculation of damage patterns in next generation sequencing data from ancient DNA

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Compared to modern DNA, the analyses of ancient DNA (aDNA) pose challenges, such as the identification of contamination by exogenous DNA of other species from the environment and modern DNA of the species of interest. Furthermore, post-mortem damage complicates the analysis, especially nucleotide misincorporations that are caused by deamination of cytosine to uracil that is read as thymine by polymerases. These occur increasingly towards the ends of the DNA molecules and have been suggested as the main diagnostic feature to authenticate aDNA. There exist several tools, which can be used to calculate damage patterns, for example mapDamage. This package includes a statistical approach to rescale quality scores of high probable damaged bases to compensate for nucleotide misincorporations. We have developed DamageProfiler, an alternative to mapDamage. It is a user-friendly, java-implemented tool, which is also available as part of EAGER, a pipeline for reconstructing ancient genomes. It provides an attractive graphical representation of damage patterns in aDNA as well as fragment size distribution, which both can be used to verify the ancient origin of a sample. The calculation of damage patterns is done in a fast and efficient way, and is up to 10 times faster as mapDamage for larger datasets. Moreover, DamageProfiler calculates within the first and last ten bases of the DNA fragment for each position independently the probability whether the base at the specific position originates from damage by using a Monte Carlo Markov Chain model. Based on the results, the base is flagged as probably being damaged.

Evolution history over millenia of sub-lineages of invasive *Salmonella enterica*

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Most cases of mammalian salmonellosis are caused by subspecies I of *Salmonella enterica*. One particular lineage in that subspecies contains sub-lineages that cause invasive disease of humans (Paratyphi C), swine (Typhisuus) and both of them (Choleraesuis). Metagenomic analyses of bones and teeth from a 25 year old woman who was buried in Trondheim, Norway in 1200±25CE yielded a genome (7x coverage) which was closely related to Paratyphi C. Our analyses showed that Paratyphi C originated in Europe but has disappeared there and is now endemic in Asia and Africa. We calculated tMRCA for all of Paratyphi C as 1380±175 ya, and 3950±140 ya for the entire lineage. Our extrapolation indicated a date of approximately 72,000±12,000 years for all of subspecies I. All 219 genomes of modern Paratyphi C, Choleraesuis and Typhisuus are very highly related, with only a few 1000 SNPs scattered across their core genomes. The pan-genome is quite diverse due to the gain and loss of genomic islands, including bacteriophages and plasmids, but most of these changes in the accessory genome are transient and are only found in single bacteria. The dated evolutionary tree of this lineage shows only few persistent changes in the accessory genome over the last 4000 years, most of which seem to reflect random events rather than natural selection. Thus, the analysis of extant bacteria overemphasizes the rate of evolutionary change within these pathogens. This analysis exemplifies the advantages gained by combining aDNA with modern population genetics.

The 5,300-year-old *Helicobacter pylori* genome of the Iceman

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The stomach bacterium *Helicobacter pylori* is one of the most prevalent human pathogens. It has dispersed globally with its human host, resulting in a distinct phylogeographic pattern that can be used to reconstruct both recent and ancient human migrations. The modern *H. pylori* strain found in most

Europeans (hpEurope) has putatively originated from recombination of the two ancestral populations Ancestral Europe 1 and 2 (AE1 and AE2). However, there exist different hypotheses about when and where the hybridization took place, reflecting the complex demographic history of Europeans.

In this study, we screened biopsy samples from the gastrointestinal tract of the Iceman, a 5300-year-old European Copper Age mummy, for the presence of *H. pylori*. By using metagenomic diagnostics and targeted genome capture, we determined the presence of *H. pylori* and reconstructed its complete genome. Comparison with contemporary *H. pylori* sequences and proteomics analysis classified the ancient *H. pylori* as cytotoxic type strain that triggered already calprotectin release as a result of host inflammatory immune responses.

Comparative analysis of ancient housekeeping gene fragments with a global multilocus sequence typing (MLST) database and comparative whole-genome analyses assigned the 5,300-year-old bacterium to the modern population hpAsia2 commonly found in Central and South Asia. The “Iceman” *H. pylori* is a nearly pure representative of the bacterial population of Asian origin (AE1) that existed in Europe before hybridization, suggesting that the African population (AE2) arrived in Europe within the past few thousand years, which is much later than previously proposed.

0099

Reconstructing population history in East Asia

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The deep population history of East Asia remains poorly understood compared to that of West Eurasia, due to the lack of ancient DNA data as well as limited sampling of present-day populations especially on the Tibetan Plateau and in southern China. We report a fine scale survey of East Asian history based on genome-wide data from ancient samples in the Amur River Basin, as well as 435 newly reported individuals from 53 populations. Present-day groups can be broadly classified into highly differentiated clusters, corresponding to Amur River Basin, Tibetan Plateau, southern natives and Han Chinese. Populations of the Amur River Basin show a high degree of genetic continuity from seven thousand years ago until today, and are closely related to the strain of East Asian related ancestry present in Native Americans. Tibetan Plateau populations are all admixed, deriving about 5%-10% of their ancestry from an anciently divergent population that plausibly corresponds to the Paleolithic population on the Plateau, and the remaining part from an ancient population that no longer exists in unmixed form but that likely corresponds to expanding farmers from the Middle and Upper Yellow River Basin who also contributed 40-90% of the ancestry of Han Chinese. A total of 10-60% of Han Chinese ancestry derives from southern Native populations, and we show that the type of southern Native ancestry that contributed to Taiwan Island Austronesian speakers is most closely related to present-day speakers of Tai-Kadai languages in southern mainland China.

Mitochondrial DNA Analysis of Human Remains from Estonia

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The transition from hunter-gatherer subsistence to farming is one of the most important processes in human history. In Europe, it has been found to be a result of demic diffusion originating from the Near East. The arrival of the first farmers in Europe led to an increase of genetic diversity as well as genetic admixture of local hunter-gatherer and the migrating farmers. Previous studies investigating European human history using mitochondrial and genome-wide nuclear data from early farmers and hunter-gatherers have provided detailed insights into the process of admixture and replacement throughout the Neolithic period. However this process has been poorly studied in the Baltic region where archaeological research suggests more extensive scenarios. Here we reconstructed the complete mtDNA of 19 individuals from different archaeological sites of Estonia covering the timespan from the Narva Culture to the Corded Ware Culture and determined their mitochondrial haplogroups. The results show that the typical European hunter-gatherer maternal lineages are represented exclusively in all individuals from until the Middle Neolithic. From the Late Neolithic on, haplogroups that are associated with European Neolithic farmers are detected. The results indicate genetic continuity of foraging cultures of Mesolithic and early Neolithic backgrounds and a late demic diffusion into the territory of Estonia associated with people of the Corded Ware culture. In addition, the generated genetic data are used to gain insights into the demography of burial complexes by sex determination and maternal kinship analysis.

Genome sequences of 6000-year old barley provide new insights into the history of crop domestication

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Barley, known as one of the founder crops of the Neolithic in Europe and West Asia, was domesticated around 10,000 years ago in the Fertile Crescent. To address questions of its origin, initial domestication and subsequent dispersal and genetic diversity we sequenced ancient DNA from five directly dated 6,000-year-old barley grains recently excavated at Masada Fortress in the Judean Desert, Israel.

A comparison to whole exome sequence data from contemporary wild and domesticated barley varieties reveals a close relation of the ancient genome sequences to present-day landraces from the Southern Levant and Egypt. This points to continuity in the contemporary lineages of the barley landraces in Israel in past 6,000 years and supports the suggested origin of domesticated barley in the Upper Jordan Valley. In addition, we could also detect evidence for gene flow between cultivated and contemporaneous wild populations since the Neolithic era.

These results from the oldest plant genome sequenced so far develop and refine previous models of barley domestication and point out the necessity of studying ancient DNA from archaeobotanical

remains to understand the history of crop domestication and to support the identification of their potential origins.

0102

The efficacy of high-throughput sequencing and target enrichment on charred archaeobotanical remains.

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The majority of archaeological plant material is preserved in a charred state and obtaining reliable ancient DNA data from these remains has presented challenges due to problems associated with high rates of nucleotide damage, short DNA fragment lengths, low endogenous DNA content and the potential for modern contamination. High-throughput sequencing (HTS) technologies coupled with DNA capture enrichment techniques have the potential to overcome some of these limitations. Here we report the findings of HTS and target enrichment on four important archaeological crops (barley, grape, maize and rice) performed in three different laboratories, presenting the largest HTS assessment of charred archaeobotanical specimens to date. Rigorous analysis of our data indicated a lack of endogenous DNA in nearly all samples, with the exception of one lightly-charred maize cob. Even with target enrichment, this sample failed to yield adequate data required to address fundamental questions in archaeology and biology. We suggest these technologies are not suitable for use with charred archaeobotanicals and urge great caution when interpreting HTS data generated from these remains.

0103

Can the use of querns and millstones make a contribution of Sr to the human diet: An experiment in digestive Sr-isotope uptake.

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Strontium isotope analysis is used in many disciplines to track the movement and provenance of modern and ancient humans. However there are aspects of human activity that are not currently taken into account in our interpretations of human ⁸⁶Sr/⁸⁷Sr. For example, the ingestion of non-food components such as soil or rock grit either accidentally via the grinding of querns and millstones, or intentionally as a result of geophagy or pica. Whether ingested non-food components contribute to human ⁸⁶Sr/⁸⁷Sr has not been explored and is rarely, if ever, taken into account in interpretations. Can the likes of radiogenic micas (as found in the stomach of the Alpine Ice Man), or other minerals, provide a substantial strontium component when ingested regularly and made bioaccessible by gastric acid?

Using three known rock types used for querns and millstones in Britain, Millstone Grit, Pennant Sandstone and Eskdale Granite, 'rock flour' was produced to represent the non-food component that could have been ingested when preparing food with a quern or millstone in the past. These rock flours underwent the Unified Bioaccessibility Method (UBM), developed by the Bioaccessibility Research Group of Europe (BARGE) for examining bioavailable components in soils by simulating the human digestive system. This study is the first of its kind to conclude whether ingested non-food components can contribute to human ⁸⁶Sr/⁸⁷Sr and whether human activities that result in the ingestion of non-food components need to be considered in our interpretations when using Strontium isotope analysis.

Stable isotope evidence for diet and subsistence patterns of the prehistoric populations of south-eastern Uruguay

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Several models have been proposed to explain the economy of the prehistoric inhabitants of south-eastern Uruguay. One of the central aspects of these models is the importance given to farming practices as an indicator of complexity, particularly regarding maize consumption. Another issue is concerning marine resources, as the suggested seasonal exploitation of those resources implies a high mobility pattern for these groups. In this work, new stable isotope data from human bone apatite ($\delta^{13}\text{C}$) and collagen ($\delta^{13}\text{C}$, $\delta^{15}\text{N}$) were generated in order to contribute to this discussion. The skeletal sample was taken from two archaeological sites characterized by the presence of mound structures and dated at 3660-1500 years BP.

Isotope patterns show that protein intake in the region is consistent with a continental diet, with homogenous values among individuals. Contradicting hypotheses that propose high mobility and a link between coast and continent, no evidence of consumption of marine resources was found. Apatite $\delta^{13}\text{C}$ was more variable, with values indicating that some individuals incorporated C4 items as a complement to a predominantly C3 diet. Likewise, this more ^{13}C enriched diet is seen in more recent individuals, indicating that it may correspond to a temporal trend. The isotopic data is consistent with the archaeofaunal record which evidences a preferential exploitation of continental animal species between 3000 A.P. and European contact, and with the archaeobotanical record that identifies the presence of cultigens, including *Zea mays*.

Origins and genetic legacy of the first people in Remote Oceania

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The appearance of people associated with the Lapita culture in the South Pacific ~3,000 years ago marked the beginning of the last major human dispersal to unpopulated lands, culminating in the settlement of eastern Polynesia ~1,000-700 years ago. However, the genetic relationship of these

pioneers to the long established Papuan peoples of the New Guinea region is debated. We report the first genome-wide ancient DNA data from Asia-Pacific region, from four ~2,900 to ~2,500 year old Lapita culture individuals from Vanuatu and Tonga, and co-analyze them with new data from 356 present-day Oceanians. Today, all indigenous people of the South Pacific harbor a mixture of ancestry from Papuans and a population of East Asian origin that we find to be a statistical match to the ancient Lapita individuals. Most analyses have interpreted the ubiquitous Papuan ancestry in the region today—at least 25%—as evidence that the first humans to reach Remote Oceania and Polynesia were derived from mixtures near New Guinea prior to the Lapita expansion into Remote Oceania. Our results refute this scenario, as none of the geographically and temporally diverse Lapita individuals had detectable Papuan ancestry. These results imply later major human population movements, which spread Papuan ancestry through the South Pacific after the islands' first peopling.

0106

The preservation of DNA from bone, dentin, and calculus from Gombe National Park and Pinnacle Point in Africa.

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Because of the challenges of extracting ancient DNA from bones found in warm environments, few studies have successfully examined remains from African archaeological and paleontological sites. Here we report efforts to extract DNA from faunal remains from two sites, Gombe National Park in Tanzania and Pinnacle Point in South Africa, with samples ranging in age from ~45-14 years and ~50,000-190,000 years, respectively. The Gombe chimpanzees were buried from 1-3 years after death and then the remains were excavated and stored. We extracted DNA from both dentin and dental calculus. Extracts from calculus yielded DNA and were subjected to subsequent mtGenome in-solution capture and sequencing. Mean coverage ranged from 2.6-122x in 19 individuals. Complete genome capture using human baits (MYcroarray) is currently underway for two samples. At Pinnacle Point, DNA was extracted from 44 bovid bone and dentin samples distributed across the time periods represented at the sites. Initial results from mtGenome capture using Springbok baits for seven samples suggest little to no DNA is preserved, though additional attempts are in progress using diverse synthetic baits from more than 20 bovid species mtGenomes (Agilent) and single stranded library preparation techniques. Advances in ancient DNA methods are providing results from unexpected contexts though more work is needed to fully understand the conditions under which DNA is preserved across time and geography. These technical advances will aid in the identification of unknown faunal remains and benefit in-depth phylogenetic and population history analyses in areas of the world where DNA is not commonly well-preserved.

0107

Stable isotope ($\delta^{13}\text{C}$, $\delta^{15}\text{N}$ and $\delta^{34}\text{S}$) and elemental analysis as markers for cultural heterogeneity and causes of death of a miner's population from Silbojokk in northern Fennoscandia during

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The silver mine of Nasafjäll in Swedish Lapland was established in 1635 and has known several phases placing its time of use to the 19th century. Excavations in Silbojokk, further down from Nasafjäll have been revealing buildings as a smelter, living quarters, a bakery, a church and its churchyard and many others. Already at the beginning, foreigners and swedes were travelling to Silbojokk in order to help work the mine. Local Sámi were also employed, especially in order to transport silver down to the Swedish coast. Even though the hard working climate in its harsh environment these sites are still places of meeting and bonding between different groups. Historic facts and archaeology have placed

the site in a Sámi context due to its finds and at least 36 excavated individuals from the churchyard have been osteologically determined as men, women and children of different ages. Most of the adults died quite young around the age of 25-30. Within this study I aim to study diet and mobility patterns of these past populations and as they mostly died of young age and according to historical sources of sickness due to hard working in the mines, elemental analyses is being done on the bones as to trace lead poisoning.

0108

Ancient DNA from cats - a paleogenetics perspective into past distributions and patterns of dispersal of *Felis silvestris*

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Until recently the general belief was that the initial domestication of cats took place in Egypt at least by 1,700 BC, based on evidence from figurative art. Recent zooarchaeological evidence suggests possible attempts of cat taming in Egypt even earlier, probably by ~3,700 BC. However, a complete cat skeleton found in association with a human burial dated to ~7,500 BC in Cyprus suggests that early taming of cats has arisen in the Neolithic agricultural societies of the Near and Middle East. Genetic evidence showed that only one of the four *Felis silvestris* subspecies in the Old World contributed to the genetic pool of modern domestic cats, the North African/Southwest Asian *Felis silvestris lybica*.

In this study, by analyzing mtDNA sequences of 197 ancient cats from Europe, Africa and the Near and Middle East, chronologically spanning from the Paleolithic to the 18th century AD, we showed that *F. s. lybica* lineages from both the Near East and Egypt contributed to the gene pool of the domestic cat at different historical times, with Near Eastern cats providing the first major contribution during the Neolithic and Egyptian cats spreading across the Old World during the Classical period. The expansion pattern and range suggest dispersal along maritime and terrestrial routes of trade and connectivity.

Lastly, by analyzing a SNP in the nuclear *Taqpep* gene, we also showed that the recessive allele associated with the blotched-tabby coat pattern in domestic cats appeared recently in the history of cat domestication, probably not earlier than Medieval times.

A new methodological approach for the extraction and derivatization of absorbed lipid residues from very small and very old sample amounts of ceramic potsherds for molecular analysis by Gas Chromatography-Mass Spectrometry (GC-MS) and single compound stable carbon isotope analysis by Gas Chromatography-Combustion-Isotope Ratio Mass Spectrometry (GC-C-IRMS)

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Working with very small sample amounts of archaeological ceramics is a challenge for biomolecular archaeologists that use lipid analysis as diagnostic tool to investigate past pottery uses. This endeavor gets even more challenging with very old ceramics, as the further back in time we go the less of the original material survives, which may have also undergone multiple structure alterations during the long deposition times. Moreover, a series of chemical reactions triggered by the use history and deposition of the vessels may have led to the formation of molecular products that are strongly bound within the crystalline matrix, and therefore less amenable to the commonly used solvent extractions. In that sense, application of a suitable extraction and derivatization protocol is crucial to increase the lipid recovery possibilities and to offer interpretation potentials.

Our intention is to present the results of the successful application of an acid-catalyzed direct extraction and methylation technique on the absorbed residues of extremely small sample amounts of ceramic powder (<0.1 g). They belong to one of the earliest so far reported pottery sequences in the world, the Japanese Incipient Jōmon (~13,900-13,300 cal BP). The technique was applied after the commonly used ultrasonically aided solvent extraction followed by silylation that gave no measurable yields. Interpretations on pottery use were possible through molecular analysis of the extracted lipids by Gas Chromatography-Mass Spectrometry (GC-MS) and stable carbon isotope analysis of the identified target C_{16:0} and C_{18:0} fatty acids by Gas Chromatography -Combustion-Isotope Ratio Mass Spectrometry (GC-C-IRMS).

Stable Isotope Analysis of the Blick Mead Dog: A proxy for dietary reconstruction of Mesolithic Hunter-Gatherers

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Domestic dogs can be used as proxies for humans in dietary reconstruction, because it is likely that their diet will to some extent be similar to those of the humans. At the Mesolithic site of Blick Mead in the Stonehenge landscape no human remains have been recovered to date. However, excavations in 2013 recovered an upper, left 4th premolar from an early domestic dog. In this study, incremental dentine sampling was carried out on the tooth for collagen isotope analysis: nine incremental samples from the crown and one from the partially surviving root were obtained. Carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) analysis show that there is little variation in the dog's diet in its early life (3-5 months). The $\delta^{15}\text{N}$ values range between +7.9‰ to +8.7‰, averaging +8.5‰, whereas $\delta^{13}\text{C}$ values range between -21.3‰ and -20.5‰, averaging -20.9‰. While different from the isotope ratios produced by the Star Carr and Seamer Carr dogs, the Blick Mead dog had $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values suggesting a diet consistent with the consumption of large terrestrial mammals found at the site. Further $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ analyses were conducted on the astragali of two aurochs from the site and recorded an average $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ value of -23.7‰ and +3.7‰, respectively. Forthcoming $\delta^{13}\text{C}$ and $\delta^{18}\text{O}$ values from the enamel will provide additional information to corroborate the dentine data and shed light on seasonality. By

extrapolating these results to the humans who kept the dog we hope to widen our understanding of Mesolithic hunter-gatherers in Britain.

0111

Towards the identification of plant residues in prehistoric archaeological artefacts: integrating lipid and protein approaches

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In the last decades organic residue analysis of ceramic artefacts have advanced our understanding of culinary practices and economies in the past. Current approaches, deploying lipid residue analysis, have allowed a wide range of prehistoric commodities processed in pottery to be identified. Much of this research however has focused on identifying animal fats, whilst plant products have been notoriously difficult to evidence, partly due to their low lipid content. Here we present the results of an integrated approach involving lipid and protein analysis of an amorphous organic deposit recovered from an extraordinarily well-preserved wooden artefact from Bronze Age Switzerland. The lipids analysis revealed molecular compositions typically associated with plant products, notably phytosterols and long-chain fatty acids but also specific plant lipid biomarkers attributable to cereal grains. The lipid results were confirmed by LC-MS/MS analysis of extracted proteins, which identified wheat proteins specific to the endosperm of the grain. The results demonstrate the benefit of such integrated methodologies for understanding vessel contents, and calls for application to a wider range of archaeological contexts.

0112

Metagenomic analysis of a permafrost-preserved woolly mammoth calf

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In 2007, a frozen mummified woolly mammoth (*Mammuthus primigenius*) calf ('Lyuba') was found along the Yuribey river on the Yamal peninsula, northwestern Siberia. Radioisotopic dating indicated that it lived approximately 42'000 years before present. Anatomical and histological investigations revealed that the calf was female, between one and three months old, was in a good nutritional state, lived in a tundra-like landscape, and that the cause of death was likely to be drowning. Histological examination also identified parasitic nematodes in Lyuba's tissues. Furthermore, Lyuba's mummy likely endured at least one cycle of thawing and freezing before discovery. Here we investigate metagenomic profiles of soft tissue samples collected during endoscopy and autopsy of Lyuba. We observe a variable range of endogenous mammoth DNA preservation and limited diversity of environmental taxonomic profiles despite all samples having been collected internally and from different organs. Furthermore, we detected DNA derived from parasitic nematodes, corroborating histological findings.

The organic coating from a decorated human skull from the Neolithic site of Nahal Hemar (Israel): molecular evidence for the use of a vegetal substance

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Human modeled skulls, a feature of the Pre-Pottery Neolithic B (PPNB) period in the Near East (ca. 8600 to 7000 BC), have been discovered in Nahal Hemar cave (Israel) and one of them exhibits a black organic coating applied in a net pattern. Recent molecular analyses of the organic coating using pyrolysis gas chromatography-mass spectrometry (Py-GC-MS) and GC-MS have revealed the presence of cinnamate and benzoate derivatives suggesting the use of a styrax-type resin. A survey of the literature regarding the presence of cinnamate and benzoate derivatives led us to propose resins from *Liquidambar orientalis* or *Styrax officinalis* as possible botanical sources of the archaeological resin, both species growing in the Near East. GC-MS investigation of reference samples of fresh resins confirmed the presence of cinnamate and benzoate derivatives, indicating that such botanical sources were likely used among the ingredients of the organic coating of the skull. In addition, the triterpenoid distributions have been investigated in both the archaeological and botanical samples. The archaeological sample was shown to contain rather uncommon triterpenoids identified as 6-oxygenated derivatives of oleanolic acid based on their mass spectra. By contrast with the fresh resin of *L. orientalis* which does not contain such derivatives, the presence of the uncommon triterpenoids in the fresh resin *S. officinalis* indicated that the latter has been likely used during the preparation of the coating. Such a finding represents the earliest scientific evidence of a plant resin use in a cultural context.

Dietary practices in medieval Islamic Portugal: using stable isotopes to explore food consumption in 11-12th century Lisbon.

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The Iberian Peninsula, a crossroads between Africa and Europe and the Atlantic and Mediterranean, harboured one of the major multi-faith societies of medieval Europe, however, little is known on the everyday life of the Iberian population during Islamic rule. Archaeology has begun to redress this issue but although studies using stable isotopes to elucidate foodways in medieval Spain are growing in number, none have focused on Portugal. This research represents some of the first data from a larger project exploring debates on socio-culturally driven dietary practices by applying stable isotope analysis of carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) to study the diets in Islamic Portugal. This poster presents isotopic data from three burial sites in Lisbon: São Jorge Castle, the Mouraria and the Alfama neighbourhood. The exclusive burial site within Lisbon's castle suggests a high social status for this Islamic population, whose diet is compared to the urban population buried outside the city wall in the Mouraria and Alfama. Interesting dietary patterns have been identified suggesting differential food

access based on sex and age in the higher status population. Conversely, the lower status populations show a homogeneous diet in relation to sex and age, but differs significantly between the two populations. These findings open a window into the socio-economic strata and food preferences of 11th century Lisbon and represent the first application of stable isotope analysis to study the diet of medieval populations from Portugal.

0115

Unappreciated ecosystem diversity of oral microbiota detected in ancient Britain

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Human microbiota (microorganisms inhabiting the human body) play critical roles in human health and disease, and are shaped by an individual's cultural and environmental surroundings. Sequencing ancient microbial DNA preserved in calcified dental plaque (calculus), an accurate record of oral microbiota, from across Europe revealed significant changes in microbial biodiversity during major cultural and dietary revolutions, including the Neolithic and Industrial Revolutions. However, these studies could not resolve the specific factors that drove the rapid change in ancient microbiota between these revolutions. Here, we use Great Britain as a model system to study the factors that influence oral microbiota in greater detail. We examined microbial DNA within dental calculus from 54 ancient British individuals from the Bronze Age to post-Medieval (~2,000 BCE – 1700 CE), and collected detailed archaeological information for each individual. Ancient individuals displayed three ecosystems dominated by primary colonisers of the tooth surface: *Streptococcus*, *Actinomyces*, and *Methanobrevibacter* species. This is in direct contrast to modern oral microbiota, which are dominated by *Streptococcus* in nearly all industrialized populations. These three microbiota ecosystems are unique, containing distinctive functional profiles. None of the three were linked to a specific time period, archaeological site, or location in the mouth. However, functional analysis indicates that an individual's diet, which was likely linked to social rank and culture, may have been a defining factor. The depth of this study reveals previously unappreciated ecosystem diversity in past human microbiota, and demonstrates how dramatically recent alterations have shaped the modern microbiota studied today.

0116

Finns in the light of ancient mitochondrial DNA

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The past migrations and relations of mankind are studied today with a wide range of interdisciplinary methods, such as isotope analysis, genetics and statistics. Ancient DNA (aDNA) shows unprecedented precision in detecting and interpreting changes in populations. Mitochondrial DNA (mtDNA) allows the maternal lineages be followed back in time. Comparing the distributions and divergence of mitochondrial haplogroups helps revealing migration routes and shifts in the genetic structure. Modern Finns have been subject to a vast amount of genetic research, yet there are no previous ancient DNA studies focusing on Finnish population history. Here we analyze ancient mtDNA from ca 50 individuals from Finnish historical burials, ranging from Iron Age to recent historic times. Our aim is to resolve past relations of Finns with the neighboring populations, and investigate the migration patterns over time. We also hope to address the local emergence of haplogroups associated with early farmers, and its effect on the more archaic “hunter-gatherer” haplogroups in Finns.

We find a good preservation of ancient DNA in Finnish bone material over the timespan of 1,500 years. Complete mitochondrial genomes for each of the collections studied were retrieved. The

mitochondrial evidence is used to compare the ancient genetic structure of Finns with that of the modern population. Previously published aDNA data from other locations is used to estimate the order and timing of population changes in Finland over time, and to examine the past relations and possible patterns of migrations in historical Finland.

0117

Tracing the origins of 19th century enslaved Africans from the island of Saint Helena

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The transatlantic slave trade was the largest movement of people in recorded history. Between 1500 and the 1900, it is estimated that over 12 million Africans were enslaved and forcedly transported to the Americas. In 1807, the British outlawed the slave trade and during the course of the 19th century the Royal Navy tried to impose the ban by patrolling the Atlantic and intercepting slave ships that were still actively involved in the trade. At that time, the island of Saint Helena in the South Atlantic served as a way station for the British Navy and as an internment camp for "liberated" Africans who had been taken off the slave ships. Between 1840 and 1872, around 26,000 Africans were disembarked on the island. Historical records suggest that these people had originated mainly from West Central Africa, but their precise origins remain unknown. Recent studies have shown that genome-wide analysis of single nucleotide polymorphisms (SNPs) provides a powerful tool for estimating individual ancestry and for tracing origins. In the present study, we use low- coverage genome-wide data generated from enriched ancient DNA libraries to examine the geographic origins of enslaved Africans who were brought to the island of St. Helena during the second half of the 19th century.

0118

Mobility between the Aegean and the Levant in the Late Second Millennium BCE: inference from ancient DNA of pigs

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The Late Bronze and the early Iron Ages (ca. 1450-950 BCE) of the eastern Mediterranean region are characterized by dramatic historical processes. Empires emerged and collapsed, trade connections were established and severed, and at the end of this era socio-political unrest and migration of large groups of people were rife throughout the region. In the 12th century BCE the movements of the so-called "Sea Peoples" affected wide parts of the East Mediterranean. We study the nature of human movements during this period on trade connections, culture and animal husbandry using the ancient DNA of domestic animals, above all pigs. We recently showed that in Israel, European pig haplotypes appeared ca. 900 BCE, and soon after took over the gene pool, with all modern wild boars in Israel carrying European mitochondrial DNA. Here, we broadened the chronological and spatial scopes by studying ancient pig mitochondrial DNA from the southern Levant and Greece. The Near Eastern haplotype Y1 and supposedly Near Eastern haplotype Y2 were discovered in Greece in the mid to late 3rd millennium BCE, while the European haplotypes were found in Israel in the early Iron Age IIA (ca. 900 BCE). We propose that pigs were moved between Europe and Anatolia since the early Bronze Age. Connections between Greece and the southern Levant are observed in the Iron Age, and probably

result from the migration of Sea Peoples to the east. These results shed light on networks and movements of people during both times of prosperity and crisis.

0119

Genome sequence of a 5310-year-old maize cob provides insights into the early stages of maize domestication

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Genomic-level data from modern maize (*Zea mays* L. ssp. *mays*) landraces and wild teosinte grasses have helped clarify the complex evolutionary history of maize domestication and cultivation. Archaeological findings and genetic data point to domestication between 10,000 and 6,250 years ago in southern Mexico, with rapid evolution under human selection, leading to considerable morphological change and adaptations to varied environments. From the genetic perspective, however, many questions about the domestication process remain unanswered because modern specimens do not represent the full range of past diversity, due to abandonment of past lineages, genetic drift, on-going natural selection, and recent breeding activity. To more fully understand the history and spread of maize, we characterized the draft genome of a 5,310-year-old archaeological cob excavated 450 km northeast from maize's domestication center, in the Tehuacan Valley of Mexico. We compare this ancient sample with a modern reference panel of landraces and teosinte grasses, using D statistics, model-based clustering, and multidimensional scaling analyses, demonstrating the specimen derives from the same source population that gave rise to modern maize. However, many genes associated with key domestication traits existed in the ancestral state, sharply contrasting with the ubiquity of derived alleles in living landraces. These findings are consistent with maize evolving at a rapid pace, with morphologic changes occurring as a gradual process, and encourage further paleogenomic research to address provocative questions about the world's most produced cereal.

0120

Mitochondrial DNA analysis of first Neolithic farmers from Anatolia and Syria: implications for the Neolithisation of Europe

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The knowledge of the genetic make-up of the first Near Eastern farmers is crucial for the understanding of the biological processes involved in the Mesolithic-Neolithic transition in Europe. To elucidate the genetic contribution of Pre-Pottery Neolithic populations of Anatolia and the Levant to the European Neolithic and present-day gene pool DNA was extracted from 82 skeletal remains from four archaeological sites in the Levant (Tell Halula, Tell Ramad, Dja'de El Mughara and Tell Aswad) and two in Anatolia (Pınarbaşı and Boncuklu Höyük). A fragment of the Hypervariable Region I plus several haplogroup diagnostic SNPs were amplified by PCR and sequenced. Stringent criteria of authenticity were observed throughout the process, including analysis in a dedicated ancient DNA laboratory and replication of extraction and PCR procedures, some of them conducted in a separate laboratory. Reproducible results could be obtained for 10 samples. Haplogroup and haplotype distribution

showed a differentiation between the Anatolian and the Levantine samples. A statistical comparison with published Early Neolithic mitochondrial DNA profiles showed different patterns, with the Anatolian samples being genetically closer to the Starčevo-Criş-Kőrös and LBK-AVK pottery cultures and the Levantine samples showing stronger affinities to the Iberian Cardial and Epicardial cultures. These preliminary results suggest a maternal genetic input from the Levant into the first Neolithic communities of Iberia, which might have followed a sea route as well as a genetic contribution from Anatolia to Early Neolithic farming cultures of the Carpathian basin and Central Europe.

0121

Digging deep into the ancient human oral microbiome: Metaproteomics challenges and perspectives for modern bioinformatics

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Mass Spectrometry (MS) based proteomics enables the identification and quantification of a given proteome, the entire complement of proteins that is or can be expressed by an organism, cell or tissue. We are using ancient human dental calculus from the Viking period, as a source for proteins, in order to track changes in human health, nutrition and life style. This well-preserved reservoir of ancient biomolecules contains proteins from various sources, mainly of human and bacterial origin, as well as food remains. This enables a plethora of interesting questions to be asked, but also poses the following pivotal problem, amongst others. The appropriate search space of potential protein sequences is key to the successful identification of MS data. A very large, universal search space will yield very poor results, due to the inherent nature of state-of-the-art MS data analysis. Therefore, customized databases have to be created and novel methods are needed to cope with such data and for metaproteomics data in general. Apart from the fact that, proteins can be conserved for longer periods of time than DNA, their functional association can give additional insights that couldn't be derived from DNA. We are developing publicly available resources for species identification, customized protein databases and their functional annotation, and computational methods for data analysis, such as degradation pattern analysis (deamidation).

0122

The effect of trophic level on individual amino acid $\delta^{15}\text{N}$ values in a terrestrial ruminant food chain

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Bulk collagen nitrogen isotope analysis has been extensively used to investigate past diet and trophic positions of humans and animals. However, bulk values are an average of the $\delta^{15}\text{N}$ values of the constituent amino acids, reflecting both the nitrogen source and the effect of complex metabolic processes. This can complicate interpretations of bulk data; using compound-specific isotope analysis of amino acids can help to elucidate these metabolic effects on bulk $\delta^{15}\text{N}$ values. Although trophic level effects on individual amino acid $\delta^{15}\text{N}$ values have been previously investigated in aquatic ecosystems and terrestrial invertebrate food webs, most archaeological applications involve terrestrial herbivores, and therefore a greater understanding of these effects between diet and consumer in a terrestrial herbivore food chain is required. The analysis of pasture plant protein and cattle collagen from the North Wyke farm platform, a well-defined and well-controlled food web in which the animals' diet is precisely known, helps to clarify the effect of trophic position on individual amino acid $\delta^{15}\text{N}$ values. The results indicate that increasing trophic level affects each amino acid differently, and that terrestrial and aquatic food chains are not directly comparable.

Compound-specific radiocarbon dating of food residues preserved in archaeological pottery vessels

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Dating of pottery vessels is a challenge as regards to obtain of a reliable source of carbon. Sources of carbon in pottery vessel derive from the clay, the temper, the fuel in the kiln and the food residues. The invisible food residues preserved in the vessel wall is of particular interest because of their young age at the time of the deposition due to fast metabolic turnover and relative immobility in the burial environment. Animal fats that are distinctive by their high content of C16:0 and C18:0 fatty acids are often recovered in high concentration in archaeological potsherds and can therefore be targeted for dating. However when bulk dating the food residues, modern contaminants can be found in small amounts and can biased the results. Therefore isolating and dating the fatty acids is of particular interest to remove contaminants.

The isolation of fatty acids is performed by Preparative Capillary Gas Chromatography. If this instrument is powerful for isolating compounds from environmental samples however it needs to be improve to be applied archaeological problems. This method has been proved promising on food residues in the past but requires some improvement. The new protocol focusses on the characterisation and quantification of the contamination deriving from the isolation process and the removal of solvent use to recover the samples from the traps. Once the protocol is established with modern references it will be tested on archaeological materials of which context have been dated to prove the efficiency of compound-specific dating of food residues.

Identifying plague in 17th century London: a discussion of preliminary results

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Yersinia pestis is believed to be the causative agent of at least three documented plague pandemics: the Justinianic Plague of the Roman Empire (6th and 8th century), the second pandemic of Medieval Europe (Black Death mid 14th-18th century), and the third plague pandemic that began in China in the late 19th century. Recent ancient DNA studies have revealed a link between post Black Death outbreaks in Western Europe, which offered support to theory of the plague's persistence in the continent during the second plague pandemic. Still unanswered is the question of the existence of one or multiple plague foci in Western Europe or adjacent areas throughout the second pandemic. In the present study, we have analyzed 40 individuals from a mass grave and a control group of attritional burials from the New Churchyard in London, UK. Historical documentation and archaeological evidence indicates its use during the Great Plague of London (1665-1666), which is assumed to be the final major plague outbreak in England. Here, we present preliminary results revealing that five individuals from the mass grave tested positive for the plague bacillus by qPCR screening. These results are further supported by the detection of *Y. pestis* fragments via shotgun sequencing and ancient DNA authentication. The control group was screened under the same conditions but was negative for *Y. pestis*. Our current results open the possibility for acquisition of whole genomes from the Great Plague of London, which would permit comparison to other strains present in Europe during the second pandemic.

Seasonal reproductive patterns of buried sheep in the funeral Avellaner cave (Epicardial; Northeast Iberian Peninsula) by stable isotope sequences ($\delta^{18}\text{O}$) in bioapatite tooth enamel: funerary and sheep herding implications.

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The Avellaner cave is an Early Neolithic (Epicardial) funeral cave in the Northeast of the Iberian Peninsula (IP). The cave was exclusively used as funerary deposit along the beginning of the seventh millennium BP for a period of 150-200 years. During this time at least 19 individuals were buried inside (Lacan et al., 2011, *PNAS*). Animals were also buried probably as grave goods and sheep was the most used species. Sheep mortality profile show that younger age-class categories (i.e. neonates and infantile specimens younger than 12 months) are over-represented. This data suggests a long duration of the lambing period for this species. Seasonal reproductive patterns of buried sheep specimens are here investigated by stable isotopes sequences of oxygen ($\delta^{18}\text{O}$) values in bioapatite tooth enamel molars. Nine second lower molar from different specimens were sampled. Results are used to reconstruct duration of the lambing period and season of birth of sheep specimens. Data shows that lambing period of sheep buried in the Avellaner cave occurred almost along the year, except during the less optimal events: mid summer and early and mid winter. These results contribute to the better characterization of the funeral practices followed in the Avellaner cave, where young sheep specimens played an important role thanks to its availability during a long period of the year. On the other side, this longer availability give important information about the seasonal reproductive patterns of the early sheep herds introduced in the IP, at the end of the establishment of the Neolithic cultures.

Investigating the possible brotherhood of two Egyptian mummies Nakht-Ankh and Khnum-Nakht via ancient DNA analysis

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Ancient DNA analysis is conducted to investigate the possible brotherhood between two Egyptian mummies Nakht-Ankh (NA) and Khnum-Nakht (KN) from the 12th Dynasty (c. 1900-1783 BC). The two high status individuals were discovered in 1907 at Deir Rifeh in Middle Egypt, and conserved to the Manchester Museum since then. Their kinship has never been questioned before due to the existence of historical records that mention their common life together, and the fact that they were buried adjacent to each other. However, a re-evaluation of facts such as their morphological structure and 3D reconstructions, the large age difference of 20 years and the uniparental mention of a mother's name in hieroglyphics in combination with the lack of male filiation, has led to a new hypothesis, that these individuals are probably half-brothers. To examine this the non-recombining regions of the mitochondrial and Y-chromosome were analysed, namely the hypervariable regions (HVRI, HVRII) of the mitochondrial DNA (mtDNA), and NRY (non-recombining region) of the Y-chromosome. Sanger sequencing results were inconclusive for both samples, yielding contradictory results for both individuals, probably due to the degraded nature of ancient DNA and possible issues with contamination. Next generation sequencing (NGS) in combination with in-solution target enrichment results for the mitochondrial DNA, were successful for the two individuals. Bioinformatic analysis exhibited 19 common polymorphisms between the samples indicating that the two mummies are most likely maternally related. The overall coverage was preferential towards NA thus indicating a better preservation. Attempts are also being made to obtain Y-chromosome sequences.

Unspecific mapping when searching for a target organism in next-generation sequencing reads: The case-study of DNA extracts from medieval leprosy sufferers

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Ancient DNA (aDNA) extracts are composed of a mixture of DNA molecules of various origins. The DNA of interest is accompanied by large amounts of DNA from environmental organisms. With the rapid development of next-generation sequencing technologies, the risk of identifying the wrong species in a DNA extract due to sequence homology has increased. To judge whether or not a species is present in a DNA extract the level of cross-species mapping between the target species and its relatives should be carefully investigated. Here we present the case-study of DNA extracts from medieval leprosy sufferers. Leprosy is mainly caused by *Mycobacterium leprae* (*M. leprae*). Members of the *Mycobacterium* family include other human pathogens (*M. tuberculosis*) and numerous environmental bacteria. *Mycobacterial* species are genetically closely related and display strikingly conserved regions. All *mycobacterial* genomes studied showed at least 38% identity to *M. leprae*. To allow the accurate confirmation of presence of *M. leprae*, whole-genome coverage statistics and species-specific targets coverage statistics were compared. Species-specific targets were chosen as regions present in the genome of the species of interest and not in the other *mycobacterial* genomes studied. Using this approach, we confirmed the presence of *M. leprae* in the medieval leprosy sufferers aDNA extracts and ruled as unlikely the presence of another *mycobacterial* species in sufficient amount to bias subsequent analyses of the recovered *M. leprae* genomes. This approach can be adapted to most species and used to estimate the specificity of targeted enrichment methods.

Next-Generation-Sequencing of tetraploid wheat accessions and the origins of agriculture in the Near East

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Emmer (*Triticum dicoccum* L.) was one of the first crops to be domesticated in the Near East Neolithic. Based on genetics, archaeobotanical and experimental data, two models explaining how the domesticated forms and full-fledged agriculture emerged have been proposed. One postulates a fast process occurring in a core area, the other a protracted model with domestication occurring slowly after a mixing of wild genotypes with piece-meal emergence of domesticated traits all around the Fertile Crescent rather in a single or small number of core areas. The small number of genetic markers used to characterise wheat accessions has hindered the testing of these hypothesis. To investigate emmer wheat domestication we used genotype-by-sequencing (GBS) to identify genome-wide genetic markers in 77 accessions of wild emmer, 40 emmer and 50 other cultivated tetraploids from the Near East and nearby regions. We generated >1,000,000 unbiased single-nucleotide-polymorphisms (SNPs) specific to our accession panel. In addition to these bi-parentally inherited SNP markers, we sequenced the maternally inherited chloroplast genomes of these accessions. Our data suggests that introgression and lineage sorting shaped the population structure of wild and cultivated emmer in the Near East, with domesticated genotypes acquiring alleles from different wild populations. Our genetic data is in accordance with a protracted model, the archaeobotanical record, and falsifies previous studies suggesting single-domestications in a single core-area.

Genomics of elephants and their extinct relatives

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Elephantid lineages first appeared in Africa about 9 million years ago giving rise to the African and Asian elephants that survive until today as well as their extinct relatives, some of which disappeared just a few thousand years ago. Morphological and genetic analyses have shown that present-day elephants comprise two genera: the African *Loxodonta*, which is commonly argued to include two species, the savanna (*L. africana*) and forest (*L. cyclotis*) elephant, and the Asian *Elephas* (*Elephas maximus*). Extinct woolly mammoths (*Mammuthus primigenius*) have been genetically shown to be most closely related to the Asian elephant, while other taxa such as the straight-tusked European elephant (*Paleoloxodon antiquus*) have not been sequenced to date. We generated genome-wide data from 15 Proboscideans, including new high-coverage genomes from 7 elephants (2 forest, 2 savanna, 2 Asian and 1 straight-tusked) as well as low to medium coverage genomes from another 8 proboscideans (4 woolly mammoths, 1 Columbian mammoth, 1 straight-tusked elephant, and 2 mastodons (*Mammuthus americanum*, a non-elephant outgroup). We analyzed this dataset to document the evolutionary relationships among the different lineages and reconstruct admixture events, demographic changes and natural selection. Using complete genome sequences, we were able to establish the phylogeny of elephantids and resolve the topology of *P. antiquus*. We also discovered signals of inter-species gene flow, such as between woolly and Columbian mammoths, and between forest and savanna elephants, revealing a complex history of admixture within the elephantid family.

Insight into the origin and diversification of late marine hunter-gatherers groups from the Chilean Patagonia

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The human population history of Patagonia has been of great interest in the context of the peopling of the Americas. However, less attention has been paid to the local population structure of the groups that inhabited the area during later times. The main goal of this work is to investigate the population history of the Chilean Patagonia using genomic data. We sequenced four ancient genomes from late marine hunter-gatherers dated between 910±30 BP and 1320±30 BP and genotyped 95 modern individuals from Southern Chile and Patagonia. These samples were compared with genotyping data from 51 modern populations and four ancient individuals (Anzick-1, Selknam and Yámana) from America. An admixture analysis suggests the presence of two main ancestral components in South-Central Chile and Patagonia, both representing between 68-86% of the total ancestry in the ancient individuals. In addition, an outgroup-f3 analysis shows a closer proximity between the ancient individuals and modern populations from the area, suggesting their continuity in the region. Only considering the relationship between the ancient individuals, we saw an agreement between the geographical classification in a Kawéskar and Yámana territory and the genetic proximity between individuals, being the individuals inside each territory closer to each other. Furthermore, the comparison of the marine individuals with a terrestrial hunter-gatherer from Tierra del Fuego suggests a common origin for the marine individuals or recurrent admixture between them. Archaeological evidence has suggested multiple or a single origin for the coastal tradition, being this is the first genetic evidence contributing to the debate.

0131

The Skeleton Coast shipwreck: sourcing elephant ivory from a 16th century Portuguese trading vessel

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Whilst mining for diamonds in 2008, mine workers in Oranjemund, Namibia found over 40 tons of cargo from a shipwreck buried under the sand for 500 years. The ship was a Portuguese nau which wrecked off the coast of Namibia around 1530 AD, and the artefacts are vast and well preserved, revealing aspects of European trade and contact with Africa in the early 16th century. Among gold and silver coins, copper ingots, and navigational equipment, 100 complete tusks of elephant ivory were preserved in the sands of the so-called "Skeleton Coast". One of the most intriguing questions is the source of this ivory, as the variety of artefacts found on the ship suggests a number of possible voyages for the acquisition of goods. Biomolecular methods, in this case ancient DNA and stable isotope analyses (carbon, nitrogen, and oxygen), enable us to narrow down the source region of the ivory, shedding light on the journey and complex history of this trading vessel. Whilst it was expected due to the outer morphology of the tusks and from historical documents of Portuguese trading ports that the elephant ivory was from forest habitats along the western African coast, the initial results suggest that the tusks are from elephants that lived in mixed savanna grassland and woodland habitats in inland western Africa. The combination of the two techniques therefore provides separate but complementary lines of evidence and continues to develop a database that can be used to source ivory for modern and archaeological applications.

Comprehensive biomolecular analysis of faunal remains from Vindija Cave, Croatia, combining ZooMS collagen fingerprint analysis, stable isotopes, and ancient DNA.

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As assemblage of morphologically unidentifiable faunal remains from Vindija Cave, Croatia, has yielded ZooMS collagen fingerprint identifications, stable isotope data, ancient DNA, and radiocarbon dates relevant to the chronology and isotope ecology of the Early Upper Paleolithic in Europe. We have identified an additional hominin specimen from a layer with known Neanderthal remains, allowing for the analysis of its collagen fingerprint, stable carbon and nitrogen isotopes, radiocarbon, and ancient DNA. These results, in context with those of the associated fauna, provide insight into the dietary ecology of Upper Paleolithic hominins at the site, along with additional insights into the differential strengths and challenges encountered with ZooMS and stable isotope analysis in analyzing an assemblage with highly variable collagen preservation.

“Isoscapes” of tooth enamel phosphate oxygen isotopes ($\delta^{18}\text{O}_\text{p}$) help to identify human mobility in Early Bronze Age Britain

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It is well-known that mineralised tissues of humans are isotopically related to the geochemistry of the environment in which they live. On this basis, human skeletal remains are used to gather information on past people habitats and lives. Particularly, tooth apatite phosphate or carbonate oxygen isotope compositions ($\delta^{18}\text{O}_\text{p}$ or $\delta^{18}\text{O}_\text{c}$) are often employed to investigate mobility, as they can record the characteristic of the milieu of the individual during childhood, when the tooth formed. These applications are based on existing correlations between $\delta^{18}\text{O}$ values in bones and teeth and those of local environmental waters (precipitations, surface and plant water). The standard practice in these studies is to compare measured skeletal isotopic ratios with the same ratios measured on (or estimated for) local waters, once the appropriate conversion to go from $\delta^{18}\text{O}_\text{p}$ to $\delta^{18}\text{O}_\text{w}$ is applied.

In this study we instead used a new set of $\delta^{18}\text{O}_\text{p}$ values of mainly Early Bronze Age human teeth excavated from across the British Isles to create a model of skeletal $\delta^{18}\text{O}_\text{p}$ geographical variation (“isoscapes”). The geostatistical analysis for this dataset allowed the identification of outliers likely representing people non-local to the areas where they were excavated. This study has additionally shown great intra-population variability, suggesting a lot of movements within the British Isles at the time. The model proposed is a baseline for future archaeological and forensic studies and will allow evaluating the $\delta^{18}\text{O}_\text{p}$ from other individuals without the need to convert their values to water values, a process known to be flawed.

A Multi-Isotopic Investigation of a Large, Unusual Neolithic Assemblage

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The use of isotopic analyses to investigate both diet and mobility has in recent years emerged as an established approach to the study of Neolithic lifeways. Frequently, however, the sample sizes of British assemblages studied are fairly small, thus limiting the amount of detailed information which can be obtained. However, in 2011, the disarticulated remains of >165 human individuals were

recovered from a Middle Neolithic triple-ring-ditch monument in the east Midlands. The configuration of the human skeletal material excavated was highly unusual, and dates to a period for which few human remains have been recovered in Britain. Here, we present new $\delta^{13}\text{C}$, $\delta^{15}\text{N}$ and $^{87}\text{Sr}/^{86}\text{Sr}$ data obtained from these individuals, undertaken in an attempt to understand this unique assemblage. Stable isotope analysis of $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ of bone collagen revealed a remarkable degree of dietary homogeneity across such a large sample size, but interestingly, modelling of the data obtained also suggests a potential freshwater protein component within the diet. Conversely, strontium ($^{87}\text{Sr}/^{86}\text{Sr}$) isotope analysis on teeth from the site indicates a range of potential childhood mobility within the population, and childhood origins spanning different geological zones in the UK. The strontium data obtained therefore links to ideas previously suggested for the British Neolithic surrounding residential mobility, linked kinship networks, and pastoralist subsistence strategies. Overall, the assemblage presented here provides a unique opportunity to explore British Neolithic lifeways, and represents one of the largest isotopic analyses of British prehistoric human remains to date.

0135

Identify ancient microbial strains with < 100 palaeogenomic reads

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The application of revolutionary palaeogenomic technologies has largely re-defined archaeology. DNA from microbes in ancient samples were initially ignored or treated as contaminations. However, the identification of important pathogens in ancient samples in recent studies has re-written the human history. However, the genetic background of microbes is complicated. Pathogens and their commensal neighbours, as well as different lineages in the pathogens were hard to distinguish by traditional methods, which can only confidently assign aDNA at species level. Some recently developed algorithms can achieve strain-level genotyping, but only when a significant fraction of reads in the sample were from that strain, or the same strains were recovered in many samples.

Here I present a novel algorithm named MGplacer2, which can reliably identify strain-level genotypes from ancient samples, by taking advantage of 100,000s modern genomes sitting in public databases. An early version of MGplacer has successfully identified mixed genotypes of *Mycobacterium tuberculosis* from 400-year old mummies. Its accuracy was assured by targeting specific core SNP sites defined by modern genomes and ignoring the unreliable accessory regions. The latest development of MGplacer2 has improved the performance even further: 1) An automatic pipeline was integrated to reconstruct the phylogeny from modern genomes. 2) A super-tree based approach was applied to overcome the recombination problem, which disturbed genotype assignments in the earlier version. 3) A Bayesian approach was used to estimate the proportion of each genotypes, when multiple strains were found.

0136

Pasteurization, Processing, Palaeoenvironment – Applicability of modern dairy reference fats in archaeological lipid residue analysis using $\delta^{13}\text{C}$ of single fatty acids

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Milk based foods play a central role in the of subsistence of modern and prehistoric pastoral communities around the world, serving as a storable dietary staple that is often imbued with deep social, cultural and ritual significance. By comparing compositional and compound specific carbon stable isotope data of fatty acid residues with modern reference fats, dairy products have been identified in prehistoric pottery from a variety of archaeological contexts, especially relating to the secondary products revolution, the development and spread of pastoralism, and dietary continuity

across the Neolithic transition. However, while diagenetic effects and their impact on comparability between modern and archaeological fats have extensively been studied, other alterations introduced through processing, animal diet and environment have received considerably less attention. Here we establish overall stability of $\delta^{13}\text{C}$ values of single fatty acids during pasteurization and cream clotting despite substantial changes in fatty acid distribution. Small and heterogeneous isotopic changes and compositional differences reveal the complex interplay of several degradation pathways induced by heating and mechanical fat separation. At the same time, taxonomic clustering underlines the importance of considering impacts of environment, seasonality and dietary composition.

0137

Combining bleach and mild pre-digestion improves ancient DNA recovery from bones

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The feasibility of genome-scale studies from archaeological material remains critically dependent on the ability to access endogenous, authentic DNA. A number of pre-extraction protocols aimed to improve ancient DNA recovery before library amplification have recently been developed. We test the effects of combining two of such protocols, a bleach wash and a pre-digestion step, on 12 bone samples of Atlantic cod and domestic horse aged 750-1350 cal. years before present. Using high-throughput sequencing, we show that combined together, bleach wash and pre-digestion consistently yield DNA libraries with higher endogenous content than either of these methods alone. Additionally, the molecular complexity of these libraries is improved and endogenous DNA templates show larger size distributions. Other library characteristics, such as DNA damage profiles or the composition of microbial communities are little affected. Application of the combined protocol presented in this study will facilitate the genetic analysis of an increasing number of ancient remains and reduce the cost of whole genome sequencing.

0138

Investigating Viking Age trade of Atlantic cod using ancient DNA

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According to the first systematic historical records, dried Atlantic cod (stockfish) dominated the Norwegian export already in the 14th century AD, consisting of 80% of its total value. Nonetheless, the first origin of this trade and its expansion up to that period is unclear. While it has been suggested that the stockfish trade began around AD 1100, archaeological evidence is inconclusive. There is support for substantial trade starting later in both England and the eastern Baltic region, whilst this trade appears to have started earlier in the Viking Age trade settlement of Haithabu/Schleswig. Such evidence is based on the analysis of stable isotopes and/or on the lack of skull bones within Atlantic cod bone assemblages. Since fish were typically decapitated before drying for export, bone assemblages without skulls are indicative of long-distance trade. Yet fish from nearby sources could also be processed in this way, and stable isotopes only provide a low-resolution guide to source origin of traded cod. Here, we use whole genome sequencing (WGS) approaches to investigate the origin Atlantic cod during the Viking Age. We have obtained WGS data from samples between 1250 to 800 years BP, which will be compared to an extensive WGS dataset (>300 specimens) obtained from contemporary populations in the North Atlantic region. Identifying the genetic source of these samples may reveal a Viking Age origin and subsequent expansion of Norway's medieval stockfish

trade, which has implications for the timing of anthropogenic impacts on Northern Atlantic cod populations.

0139

Identification of human migrants in the archaeological record: testing the method of oxygen isotope analysis by a compilation of all relevant published data

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Oxygen isotope analysis of archaeological skeletal remains is an increasingly popular tool to study past human migrations. In use over the last 25 years, it is based on the premise that “you are what you drink and eat” – that human body chemistry preserves the oxygen isotopic value of water consumed in the oxygen isotopic value of body biominerals such as teeth and bones. But the technique relies on a series of assumptions that have been hard to test in controlled situations.

Here, we present our work on compiling and analysing the first global survey of published archaeological human oxygen isotope data to explore the technique's validity. Key outcomes were that several widely-held assumptions were untenable (including the degree of biological noise in the signal), and that the most widely-applied statistical methods were inappropriate for these datasets. These insights were not apparent at site-level, which has been the typical scale of analysis for most researchers.

Finally, through a spatial assessment of the dataset, we show that the degree of overlap in human isotope values from different locations across Europe is such that identifying individuals' homelands on the basis of oxygen isotope analysis alone is not possible for the regions analysed to date.

0140

Stable isotope analysis of parchment as an annual record of British agriculture and climate

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Between the 16th and 19th centuries, British agriculture underwent 'revolutionary' transformations. Despite the wealth of research in this area, historical and increasingly archaeological enquiry has been hampered by the scarcity of data of the geographical and chronological resolution required to explore this period of immensely rapid change. In this paper we present the use of dated sheepskin parchment as a geographically and chronologically sensitive isotopic record of British agriculture and climate.

To establish the use of parchment as an isotopic record, we present the $\delta^{13}\text{C}$, $\delta^{15}\text{N}$ and $\delta^{18}\text{O}$ isotope analysis of modern skin and bone from the same individuals to explore the isotopic relationship between skin and bone collagen, which highlight the rapid turnover of dermal collagen producing a seasonal signature in the skin. We also present the impact of parchment production on skin isotope values, validating the use of parchment as a reliable isotopic record.

Isotopic analysis has so far been conducted on over 200 dated sheepskin documents from between the 16th-20th centuries, with up to 30 skins for a single year. We present the preliminary results of this high resolution study on animal and landscape management.

Genomic History of Upper Paleolithic Europeans

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Little is currently known about the genetic history of ancient Europeans before the advent of agriculture ~8,500 years ago. Here we have analysed genome-wide data from 51 modern humans remains that span around 40,000 years of Eurasian prehistory. Over this time, the proportion of Neanderthal DNA decreased from 3–6% to around 2%, consistent with natural selection against Neanderthal variants in modern humans. Whereas the earliest modern humans in Europe did not contribute substantially to present-day Europeans, all individuals between ~37,000 and ~14,000 years ago descended from a single founder population which forms part of the ancestry of present-day Europeans. A ~35,000-year-old individual from northwest Europe represents an early branch of this founder population which was then displaced across a broad region, before reappearing in southwest Europe during the last ice age ~19,000 years ago. During the major warming period after ~14,000 years ago, a new genetic component related to present-day Near Easterners appears in Europe. These results document how population turnover and migration have been recurring themes of European pre-history.

Reconstruction of HLA genotypes in ancient human samples

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Genes of the human leukocyte antigen (HLA) system play an essential part in the immune system. HLA variation has been associated with susceptibility to a large number of infectious and autoimmune diseases. The analysis of the HLA region in ancient specimen based on high throughput sequencing (HTS) of ancient DNA (aDNA) enables the identification of unknown HLA allele variations as well as new insights into the development of immunity and susceptibility present today.

Numerous bioinformatical tools to identify HLA allele combinations based on HTS data are available, but with no established gold standard, most methods require deeply covered genomes due to the high variability of the HLA region. Unfortunately, aDNA is highly degraded, leading to a low and incomplete coverage of the region of interest. Furthermore, the allele combinations present in the samples might include unknown alleles that are undetectable by automated approaches that only compare the reads with modern reference sequences. We have therefore developed a method based on automated processing and manual curation of short read alignments against all known HLA alleles, allowing an easy to follow selection of the most likely allele combinations up to 4-digit resolution, including potentially unknown alleles.

We present preliminary results of an ongoing study showing an efficient approach on analyzing the HLA region based on HTS using aDNA samples. We compare our protocol with established software

and highlight the advantages of using a partly manual approach when reconstructing HLA allele combinations from degraded and incomplete data.

0143

Spatio-temporal mtDNA and isotope analyses of red deer (*Cervus elaphus*) in the Vosges: long-lasting co-existence of two “ecotypes” and low mtDNA diversity throughout millennia

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European red deer (*Cervus elaphus*) is one of the survivors of the Late Quaternary megafauna. After the Last Glacial Maximum, populations suffered several episodes of overhunting through the millennia. In the Vosges (north-eastern France), the last such episode was in mid 19th century, where few local groups survived and recolonized the region. Using 262 bp of concatenated *cyt b* (168 bp) and d-loop (94 bp) mtDNA fragments from 23 archaeological samples we found only two haplotypes (tentatively named A-*vsa1* and A-*vsa2*) of the western European red deer group A continuously present from 5000 BC to 600 AD in the region. Isotope analysis ($\delta^{13}\text{C}$ and $\delta^{15}\text{N}$) of the same archaeological samples suggests the existence of two “ecotypes” which correlate with the two haplotypes: A-*vsa2* feeding in forested more closed habitats, and A-*vsa1* feeding in more open landscapes throughout the time. Analysis of 116 modern red deer samples from the Vosges did not identify the haplotype A-*vsa2*. One novel haplotype appears that is unique to a small area in the Vosges, supporting recent translocation from an unknown region. A-*vsa1* continues to be present and because of the longer lengths of modern sequences examined (680 bp of *cyt b* and about 785 bp of d-loop) represents two haplotypes, one of which most probably originates from a source population in the Donon Massif (Lower Vosges), in agreement with historical records. Our results are indicative of pronounced bottleneck and small-scale phylopatric behaviour of female animals in the absence of migration barriers over several millennia.

0144

The Neolithic Transition at the Edge of Europe

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In Europe, the Neolithic transition marked the beginning of a period of innovations which saw people move from a mobile lifestyle, dependent on hunting and gathering for survival, to a more sedentary way of life based on food production. This new lifeway, which began in the Near East ~11 kya, spread quickly across the continental interior of Europe predominantly through demic diffusion.

While the genetic impact of the Neolithic transition has been well explored in central Europe, its impact on more peripheral regions of the continent has not been as extensively studied. To broaden our understanding of this dynamic phase in European prehistory, we analysed genomes from a 4,000 year temporal transect through the Baltic region spanning from the Late Mesolithic to the Late Neolithic period. We found evidence for connectivity from the Mesolithic to the Neolithic however, we also detected signals consistent with influxes from non-local populations. These influences were distinct from the early farmer admixture which transformed the genetic landscape of central Europe during the Neolithic. Interestingly, dietary stable isotope analyses ($\delta^{15}\text{N}$ and $\delta^{13}\text{C}$) show that the

genetic shifts coincide with diversifications in subsistence strategy. These results suggest that the Neolithic was a period of genetic flux in the Baltic however, the cultural and technological changes observed were largely independent of forager-farmer genetic exchange.

0145

Paired radiocarbon dating on human samples and camelid textiles from Pica 8, northern Chile

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Pica 8 is an inland cemetery of the Late Intermediate Period (AD 900-1450) in northern Chile. Burials in this cemetery present unexpectedly high variability in stable carbon and nitrogen isotope values in their skeletal tissues, implying very diverse diets. Two possible explanations can be posited to explain the observed variability. The first relates to diachronic change in diet, as might be seen, for example, with changing access to marine foods and maize over time. The second explanation emphasizes synchronic socio-cultural distinctions, revolving around identity and ethnicity. To address this, paired radiocarbon dates were obtained on human bone and camelid textiles from nine graves. The results fell into two groups, one showing an average offset of 117 ± 9 ¹⁴C years, and the other showing no significant offsets at all. Surprisingly, there is no predictive relationship between any of the stable isotope measurements on human bone ($\delta^{13}\text{C}$ on collagen and apatite, $\delta^{15}\text{N}$ on collagen) and the observed offsets in ¹⁴C years. We propose that the contribution of marine foods at Pica 8 to bone collagen was less than previously supposed, modeling it as no more than ca. 12-20%, and that other factors must be invoked to account for the unusually high human $\delta^{15}\text{N}$ values at the site. The results favour the hypothesis that the isotopic, and hence dietary, variability seen at Pica 8 is best interpreted as synchronic, implying considerable diversity in lifeways within the community.

0147

Exploring the Migration of the World's first Farmers

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A key process in the history of modern humans is the transition from a hunter-gatherer way of life to agro-pastoralism. This process began in the so-called "Fertile Crescent" that stretches west to modern-day Egypt, north to southeast Turkey and east into Iran, after which farming technology spread into Europe and elsewhere. Whether the spread of farming across the world was mediated by the exchange of ideas or the large-scale movement of peoples has been highly debated, and little is known about the genetic structure of the first farmers. We present a novel Bayesian mixture modelling approach based on chromosome painting designed to elucidate patterns of shared ancestry between modern human populations and aDNA from early Neolithic farmers. Specifically we infer proportions of shared ancestry among present-day world-wide groups and ancient farmer genomes from Greece, Anatolia, Germany, Hungary and Iran, including several sequenced to high coverage (>7X). We present strong evidence that the spread of farming from Anatolia into Europe was accompanied by extensive migration of peoples, and that modern groups in Europe descend in part from these early farmers. In contrast, we show that the early farmers of Iran share surprisingly little genetic affinity with the early farmers that spread into Europe, and also appear to be ancestors of modern day groups in Pakistan, India and Iran. By resolving these patterns of ancestry we provide evidence for strong genetic

structure in the first farmers, suggesting that multiple hunter-gatherer groups adopted farming in SW-Asia.

0148

Genetic Identification of Canid in High Altitude Palaeoindian Peruvian Site

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The Late Pleistocene saw the arrival of humans to the New World accompanied by the first domesticate, dogs. As humans progressed from Beringia to Patagonia they encountered new canid species in North America such as the grey fox and coyote, along with novel South American canid species, including maned wolves, bush dogs, and Andean foxes. Cuncacha rock shelter site in southern Peru's Pucuncho Basin, is currently one of the oldest known high altitude sites in the world, with occupation beginning approximately 12,400 years ago. A human burial from the site was found with a canid mandible in a shallow pit at the head. Radiocarbon dating of the human and canid remains established contemporary dates at approximately 9,300 to 8,800 calibrated years before present. The specimen was initially identified as a domestic dog based upon the size and morphology of the partial mandible, which would have made the specimen the world's oldest known high altitude domestic dog and the oldest South American dog. Subsequent ancient DNA analysis through shotgun sequencing and mitochondrial enrichment of the specimen revealed the 'dog' from Cuncacha shared more similarity with the Andean fox, *Lycalopex culpaeus*. Computational analysis showed more reads mapping to the *Lycalopex culpaeus* genome compared with the *Canis lupus familiaris* genome. The Andean fox has played interesting roles in the lives of humans residing in Tierra del Fuego from archaeological through to historical contexts. Cuncacha Rock Shelter now joins the list of sites with intriguing interactions between Andean foxes and humans.

0149

Illuminating the prehistory of northern Europe through lipid residue analysis of putative oil lamps.

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Organic residue analysis has been widely applied to study the preparation of foods in prehistoric contexts. Here, we consider its wider application to other commodities, including fulfilling the need for illumination. In Northern Europe, a range of shallow oblong bowls first appear in the Eastern Baltic around ca. 5100 cal BC, along with the earliest ceramic cooking pots. Similar, shaped vessels are found a few centuries later in the Western Baltic also with the earliest ceramic horizons of the Late Mesolithic Ertebølle culture. Whilst various interpretations have been proposed for these vessels, it has been

unclear what function they provided to these hunter-gatherer communities. In 1935, Therkel Mathiassen suggested that oil from seal or whale was probably the most likely fuel. Seventy-eight years later this hypothesis was confirmed by Heron et al. (2013). Building on this work, here we present the results of organic residue analysis conducted on a large collection of these vessels from 12 coastal and inland archaeological sites throughout the circum-Baltic region. Their organic contents were determined using a combination of bulk carbon and nitrogen stable isotope analysis (EA-IRMS), molecular characterisation of free or bounded lipid extracts by gas chromatography-mass spectrometry (GC-MS), and compound-specific carbon stable isotope analysis by gas chromatography-combustion-isotope ratio mass spectrometry (GC-C-IRMS). Intriguingly, the results demonstrate that oils from both freshwater and marine fish made up the bulk of the residues, consistent with their use as oil lamps.

0150

Combining ancient DNA analysis and radiocarbon dating

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Comprehensive studies of ancient skeletal remains often require both ancient DNA analysis and radiocarbon dating, leading to undesirable consumption of material from precious or limited samples. Currently, no method exists to recover DNA and collagen from the same bone or tooth powder. Here we present preliminary data from three approaches that aim at combining both analytical techniques. The first is based on releasing surface-bound DNA from the bone/tooth matrix using a neutral phosphate buffer, and the other two rely on partial digestion of the bone/tooth matrix using either EDTA or an acidic phosphate buffer prior to complete decalcification of the sample for collagen extraction. Using a set of 12 bones of different ages we demonstrate that DNA can be released from bone samples with minimal or no losses in the amount of retrieved collagen. With the limited data currently available, we also detect no evidence for contamination with modern or fossil carbon after DNA extraction, which could alter radiocarbon dates obtained from samples. While further experiments are needed to determine the reliability of these methods before they can be put into practice, our results show that ancient biological material can be more efficiently used by developing combined sample preparation strategies for different analytical techniques.

0151

Tracing changes in early life history of individuals from a Migration period cemetery

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The disintegration of the Western Roman Empire in the 5th century led to socio-economic consequences and entailed a comprehensive process of transformation. At the border regions of the Roman Empire this transformation is characterised by cultural exchange, migration, integration and acculturation. Diet does reflect individuals' residence and subsistence and can also display cultural changes. Stable isotope analysis on tooth dentine microsamples allows reconstructing a chronology of dietary intake and to detect changes in individuals' diet during early lifetime.

The cemetery of Niedernai (Upper Rhine Valley, France), located at the (former) Roman Rhine frontier, dated from 450-530 AD offers the opportunity to investigate individuals' life histories at the transition time from Late Antiquity to the Early Middle Ages, the so-called "Migration Period". We conducted carbon and nitrogen isotope analyses on tooth dentine microsamples from 1st, 2nd and 3rd molars, to reconstruct a chronology of dietary intake and to detect potential changes in their diet during early lifetime. Some individuals show no changes in their diet, data reflecting a C3 plant based terrestrial

diet as expected in this area. However, a number of individuals show significant changes in isotope ratios over time. A few show even drastic changes in the $\delta^{13}\text{C}$ ratios, indicating that they were migrating from regions where a C4-based diet was prevalent. Our results demonstrate a heterogeneous population buried in the Niedernai cemetery. Tooth dentine microsampling offered an insight into dietary changes that we would not have been able to trace by simple bone isotope analysis.

0152

Imaging-assisted tooth dentine microsampling for time-resolved isotope analysis

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Tooth dentin microsampling allows detecting changes in an individuals' diet during early lifetime. However, the current approach of using transverse tooth sections is suboptimal, due to the conical growth of dentin towards the root and changes in growth rate during tooth development. Thus, the time period covered by any microsample can change substantially and increments may overlap in the root area. A thick layer of tooth cementum can also alter the actual isotope values. Furthermore, the sample size (and accordingly the covered time span) is dependent on the minimum amount of collagen required for isotope analyses. Hence, collagen quality and local concentration are important determinants for the sample size.

We addressed the challenge to improve temporal resolution of microsampling by (1) defining the covered time spans, (2) mapping relative collagen quality, and (3) targeted sampling alongside the increments. We used a method based on high-resolution transmission and fluorescence imaging of tooth root longitudinal thin sections. Imaging the incremental lines and a previous preparation of the sample allows a more biological sensitive sampling. Further, auto-fluorescence at different wavelengths is used to evaluate collagen quantity and quality to be correlated with the respective sampling area.

0153

Paleoproteomics identifies peptides from paint binders from ancient polychrome architecture

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Most of the cultural heritage objects produced using biogenic materials are rich in protein residues. This is also the case for paint binders that were used as a medium for pigments applied to sculptures and architecture in Antiquity. So far, the research of ancient polychromy has however primarily focused on analyses and identification of pigments. The choice of the binding medium was however of crucial importance for the final polychrome appearance of an object in terms of nuance, coverage, and intensity, and therefore of paramount importance for our understanding of the original appearance of painted objects. In this pilot study we identify collagen alpha-1(I) and collagen alpha-2(I) from *Bos Taurus* in a sample from a polychrome layer from an architectural element from the Palace of Apries, Egypt, (around 589-570 BCE) using mass spectrometry-based peptide sequencing. Identifications of ancient paint binders will expand our knowledge on painting techniques of Antiquity considerably. Moreover the identifications will improve reconstructions of ancient painted objects in museum exhibitions.

Investigating breastfeeding/weaning practices and adult mobility patterns during the Western Zhou Dynasty (1122 – 771 BC) at Boyangcheng, Anhui Province, China

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In a first for China, we report stable isotope ratios of carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) to reconstruct breastfeeding/weaning practices and dietary habits for 42 individuals from the Western Zhou Dynasty (1122 – 771 BC) site of Boyangcheng, in Anhui Province. Ribs and long bones (either femurs or humeri) were analyzed, and the isotopic offsets between these different bones were used to examine short and long term dietary changes in each individual. The adult $\delta^{13}\text{C}$ ($-17.6 \pm 2.0\text{‰}$) and $\delta^{15}\text{N}$ ($10.6 \pm 0.6\text{‰}$) results indicate that mixed C_3 (possibly rice) and C_4 (millet) terrestrial diets with varying levels of animal protein were consumed. The elevated subadult $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ results reflect that solid foods were introduced to the infant's diet before the age of 2 years and that cessation of breastfeeding occurred predominately between 2-3 years of age and no later than 4. Individuals between 2-10 years old, with lower $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ results than the adult mean, possibly had a more plant-based diet with reduced amounts of animal protein during childhood. The isotopic offsets between ribs and femurs revealed that five adults experienced radical dietary shifts in their later lives; all switching from predominately C_4 to C_3 diets. Based on historical and archaeological evidence of the Jianghuai region (where Boyangcheng is located) these individuals could have been Dongyi migrants from the Shandong region of northern China.

INVESTIGATING DIETARY INPUT ACROSS EARLY IRON AGE ASSEMBLAGES FROM SLOVENIA USING STABLE ISOTOPES

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The paper will present dietary isotopic analyses of human and animal remains from Slovenia dating to the early Iron Age. This research forms part of a larger ENTRANS Project, examining Iron Age cultural encounters in south-east Europe and the east Alpine region. One stream of this research involves analysis of carbon and nitrogen isotopes to explore differences in diet and health status. Diet is seen to have played a significant role in many societies in the construction of identity attributes, such as status, age or gender. Results thus far suggest a homogenous, terrestrial C_4 plant based diet was adopted across the research area during the early Iron Age. Without evidence of marine protein, the high carbon values suggest a considerable input of C_4 plants, most likely millet. The accompanying animal baseline data suggest some variation in farming and animal husbandry strategies across the region. This paper will introduce the sites under study, results of the dietary isotopic analyses and discuss some of the issues that one might need to think about when choosing faunal specimens to construct a dietary baseline. This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no 291827. The project is financially supported by HERA.

Nitrogen isotopic enrichment in the food chain: towards a metabolic explanation

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Isotopic values of body proteins have been used for several decades to investigate individuals' dietary intake across a range of fields, particularly archaeology and (palaeo)ecology. Nitrogen isotopic values have primarily been used as a marker of trophic position, based on the observed increase in $\delta^{15}\text{N}$ with each step in the foodchain. However, the full utility of the technique is hampered by our incomplete understanding of the expected magnitude of the isotopic enrichment, as well as our ignorance of the underlying metabolic reasons. On the one hand, the nitrogen isotopic increase for each trophic level appears relatively consistent (*ca.* 3‰), but it also appears to vary considerably within and between species, depending on such variables as growth, digestive physiology, diet composition. Metabolic explanations are thought to relate to isotopic fractionation during amino acid transamination, but with little complexity in the picture that has so far been drawn.

In this paper, I draw on isotopic tracer studies of protein metabolism and physiology, and controlled animal feeding studies, together with a consideration of amino acid metabolic pathways, to assess the likely mechanisms for nitrogen isotopic enrichment during metabolism. I then explore the potential implications of these observations for the technique's use in ecology and archaeology, arguing that a limited grasp of the metabolic mechanisms must result in limited interpretations of the data. Greater consideration of physiology and metabolism should help us in better understanding the observed patterns in amino acid nitrogen isotopic data.

The Hole Story: Ancient DNA, stable isotope and radiocarbon analysis of human remains from the 'Mesolithic' cemetery at Aveline's Hole

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Aveline's Hole Cave in the Mendip Hills, Somerset, England, which was originally excavated in 1860, is renowned as the earliest known cemetery in Britain. Up to 50 individuals were interred in the cave, although remains of only around 21 individuals have survived. Dozens of radiocarbon dates obtained from this assemblage are tightly clustered in the mid-late 9th Millennium BC, the Early Mesolithic. These tight dates suggest that whole bodies were interred over a relatively short period, after which the cave was sealed, perhaps deliberately.

Here we present whole genome data, as well as further stable isotope and radiocarbon dating results from the Aveline's Hole human remains. Our results suggest that the assemblage includes remains which date to the early 4th Millennium BC, show dietary signals more consistent with a farming than a hunter-gatherer lifestyle and which have genetic affinities with European Middle Neolithic populations ultimately deriving from Anatolia. These results not only inform on the nature of the British Mesolithic-Neolithic transition, but also overturn the conventional archaeological narrative of this unique and important site.

Population continuity in the time of admixture: exploring the Neolithic transition from Anatolia to Central Europe.

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A strict definition of population continuity is a population continuous through time without admixture or replacement from neighbouring populations. While such a scenario is unlikely to hold for most population histories, it does form a natural null-hypothesis in archaeogenetics. Following this definition, we present a method that allows to test population continuity using a single ancient genome and a sample of modern genomes. This method is based on forward simulations of genetic drift and the comparison of observed and expected proportions of allele sharing classes for all overlapping variable positions in both the ancient and modern genome data. We apply our continuity test to different datasets to investigate a topic that has been the subject of particular intense archaeological research and conspicuous long-standing controversy; the Neolithization of Europe. We explore the relative roles of admixture, demic and cultural diffusion during the Neolithic transition in Europe by tracing direct ancestry relationships between ancient inhabitants of Anatolia, the Balkans and Central Europe, and modern Sardinians, Greeks and Turks. Our results suggest that population continuity cannot be fully considered between any of the tested ancient and modern genomes, highlighting the prominent role of admixture in the origin of modern European populations.

Human Adaptation to Dietary Changes: Are we optimised to an ancient Palaeolithic diet?

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In this multidisciplinary study I am quantifying the differences in inferred nutrient profiles between the ancient and modern diets to investigate the following questions: What nutrients have changed the most since the transition to agriculture, and with the development of modern food production technologies? Have we evolved taste avidities for proxy nutrients which in a Palaeolithic setting would have selected a complement of nutrients required for a healthy diet? It has been suggested that many complex and chronic diseases today, including obesity, type II diabetes, some cancers and coronary heart disease, may be caused in part by a mismatch between modern diets and our ancestral diets to which our metabolism should be optimised. There is also clear evidence that some human populations have adapted genetically to some changes in diet over the last 10,000 years e.g., lactase persistence possibly amylase copy number variation and polymorphisms in detoxification genes. This study will systematically quantify these dietary changes at the individual nutrient level. I will identify nutrients enriched in modern diets, test if those nutrients act as avidity proxies for larger nutrient clusters in an ancestral setting, and test if genes involved in the digestion, transport and utilisation of those nutrients show elevated signatures of natural selection.

Gone to seed? Earliest direct evidence of plant processing in prehistoric Saharan pottery

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Over twenty years of investigations of lipid biomarkers contained in food residues has routinely demonstrated the importance of prehistoric cooking pots for the processing of animal products across the world. Remarkably, however, direct evidence for plant processing in prehistoric pottery has not been forthcoming. This is particularly surprising as the ability to cook otherwise unpalatable or even toxic plants would have rendered them edible and unlocked their nutritional potential. Archaeobotanical evidence in the form of charred and desiccated plant organs is the primary source of evidence for plant exploitation, and in North Africa such evidence shows Early Holocene hunter-gatherers routinely exploited a wide range of plant resources. Significantly, since pottery production also begins around this time the potential exists to investigate early plant processing and consumption through lipid biomarker residues of plant foods using gas chromatography (GC), mass spectrometry (MS) and stable isotope ratio MS. Our findings reveal the earliest direct evidence for plant processing in pottery globally, from the sites of Takarkori and Uan Afuda in the Libyan Sahara, dated to 8200-6400 calBC. Characteristic carbon number distributions and $\delta^{13}\text{C}$ values for plant wax-derived *n*-alkanes and alkanolic acids indicate sustained and systematic processing of C_3/C_4 grasses and aquatic plants, gathered from the savannahs and lakes in the Early to Middle Holocene green Sahara. The dominance of plant over animal lipids, a unique feature of prehistoric lipid records, suggests that early North African pottery was used very extensively by foraging groups to process wild plants, long before the exploitation of domesticated animals or plants.

Ancient DNA reveals differences in behaviour and sociality between brown bears and extinct cave bears.

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Ancient DNA studies have revolutionised the study of extinct species and populations, providing insights on phylogeny, phylogeography, admixture and demographic history. However, inferences on behaviour and sociality have been far less frequent. Here, we investigate the complete mitochondrial genomes of extinct Late Pleistocene cave bears and middle Holocene brown bears that each inhabited multiple geographically proximate caves in northern Spain. In cave bears, we find that, although most caves were occupied simultaneously, each cave almost exclusively contains a unique lineage of closely related haplotypes. This remarkable pattern suggests extreme fidelity to their birth site in cave bears, best described as homing behaviour, and that cave bears formed stable maternal social groups at least for hibernation. In contrast, brown bears do not show any strong association of mitochondrial lineage and cave, suggesting that these two closely related species differed in aspects of their behaviour and sociality. This difference is likely to have contributed to cave bear extinction, which occurred at a time in which competition for caves between bears and humans was likely intense and the ability to rapidly

colonise new hibernation sites would have been crucial for the survival of a species so dependent on caves for hibernation as cave bears. Our study demonstrates the potential of ancient DNA to uncover patterns of behaviour and sociality in ancient species and populations, even those that went extinct many tens of thousands of years ago.

0163

Ancient Invasive Species? The Origins of the Endemic Mammals of the California Channel Islands

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As many recent genetic and archaeological studies have shown, humans have intentionally and unintentionally moved plants and animals around the world. The California Channel Islands provide a unique environment to explore ancient translocations due to their close proximity to the California mainland, long human occupation (~13,000 years) and limited terrestrial diversity. Here we present our interdisciplinary approach to investigating the origins of California Channel Island mammals integrating archaeological, isotopic, genomic and radiometric datasets to explore the role of human agency in island biogeography. Additionally we propose a number of possibilities for why ancient peoples might have introduced these taxa.

0164

Comparison of Five Different DNA Extraction Methods for Reconstructing Ancient Gut Microbiomes from Coprolites

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The human microbiome is being increasingly recognized as an import factor for understanding health and disease in relation to diet and the environment. New discoveries are being made in this area of research at a rapid pace, and interest in extending the study of microbiomes into ancestral populations through aDNA represents a new frontier for the fields of metagenomics and biomolecular archaeology. While several studies have characterized the gut microbiomes of past peoples using coprolites as a source material, the effect of extraction methods on aDNA recovery from coprolites still remains to be evaluated. In this study we compared a variety of commonly employed extraction methods for reconstructing the gut microbiome on three well-preserved coprolites from the Río Zapé site in Northern Mexico. These extraction methods included the standard protocol for the Human Microbiome Project, as well as modified silica column extractions specifically designed for aDNA. Our results suggest that extraction methods modified specifically for aDNA research outperform commercially available soil and fecal extraction kits for recovering aDNA from coprolite samples. More specifically, the modified silica column methods resulted in significantly higher concentrations of extracted DNA, providing a greater number of starting molecules from which sequencing libraries could be prepared. These findings highlight the importance of selecting appropriate strategies for extracting aDNA from coprolites when attempting to accurately reconstruct microbial communities. The emerging field of ancient metagenomics offers a rare opportunity to understand human health at a deep timescale, and methodological studies are critical to ensure accurate ancient microbiome reconstruction.

Integrated approaches to animal exploitation in the Central European Early Neolithic: a case study from Ludwinowo 7 (Kuyavia, Poland; 5250-5000 cal BC)

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The introduction and spread of cattle-based agriculture by Europe's Neolithic farming groups re-shaped prehistoric culture, biology and economy in ways that underlie modern life virtually worldwide. Recent genetic studies point towards 6th millennium BC central Europe as the core region for the emergence of the lactase persistence allele -13,910*T. However, it is not known if milking was part of the LBK Neolithic 'package' from the start, or if it emerged as a new technology in specific regions during the development of the LBK, or indeed was not intensively practiced in the LBK. Determining when, where and why the transition to full domesticate-based farming occurred requires integrating multiple strands of evidence.

Here we detail ongoing multi-proxy research into the intensification of dairying in Neolithic Europe, using the site of Ludwinowo (late 6th millennium BC, central Poland) as a case study, one example of what likely was a diverse array of animal management strategies. Lipid biomarker and stable isotope compositions of food residues from vessels provide qualitative and quantitative assessments of the major animal products acquired and processed within LBK society. As well as the composition of wild and hunted species, state-of-the-art zooarchaeological analyses are identifying herding and slaughtering practices, butchery practices and the nature of meat and fat exploitation. A range of isotope analyses on domesticated animal teeth are also being undertaken to define seasonal herd management.

This multi-proxy approach offers a fully integrated picture of animal exploitation and milk use at the central European LBK site of Ludwinowo.

Europeans, Polynesians and Chickens: An archaeological and genetics approach to the natural and cultural history of chickens in South America

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The arrival of the chicken in South America has drawn much attention, yet it remains unresolved. One scenario sees a pre-Columbian Polynesian introduction via the western coast in Chile while another argues for a European introduction in the east. This debate has relied almost solely on a few bones found at the site of El Arenal-1 in Chile, and radiocarbon dated to 50 years prior to the arrival of the

Europeans in this region. However, this radiocarbon date could be pushed back to post-date the European arrival due to the marine reservoir effect, as the bones were recovered from a context heavy in marine resources and the site is located only 3kms from the coast. Most surprisingly, no radiocarbon dating or genetic analyses have been conducted on archaeological chicken bones from other colonial and post-colonial sites across South America. Combining history, archaeology and genetics, our research aims to establish the geographical distribution and genetic diversity of chickens in Chile and Argentina at the onset of the colonial period as well as assess the chickens' social, ecological and economic impact on Chilean and Argentinian societies and native biota from their introduction to the present day. This paper presents a review of what recent genetic research have revealed on the introduction of chickens in South America before presenting preliminary observations and results conducted on a chicken bone assemblage from Fuerte San Rafael del Diamante (Mendoza, Argentina), first Spanish colonial fort of the region.

0167

An ancient DNA analysis of the extinct Caribbean primate *Xenothrix mcgregori*

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Xenothrix mcgregori (MacPhee & Fleagle, 1991) is an extinct Caribbean primate that inhabited Mid Holocene Jamaica (6730 ± 110 bp; 14C dates; McFarlane, Lundberg, & Fincham, 2002). Morphological differences between Caribbean primates and their prospective living mainland forms have generated debate over the phylogenetic origins of the group. Caribbean platyrrhines exhibit features similar to those found in middle Miocene Patagonian fossils (Cooke et al., 2011). Suggesting that Caribbean primates diverged from mainland species before the modern morphological divergence of mainland species arose. Studies of the origins of the extinct Caribbean primate fauna that incorporate genetic evidence are therefore important in producing an informed understanding of the parallel radiation of island primates. Five families of New World monkeys have been allied to *Xenothrix* by morphological studies. Williams and Koopman (1952) classified *Xenothrix* as a non-callitrichid platyrrhine. Hershkovitz (1977) placed *Xenothrix* in its own family. Rosenberger (1977, 2002) made two proposals: first that *Xenothrix* is closely related to *Callicebus* (titi monkeys) and second that its closest living relatives are *Aotus* (owl monkeys). The most recent studies by MacPhee and Horowitz (2002, 2004) argued a close relation to *Callicebus*. This study attempts to resolve some of the ambiguities surrounding the phylogenetic relationships in these taxa by incorporating evidence from ancient DNA. For the first time in Caribbean primates, capture enrichment Next Generation Sequencing techniques have been used to extract and sequence mitochondrial and nuclear genetic data, that can answer key questions about the origins of the enigmatic, extinct Caribbean primate fauna.

0168

Searching for pathogens in a New World colonial epidemic burial.

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While methodological advancements in ancient DNA research have permitted the reconstruction of ancient bacterial genomes, pathogen detection has thus far been limited to capture-based approaches that carry with them an assay-specific ascertainment bias. Such biases are reduced when historical or archaeological contexts implicate a particular disease, but examples of this are rare in the archaeological record. Few clues exist, for example, to identify those infectious diseases thought to

have contributed to high mortality in New World populations in the colonial period. Here, we apply an approach for the analysis of non-enriched sequencing data that permits a fast and precise assignment of DNA reads to microbial taxa. This circumvents known biases common to capture-based screening techniques. Our strategy and experimental design will be discussed with reference to material from the project Pueblo Viejo de Teposcolula Yucundaa, which involves excavations at one of the oldest securely dated post-colonial epidemic cemeteries thus far identified in Mexico. This collection could be instrumental in our ultimate goal of understanding disease exchange in the colonial period.

0169 Testing continuity of ancient samples using SNP data

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Recent technological developments enabled a major paradigm shift in population genetics: it is now feasible to obtain ancient DNA (aDNA) from individuals across a variety of species and in a variety of climates. A key interest in many aDNA studies is assessing how the ancient sample is related to modern day populations. A specific question of interest is whether the ancient sample was a member of a population directly ancestral to a modern population. While some work has examined this question, it has primarily been in the context of having a number of ancient samples at a single locus. However, an ongoing trend is to collect genome-wide SNP data from single individuals. To make use of this kind of data, I developed a fast method to assess the continuity of an ancient individual with a modern reference population. Using simulations, I show that this method is effective and insensitive to population size history. I also apply it to SNP data from ancient humans.

0170

Industrialization-associated changes in oral microbiome ecology

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The oral microbiome is a complex microbial community that is surprisingly resistant to perturbation in the face of strong selective pressures, and is involved in oral health and disease processes. Periodically this biofilm calcifies into dental calculus, which, although rarely seen in industrialized societies today, was once nearly ubiquitous in humans. However, the prevalence of periodontal disease appears unchanged between pre- and post-industrial Western populations, despite the paucity of calculus in modern individuals, supporting the theory that oral microbiota changes are a result of disease initiation and not a causative factor. This study aims to explore oral biofilm ecology within ancient dental calculus to understand how modern hygiene influences biofilm development and its association with disease. DNA was extracted and sequenced from dental calculus from 50 individuals living in Britain during the Industrial Revolution, and the microbial community composition was assessed by 16S sequence identification. Sample metrics including skeleton age and sex, calculus characteristics, and calculus location were collected. Associations between specific microbial community members and sample metrics were evaluated with LEfSe, while alpha diversity was used to assess differences in community diversity within sample metrics. Community composition was shown to be largely oral microbiome-derived by SourceTracker, indicating minimal contamination. Alpha diversity was not significantly different between subgroups within any of the sample metrics used. Specific organisms were found to discriminate subgroups of all metrics assessed. These results suggest that biofilm diversity does not influence calculus development or its associations with disease, although specific organisms may play a role.

Examining rabbit domestication: an historical, archaeological and genomic approach

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Demographic modelling, based on the joint site frequency spectrum, is an increasingly popular technique to estimate ancestral population sizes, migration rates and split times. Recent studies have applied these techniques to a diverse range of species and evolutionary contexts—from the out of Africa expansion, to the domestication of rice. Validation of these demographic models, and the software which implement them, is often based on simulated data, or by comparison to estimates made by other techniques. The relatively recent domestication of rabbits provides a novel case study for examining the use of demographic modelling, in a context where expected parameter ranges have a relatively narrow bound.

Despite a long history of study, including pioneering work by Darwin, many of the specifics of rabbit domestication remain unknown. The most commonly cited story, that rabbits were domesticated by French monks, c. 600 AD, as a source of foetal rabbits for consumption during Lent, is based on a widely misquoted passage from the chronicles of St Gregory of Tours. In concert with the historical and archaeological lines of evidence, the demographic history of domestic rabbits was inferred, using modern genomic data and *ðaði*—a composite likelihood coalescent method, based on the joint site frequency spectrum.

Ancient Mitogenomes Shed Light on Population Affinity and Mortuary Practices in Southern Caucasus

Luka Papac¹, Bastien Llamas², Guido Valverde², Alan Cooper², Nadin Rohland³, Swapan Mallick³, David Reich³, Antonio Sagona¹, Varsha Pilbrow¹, Wolfgang Haak⁴

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The Samtavro cemetery, used from the Late Bronze Age through to the Early Middle Ages, is the largest known ancient burial ground in Georgia and the Caucasus. Centrally located at the crossroads of major continents and trading networks, archaeological investigations have revealed a diverse assemblage of artefacts and cultural practices, including Greek, Roman, Persian, Sarmatian, Scythian and Hunnic influences. In order to gain insight into the origin, affinity and legacy of the Late Antique (300-500AD) Samtavro population, we sequenced whole mitogenomes from 16 individuals buried in 13 tombs. We also sampled two individuals from three tombs each to test for maternal relatedness within tombs. We find high mtDNA diversity with all individuals from different tombs carrying unique mtDNA haplotypes. Identical mtDNA haplotypes were found in two of the three tombs from which two individuals were sampled, probably reflecting the co-burial of kin. PCA of haplogroup composition and MDS of Slatkin's *F_{st}* values show a strong west Eurasian influence with close affinity to populations from the Caucasus, Middle East and Europe. All mitochondrial lineages belong to West Eurasian haplogroups suggesting minimal impact of ancient nomads of the Eurasian steppe. Shared haplotype analysis revealed more than half (8/14=57%) of the HVSI haplotypes from Samtavro were previously reported in modern day Georgians. Similar haplogroup composition, low *F_{st}* values and a high haplotype sharing with modern day Georgians suggests an autochthonous origin of the Samtavro population followed by a high degree of population continuity in the region over the last 1,500 years.

Investigating vessel-usage in the Indus Civilisation using ceramic lipid analysis

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The Indus Civilisation (c.3000-1500 B.C) was one of the great early complex civilisations of the Old World, occupying a large area in northwest South Asia, and is best known for its urban phase, known as the Mature Harappan Period (c.2500-1900 B.C). Research has primarily focused on the supposed homogeneity of material culture and subsistence patterns across settlements in this period, as well as the abrupt decline of the urban phase after c.1900 B.C, which broadly coincides with the sudden weakening of the Indian Summer Monsoon around c.2100 BC. Recently, however, scholars have recognised significant regional variations in environmental conditions, subsistence practices and ceramic assemblages, as well as variations between urban and rural settlements. This diversity suggests that populations may have been uniquely adapted to the shifting environmental parameters of the post-urban phase. My PhD focuses on examining whether these variations are reflected in everyday acts of cooking and storing using ceramic lipid analysis, specifically gas chromatography (GC), gas chromatography-mass spectrometry (GC/MS) and gas chromatography and combustion isotope ratio mass spectrometry (GC-C-IRMS). I will investigate the relationship between urban and rural vessel-usage, and examine shifts in vessel-usage in the face of climatic instability across sites. Preliminary results from a pilot study indicate that interpretable concentrations of lipid are extractable from a range of Indus vessels, revealing promising directions for future analyses. Such a study will for the first time address the use of Indus cooking vessels from urban and rural sites, revealing patterns of consumption across space, time, and settlement hierarchies.

Phylogeography and British population history of the European wildcat *Felis silvestris silvestris* inferred from ancient DNA.

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The closing stages of the Devensian glacial (c. 15 000 cal BP) into the Holocene interglacial (commencing c. 11 500 cal BP) saw a series of rapid oscillations in global climate associated with major faunal turnover events. Such abrupt climatic fluctuations are likely to have exerted strong selection pressures on mammal fauna over a period also associated with dramatic increases in anthropogenic activity. Britain is ideally placed to examine the question of faunal turnover on account of its sensitivity to climate change driven by its proximity to the North Atlantic, its rich fossil assemblages and its geographical position, formerly connected by a landbridge to the European mainland. The research presented here focuses on preliminary findings from ancient DNA analysis on the European wildcat *Felis silvestris silvestris*, a temperate adapted taxon associated with woodland habitat. This subspecies has suffered catastrophic population declines in Britain over the Late Holocene as the result of human-mediated habitat loss, persecution and introgression with the introduced domestic cat *Felis catus*. Here, in-solution capture enrichment and NGS technologies have been used to generate the oldest whole mitogenomes from this subspecies spanning the Early to Late Holocene. In addition the first ancient light-coverage whole nuclear genome is presented from a Roman age wildcat excavated from the Isle of Bute. The utility of these data in examining *i*) the population history of *F. s. silvestris*, *ii*) the European phylogeography of the subspecies and *iii*) the application of ancient DNA in quantifying introgression levels in modern populations is discussed.

It's a dog's life! What can we tell from sequencing 1000 ancient samples?

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By extracting and sequencing over a thousand ancient wolf and dog samples, we will try and answer some important archaeological questions. Such as, were and when did the dog become domesticated and how many times did it happen?

Our samples span both time and space, we have samples from across the Old World going back to the Pleistocene and reaching modern day populations. With the introduction of Next Generation Sequencing the game changed. From looking at single short fragment we can now shotgun sequence whole genomes or capture specific genes or SNPs. In this project we are doing a combination of both these methods. In my presentation I will give you an early and preliminary glimpse into our dataset and our findings.

Contemporary wolves trace their ancestry to an expansion from Beringia following the Last Glacial Maximum

Liisa Loog^{1,2}

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The grey wolf was one of the most successful predators since the beginning of Pleistocene and among the very few large carnivores that survived the megafaunal extinctions at the end of the Pleistocene. The grey wolves are also widely believed to have been the source population for all modern domestic dog populations. Today grey wolves play an important ecological role as a key top predator across Eurasia. Nevertheless, very little is known about the demographic history of this large carnivore. We explicitly tested different wolf demographic scenarios, including variation in population size and range expansions with origins in different parts of the Northern Hemisphere, by combining a large set of whole mitochondrial genomes, from both ancient and contemporary wolf populations with spatially and temporally explicit population genetic modeling. The demographic scenario best supported by our analyses is a model of a post Last Glacial Maximum expansion of Beringian wolves across Eurasia and North America, which to a large extent replaced the local native wolf populations. The inferred timing of this expansion coincides with previously described demographic turnovers in other species such as aurochs and humans. These results have major implications for the studies of geographic origin of domestic dogs, which up until now have all assumed a static wolf population structure throughout Pleistocene.

Selection analysis applied to time series of ancient genotype data reveals how medieval religious reform shaped the genomes of modern chickens.

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A number of statistical approaches have been developed in recent years to detect and quantify the strength of natural selection using modern genomic data. However, these approaches all have poor temporal resolution and limited power to detect selection acting on standing genetic variation. Ancient DNA allele frequency data provides the most direct and sensitive alternative for detecting selection at specific loci, and offers the possibility of resolving temporal variation in selection strength.

However, ancient DNA sample sizes are typically small, and samples tend to be sparsely and unevenly distributed in space and time. In addition, all approaches are sensitive to confounding effects of demography. Here we present a Bayesian framework for reconstruction allele frequency trajectories through time from ancient allele frequency data that can explicitly accommodate the confounding effects of gene flow between populations and uncertainty in sample ages. We applied this method to ancient European domestic chicken genotype data from TSHR locus, which has been argued to be under strong and recent selection in domestic chickens. We find that the hypothesized sweep allele shows a pattern of strong selection starting 1100 years ago, coinciding with a European-wide known shift in poultry management between the mid-ninth to mid-eleventh century. This shift is associated with religious but also a legal rule that required people to abstain from quadruped meat, brought in as part of the Benedictine reform. This work directly highlights the importance of ancient DNA and statistical modeling for understanding how cultural practices in the past have shaped modern domesticated species.

0178

Seeing Beyond the Science: Multi-Strand Approaches to Human-Chicken Interactions

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This paper focuses on the chicken, an introduced bird species to Europe. Today chickens provide huge quantities of food products – both as meat and eggs, but they also are valued as pets, show animals, companions, and in some contexts as religious sacrifices. The domestication and subsequent introduction of animals in the past is frequently seen in terms of food. However, this is not always the case. Integrating scientific, archaeological and anthropological analyses allows insights into the varied roles that the chicken also held within ancient societies which included status symbolism, exoticism, religion/belief systems, sport, and food. Using case studies from across Europe, this talk explores how archaeological bone and eggshell can be analysed to reveal specific actions and activities in human-animal interaction. Isotopic bone data are used to explore shared and differential access to food resources between humans and chickens, providing information on animal husbandry and social perceptions of these animals. Archaeological eggshell can be challenging to investigate due its fragility in acidic soil conditions, the necessity of rigorous retrieval processes, and the resources needed to identify it taxonomically. However recent refinements in identifying eggshell to species via ZooMS (Zooarchaeology by Mass Spectrometry) have expanded the research possibilities. Such analyses can be combined with microscopy to identify the developmental stage of the eggs which can in turn be used to examine egg and meat production, use, consumption, and associated symbolism. By considering something as familiar as a chicken, this paper seeks to demonstrate the importance of looking beyond the science that provides the answers by relating these results to real life animal-human interactions.

0179

Analysis of Ancient Dental Calculus Proteins from Northern European Viking Samples

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Ancient dental calculus has recently been proven as a valuable and high-quality reservoir of ancient biomolecules. Through examining dental calculus from archaeological sites, we can now gain a better understanding of the oral microbiomes of past individuals. The human oral microbiome consists of a very complex mixture of bacteria, fungi and archaea and the composition of these microbiomes alters

with disease states or dietary changes, which can be reflected in these archaeological samples. With the use of high-resolution mass spectrometry we aim to reveal and analyse the protein profiles for different Northern European calculus samples dating from the Viking period. In the preliminary data we find that the most abundant species are *Actinomyces dentalis*, *Lautropia mirabilis*, *Propionibacterium propionicum*, *Homo sapiens* and *Corynebacterium matruchotii*. Gene Ontology analysis of the human proteins shows that they are enriched in extracellular proteins and are known to be involved in different immune responses. In terms of paleopathological information, we also identify proteins in several samples from the bacterial species belonging to 'the red complex' comprised of *Porphyromonas gingivalis*, *Tannerella forsythia* and *Treponema denticola*. This complex of oral bacteria is associated with severe periodontitis. Different Viking samples originating from Denmark, Sweden, Faroe Islands and Iceland are compared for any variations in diet and health which might be related to different lifestyles and food sources. Besides host and microbiota derived proteins we also identify proteins from dietary sources including the milk consumption marker, bovidae beta-lactoglobulin, which we found in several samples.

List of ISBA7 conference attendees

- Abbona, Cinthia** (The San Rafael Museum of Natural History, AR). Abstract submitted: 86 - Genetic structure and geographic partitioning of Lama guanicoe sub-populations during the late Holocene (Poster)
- Abumandil, Naglaa** ().
- Achtman, Mark** (University of Warwick, GB). Abstract submitted: 97 - Evolution history over millenia of sub-lineages of invasive Salmonella enterica (Talk)
- Alexander, Michelle** (University of York, GB).
- Alikhan, Muhammed** (University of Warwick, GB).
- Allaby, Robin** (University of Warwick, GB).
- Allen, Richard** (University of Oxford).
- Altena, Eveline** (Leiden University, NL). Abstract submitted: 51 - A stable story: insights in the development of a (post)medieval population in the east of the Netherlands. (Talk)
- Ameen, Carly** (University of Oxford).
- Andrades Valtueña, Aida** (Max Planck Institute for the Science of Human History, DE).
- Barnes, Ian** (Natural History Museum, GB).
- Barnett, Ross** (GB).
- Bennett, Andrew** (Institut Jacques Monod - CNRS).
- Best, Julia** (University of Bournemouth, UK). Abstract submitted: 178 - Seeing Beyond the Science: Multi-Strand Approaches to Human-Chicken Interactions (talk)
- Birolo, Leila** (Università Federico II Napoli, IT). Abstract submitted: 64 - The painting technique of the giant buddhas of Bāmiyān (Afghanistan) (talk)
- Boehme, Lisa** (Kiel University, DE). Abstract submitted: 87 - Comparison of human and leprosy DNA content in petrous bones and teeth from St. Jorgen, Denmark (1270 - 1350 AD) (Poster)
- Boessenkool, Sanne** (University of Oslo, NO). Abstract submitted: 137 - Combining bleach and mild pre-digestion improves ancient DNA recovery from bones (Poster)
- Boivin, Nicole** (Max Planck Institute for the Science of Human History, Germany).
- Booth, Tom** (Natural History Museum, GB). Abstract submitted: 158 - The Hole Story: Ancient DNA, stable isotope and radiocarbon analysis of human remains from the 'Mesolithic' cemetery at Aveline's Hole (Talk)
- Brace, Selina** (Natural History Museum, GB). Abstract submitted: (N/a (no abstract submitted))
- Brandt, Luise Ørsted** (Aarhus University, DK). Abstract submitted: 153 - Paleoproteomics identifies peptides from paint binders from ancient polychrome architecture (Poster)
- Breu Barcons, Adrià** (Autonomous University of Barcelona, ES). Abstract submitted: 61 - Lipids absorbed in Epicardial pottery reveal large-group meat consumption in the oldest known domestic structure on the Barcelona plain. (Poster)
- Bro-Jørgensen, Maiken Hemme** (University of Copenhagen, DK). Abstract submitted: 78 - Ancient DNA analysis of Scandinavian medieval drinking horns and the horn of the last aurochs bull (Talk)
- Brown, Keri** (University of Manchester, GB).
- Brown, Terry** (University of Manchester, GB).
- Bunce, Mike** (Curtin University, AU). Abstract submitted: 17 - 20,000 bones and counting - Insights into zooarchaeology and Ancient DNA Preservation using Bulk-Bone Metabarcoding. (Talk)
- Callaway, Ewen** (Nature Journal).
- Campana, Michael** (Smithsonian Conservation Biology Institute, US).
- Capelli, Cristian** (University of Oxford, GB).
- Cappellini, Enrico** (University of Copenhagen, DK). Abstract submitted: 54 - Paleoproteomic analysis of early Pleistocene fossil remains & 55 - Paleoproteomics for cultural heritage investigation, state of the art and perspectives. (Talk)
- Casanova, Emmanuelle** (University of Bristol, GB). Abstract submitted: 123 - Compound-specific radiocarbon dating of food residues preserved in archaeological pottery vessels (Talk)
- Charlton, Sophy** (University College London, UK). Abstract submitted: 134 - A Multi-Isotopic Investigation of a Large, Unusual Neolithic Assemblage (Talk)

- Coia, Valentina** (European Academy of Bozen/Bolzano, IT). Abstract submitted: 44 - Whole mtDNA sequencing in Alpine populations and the genetic history of the Neolithic Tyrolean Iceman (Poster)
- Collins, Matthew** (University of York, GB).
- Colominas, Lidia** (). Abstract submitted: 21 - Osteometric and mtDNA analyses from the trading post of Empúries (north-east of the Iberian Peninsula) show first evidence of cattle trade during the Early Roman period (Poster)
- Colonese, Andre Carlo** (University of York, GB). Abstract submitted: 111 - Towards the identification of plant residues in prehistoric archaeological artefacts: integrating lipid and protein approaches (Talk)
- Courel, Blandine** (University of Strasbourg, France). Abstract submitted: 113 - The organic coating from a decorated human skull from the Neolithic site of Nahal Hemar (Israel): molecular evidence for the use of a vegetal substance (Talk)
- Coutinho, Alexandra** (Uppsala University, SE). Abstract submitted: 43 - Genetics as a means of investigating cultural contact: The case of the Pitted Ware grave sites of the Island of Gotland in Scandinavia. (Poster)
- Coutu, Ashley** (University of Cape Town/ University of York, GB). Abstract submitted: 131 - The Skeleton Coast shipwreck: sourcing elephant ivory from a 16th century Portuguese trading vessel (Poster)
- Craig, Oliver** (University of York, GB).
- Cramp, Lucy** (University of Bristol, GB).
- Crowder, Kayla** (Durham University, GB).
- Cucchi, Thomas** (CNRS - Muséum national d'Histoire naturelle).
- Czajkowska, Beata** (University of Manchester, GB). Abstract submitted: 18 - The identity of the mysterious 'new glume wheat' of early European agriculture (Poster)
- Czermak, Andrea** (University of Oxford, GB). Abstract submitted: 151 - Tracing changes in early life history of individuals from a Migration period cemetery & 152 - Imaging-assisted tooth dentine microsampling for time-resolved isotope analysis (Poster)
- Dalén, Love** (Swedish Museum of Natural History, SE).
- de la Fuente, Constanza** (University of Copenhagen, DK). Abstract submitted: 130 - Insight into the origin and diversification of late marine hunter-gatherers groups from the Chilean Patagonia (Poster)
- De Oliveira Freitas, Fabio** (University of Warwick, GB).
- Der Sarkissian, Clio** (Natural History Museum of Denmark, DK). Abstract submitted: 33 - Demonstrating mollusc seashells as new genetic archives of the past (Talk)
- Diekmann, Yoan** (University College London, GB).
- Díez del Molino, David** (Swedish Museum of Natural History, SE). Abstract submitted: 159 - Population continuity in the time of admixture: exploring the Neolithic transition from Anatolia to Central Europe. (Talk)
- Doherty, Sean** (University of York, GB). Abstract submitted: 140 - Stable isotope analysis of parchment as an annual record of British agriculture and climate (Poster)
- Drosou, Konstantina** (University of Manchester, GB). Abstract submitted: 126 - Investigating the possible brotherhood of two Egyptian mummies Nakht-Ankh and Khnum-Nakht via ancient DNA analysis (Poster)
- Dunne, Julie** (University of Bristol, GB). Abstract submitted: 161 - Gone to seed? Earliest direct evidence of plant processing in prehistoric Saharan pottery (Talk)
- Dury, Jack** ().
- Eriksen, Anne Marie** (Natural History Museum of Denmark / National Museum of Denmark, DK).
- Eriksson, Anders** (University of Cambridge).
- Eriksson, Gunilla** (Stockholm University, SE). Abstract submitted: 22 - Resuming Resmo - sorting out mobility from diet using microsampling, multi-isotope analysis and modelling (Talk)
- Ersmark, Erik** (Swedish Museum of Natural History, SE). Abstract submitted: 76 - Genetic turnovers and northern survival during the last glacial maximum in European brown bears (Talk)
- Evans, Jane** (British Geological Survey, GB). Abstract submitted: 59 - Biosphere mapping- the next step. (Poster)

- Fages, Antoine** (, DK). Abstract submitted: 48 - Identifying experimental conditions improving in solution target enrichment for ancient DNA (Talk)
- Farrer, Andrew** (University of Adelaide, AU). Abstract submitted: 115 - Unappreciated ecosystem diversity of oral microbiota detected in ancient Britain (Talk)
- Feldman, Michal** (, DE). Abstract submitted: 74 - A high-coverage Yersinia pestis Genome from a 6th century Justinianic Plague Victim (Poster)
- Fellows Yates, James** (Max Planck Institute for the Science of Human History, DE). Abstract submitted: 20 - Full Mitochondrial Genomes of Central European Upper Palaeolithic Woolly Mammoths (Mammuthus primigenius) (Poster)
- Fernandez, Eva** (Durham University, GB).
- Ferrari, Giada** (University of Zurich, CH). Abstract submitted: 112 - Metagenomic analysis of a permafrost-preserved woolly mammoth calf (Talk)
- Feuerborn, Tatiana** (, DE). Abstract submitted: 148 - Genetic Identification of Canid in High Altitude Palaeoindian Peruvian Site (Poster)
- Fjallström, Markus** (Stockholm University, SE). Abstract submitted: 107 - Stable isotope ($\delta^{13}\text{C}$, $\delta^{15}\text{N}$ and $\delta^{34}\text{S}$) and elemental analysis as markers for cultural heterogeneity and causes of death of a miner's population from Silbojokk in northern Fennoscandia during the 17th century. (Talk)
- Forst, Jannine** (University of Manchester, GB). Abstract submitted: 25 - Burnt to a crisp? The high-throughput DNA sequencing of charred grains. (Poster)
- Fotakis, Anna** (University of Copenhagen, DK).
- Frantz, Laurent** (University of Oxford).
- Fuller, Benjamin** (University of Oxford). Abstract submitted: 154 - Investigating breastfeeding/weaning practices and adult mobility patterns during the Western Zhou Dynasty (1122 – 771 BC) at Boyangcheng, Anhui Province, China (Poster)
- Furtwängler, Anja** (University of Tübingen, DE). Abstract submitted: 91 - Genetic Analysis of Neolithic individuals from Switzerland (Poster)
- Garcia Reig, Sheila** (Universitat Autònoma de Barcelona, Spain). Abstract submitted: 125 - Seasonal reproductive patterns of buried sheep in the funeral Avellaner cave (Epicardial; Northeast Iberian Peninsula) by stable isotope sequences ($\delta^{18}\text{O}$) in bioapatite tooth enamel: funerary and sheep herding implications. (Talk)
- Gaunitz, Charleen** (Natural History Museum of Denmark, DK). Abstract submitted: 50 - Zonkey: a simple, accurate and sensitive method to identify first generation equid hybrids in archaeological assemblages (Talk)
- Geigl, Eva-Maria** (Institut Jacques Monod - CNRS/ University Paris Diderot, FR). Abstract submitted: 83 - Degradation and recovery of DNA from 44,000 year-old rodent samples from Africa (Talk)
- Gibbons, Ann** (SCIENCE, US).
- Gilbert, Tom** (Natural History Museum of Denmark, DK).
- Girdland Flink, Linus** (GB).
- Glocke, Isabelle** (Max Planck Institute for Evolutionary Anthropology, DE). Abstract submitted: 85 - Improving The Recovery Of Ancient DNA Sequences From Highly Degraded Material (Talk)
- Gondek, Agata** (University of Oslo, NO).
- Gonzalez Fortes, Gloria** (University of Ferrara). Abstract submitted: 162 - Ancient DNA reveals differences in behaviour and sociality between brown bears and extinct cave bears. (Talk)
- Gopalakrishnan, Shyam** (Natural History Museum of Denmark, DK).
- Granado, José** (University of Basel, CH). Abstract submitted: 143 - Spatio-temporal mtDNA and isotope analyses of red deer (Cervus elaphus) in the Vosges: long-lasting co-existence of two "ecotypes" and low mtDNA diversity throughout millennia (Talk)
- Grange, Thierry** (Institut Jacques Monod - CNRS, FR).
- Guellil, Meriam** (University of Oslo, Norway). Abstract submitted: 88 - The Need for Resolution: Addressing the lack of multidisciplinary integration in Medieval plague research. (Poster)
- Guiry, Eric** (University of British Columbia, CA). Abstract submitted: 89 - Reconstructing the migratory behaviours of extinct fish populations using stable isotope analyses (Talk)

- Günther, Torsten** (Uppsala University, SE). Abstract submitted: 23 - Relationship estimation from ancient DNA (*Talk*)
- Hagan, Richard** (University of Oklahoma). Abstract submitted: 164 - Comparison of Five Different DNA Extraction Methods for Reconstructing Ancient Gut Microbiomes from Coprolites (*Poster*)
- Haile, James** (University of Oxford).
- Hammann, Simon** (University of Bristol, GB). Abstract submitted: 77 - Palaeolipidomics: developing a new lipid biomarker proxy to detect cereal processing in archaeological pottery (*Poster*)
- Hanghøj, Kristian** (, DK). Abstract submitted: 52 - Automated reconstructions of nucleosome and methylation maps with epiPALEOMIX (*Talk*)
- Hendy, Jessica** (University of York, GB).
- Herbig, Alexander** (Max Planck Institute for the Science of Human History, DE). Abstract submitted: 49 - MALT: Fast alignment and analysis of metagenomic DNA sequence data applied to the Tyrolean Iceman (*Talk*)
- Hermes, Taylor** (University of Kiel, DE). Abstract submitted: 36 - Using $\delta^{13}\text{C}$ and $\delta^{18}\text{O}$ time series from livestock teeth to reveal the seasonality of mobility, foddering, and stress during the Bronze and Iron Ages in eastern Kazakhstan (*Talk*)
- Heron, Carl** (British Museum, GB). Abstract submitted: 84 - First molecular and isotopic evidence of millet processing in prehistoric pottery vessels (*Talk*)
- Hofman, Courtney** (University of Oklahoma). Abstract submitted: 163 - Ancient Invasive Species? The Origins of the Endemic Mammals of the California Channel Islands (*Poster*)
- Hu, Yaowu** (University of Chinese Academy of Sciences, CN). Abstract submitted: 60 - Direct earliest evidence of dog domestication in East Asia (*Talk*)
- Huffer, Damien** (, US). Abstract submitted: 28 - Trade and Empire in Ancient Bahrain: Bioarchaeological and Isotope Geochemical Perspectives (*Talk*)
- Hulda Palsdottir, Albina** (The Agricultural University of Iceland, IS).
- Hulme-Beaman, Ardern** (University of Oxford, GB).
- Immel, Alexander** (Max Planck Institute for the Science of Human History, DE). Abstract submitted: 6 - Effect of x-ray irradiation on ancient dna in sub-fossil bones – Guidelines for safe x-ray imaging. (*Talk*)
- Irving-Pease, Evan** (University of Oxford). Abstract submitted: 171 - Examining rabbit domestication: an historical, archaeological and genomic approach (*Talk*)
- Jay, Mandy** (Durham University, GB).
- Jersie-Christensen, Rosa** (University of Copenhagen, DK). Abstract submitted: 70 - Analysis of Ancient Dental Calculus Proteins from Northern European Viking Samples (*Talk*) and (179) Analysis of Ancient Dental Calculus Proteins from Northern European Viking Samples (*Poster*)
- Johannes Hansen, Anders** (University of Copenhagen, DK).
- Johnson, Lucie** (Durham University, GB). Abstract submitted: 103 - Can the use of querns and millstones make a contribution of Sr to the human diet: An experiment in digestive Sr-isotope uptake. (*Poster*)
- Jones, Eppie** (University of Cambridge, GB). Abstract submitted: 144 - The Neolithic Transition at the Edge of Europe (*Talk*)
- Karlstrøm, Aina** (, DK). Abstract submitted: 31 - Identifying *Mycobacterium tuberculosis* in ancient bone and dental calculus through DNA and protein analysis. (*Poster*)
- Kastilan, Sonja** (Frankfurter Allgemeine Sonntagzeitung, DE).
- Keller, Marcel** (Max Planck Institute for the Science of Human History, DE). Abstract submitted: 73 - The First and Second Plague Pandemic in Bavaria, Germany - Preliminary Screening Results (*Poster*)
- Kendall, Iain** (University of Bristol, GB). Abstract submitted: 122 - The effect of trophic level on individual amino acid $\delta^{15}\text{N}$ values in a terrestrial ruminant food chain (*Talk*)
- Kerudin, Ammielle** (University of Manchester, GB).
- Kistler, Logan** (University of Warwick, GB). Abstract submitted: 41 - A new general model for ancient DNA decay based on paleogenomic meta-analysis (*Talk*)
- Koon, Hannah** (University of Bradford, GB). Abstract submitted: 156 - INVESTIGATING DIETARY INPUT ACROSS EARLY IRON AGE ASSEMBLAGES FROM SLOVENIA USING STABLE ISOTOPES (*Talk*)
- Kootker, Lisette** (VU Amsterdam, NL).

- Korlevic, Petra** (Max Planck Institute for Evolutionary Anthropology, DE). Abstract submitted: 150 - Combining ancient DNA analysis and radiocarbon dating (*Talk*)
- Kornell, Sabin-Christin** (Kiel University, DE). Abstract submitted: 81 - 6380-year-old oral pathogens from hunter-gatherer remains found in Kiel bay: A metagenomic approach to ancient DNA (*Poster*)
- Krause-Kyora, Ben** (Max Planck Institute for the Science of Human History, DE). Abstract submitted: 98 - The 5,300-year-old Helicobacter pylori genome of the Iceman (*Poster*)
- Kubiak, Cara** (University of Oxford). Abstract submitted: 132 - Comprehensive biomolecular analysis of faunal remains from Vindija Cave, Croatia, combining ZooMS collagen fingerprint analysis, stable isotopes, and ancient DNA. (*Poster*)
- Kumar Lankapalli, Aditya** (Max Planck Institute for the Science of Human History, DE).
- L. Pichler, Sandra** (University of Basel, CH).
- Laffoon, Jason** (Vrije Universiteit Amsterdam, US).
- Lanigan, Liam** (University of Saskatchewan).
- Lantos, Irene** (University of Buenos Aires, AR). Abstract submitted: 63 - Drinking in the Andes: organic residue analyses of Inca aríbalo jars from Catamarca, Argentina. (*Poster*)
- Larson, Greger** (University of Oxford, UK). Abstract submitted: 177 - Selection analysis applied to time series of ancient genotype data reveals how medieval religious reform shaped the genomes of modern chickens.
- Lebrasseur, Ophelie** (University of Oxford). Abstract submitted: 166 - Europeans, Polynesians and Chickens: An archaeological and genetics approach to the natural and cultural history of chickens in South America (*Poster*)
- Lee-Thorp, Julia** (University of Oxford, UK).
- Lewis, Jamie** (University of Bristol, GB).
- Li, Xiaoqiang** (Chinese Academy of Sciences, CN). Abstract submitted: 40 - The early agriculture and its impact in NW China (*Poster*)
- Librado, Pablo** (University of Copenhagen, DK). Abstract submitted: 46 - LSD: a novel method to detect positive selection in tree time-slices (*Talk*)
- Lidén, Kerstin** (Stockholm University, SE).
- Linderholm, Anna** (University of Oxford). Abstract submitted: 175 - It's a dog's life! What can we tell from sequencing 1000 ancient samples? (*Talk*)
- Liu, Hsiao-Lei** (The University of Warwick, GB). Abstract submitted: 32 - Story Hidden in the Cabinet? -Unveiling the Grape Evolution by Using Historical Herbarium Specimens (*Poster*)
- Llorente-Rodriguez, Laura** (University of York, GB).
- Loog, Liisa** (University of Oxford). Abstract submitted: 176 - Contemporary wolves trace their ancestry to an expansion from Beringia following the Last Glacial Maximum
- Lorenzen, Eline** (Natural History Museum of Denmark, DK).
- Lundstrøm, Inge** (, DK). Abstract submitted: 24 - Genome Evolution of Trondheimers Through the Last 1000 Years (*Poster*)
- Lundström, Maria** (Linköping University, SE). Abstract submitted: 93 - DNA quality in different types of archaeological plant materials (*Poster*)
- Lyon, David** (University of Copenhagen, DK). Abstract submitted: 121 - Digging deep into the ancient human oral microbiome: Metaproteomics challenges and perspectives for modern bioinformatics (*Talk*)
- Mackie, Meaghan** (University of Copenhagen, DK).
- Majander, Kerttu** (University of Tübingen, DE). Abstract submitted: 116 - Finns in the light of ancient mitochondrial DNA (*Poster*)
- Makarewicz, Cheryl** (Christian Albrechts University, Germany).
- Mann, Allison** (University of Oklahoma).
- Marion, Bonazzi** (Kiel University, DE).
- Marom, Nimrod** (University of Haifa, IL).
- Marr, Melissa** (Royal Holloway/Natural History Museum, GB). Abstract submitted: (174) Phylogeography and British population history of the European wildcat Felis silvestris silvestris inferred from ancient DNA. (*Poster*)

Massilani, Diyendo (Institut Jacques Monod - CNRS, FR). Abstract submitted: 79 - The evolution of bison in Europe during the last 50,000 years (*Talk*)

Matheson, Carney (Lakehead University).

Mathieson, Iain (Harvard University, US).

Meiri, Meirav (Tel Aviv University, IL). Abstract submitted: 118 - Mobility between the Aegean and the Levant in the Late Second Millennium BCE: inference from ancient DNA of pigs (*Poster*)

Meltzer, David (SMU, US).

Millard, Andrew (Durham University, GB). Abstract submitted: 14 - Identifying Scottish Soldiers from the Battle of Dunbar (1650) (*Talk*)

Miller, Holly (University of Nottingham, GB).

Minnikin, David (University of Birmingham, GB). Abstract submitted: 3 - Detecting ancient tuberculosis beyond the reach of ancient DNA with lipid biomarkers and characteristic bone lesions (*Talk*)

Montgomery, Janet (Durham University, GB).

Moore, Jo (Durham University, GB).

Moreno Mayar, Jose Victor (University of Copenhagen, DK).

Mut, Patricia (). Abstract submitted: 104 - Stable isotope evidence for diet and subsistence patterns of the prehistoric populations of south-eastern Uruguay (*Poster*)

Nelson, Elizabeth (Max Planck Institute for the Science of Human History, DE). Abstract submitted: 124 - Identifying plague in 17th century London: a discussion of preliminary results (*Poster*)

Neukamm, Judith (University of Tübingen, DE). Abstract submitted: 96 - DamageProfiler: Calculation of damage patterns in next generation sequencing data from ancient DNA (*Poster*)

Nicholson, William (University of Warwick, GB). Abstract submitted: 34 - Nubian Barley evolution in a drought stress environment (*Poster*)

Niemann, Jonas (, DE).

Nistelberger, Heidi (University of Oslo, NO). Abstract submitted: 102 - The efficacy of high-throughput sequencing and target enrichment on charred archaeobotanical remains. (*Poster*)

Nutsua, Marcel (Kiel University, DE). Abstract submitted: 142 - Reconstruction of HLA genotypes in ancient human samples (*Poster*)

Nyström von Seth, Johanna (, SE).

O'Connell, Tamsin (University of Cambridge, GB). Abstract submitted: 139 - Identification of human migrants in the archaeological record: testing the method of oxygen isotope analysis by a compilation of all relevant published data; and 157 - Nitrogen isotopic enrichment in the food chain: towards a metabolic explanation (*Poster*)

Oliveira, Hugo (University of Manchester, GB). Abstract submitted: 128 - Next-Generation-Sequencing of tetraploid wheat accessions and the origins of agriculture in the Near East (*Talk*)

Onkamo, Päivi (University of Helsinki).

Oras, Ester (University of Tartu, EE). Abstract submitted: 71 - MALDI-FT-ICR-MS for archaeological lipid residue analysis (*Poster*)

Orlando, Ludovic (Natural History Museum of Denmark, DK). Abstract submitted: 42 - An ancient genomic perspective on the horse domestication process (*Talk*)

O'Sullivan, Niall (University College Dublin, IE). Abstract submitted: 35 - Capture of ancient genomic DNA of individuals recovered from a Medieval Alemannic gravesite provides evidence for high mobility of fellowships during the 7th century CE.; and 58 - Multi-omics study of the Iceman's stomach content shows main component (*Talk*)

Otoni, Claudio (KU Leuven, NO). Abstract submitted: 108 - Ancient DNA from cats - a paleogenetics perspective into past distributions and patterns of dispersal of *Felis silvestris* (*Poster*)

Pacheco, George (Natural History Museum of Denmark, DK).

Palkopoulou, Eleftheria (Harvard Medical School, US). Abstract submitted: 129 - Genomics of elephants and their extinct relatives (*Talk*)

Palmer, Karren (University of Manchester, GB).

Papac, Luka (University of Melbourne).

Papakosta, Vasiliki (Stockholm University, SE). Abstract submitted: 109 - A new methodological approach for the extraction and derivatization of absorbed lipid residues from very small

- and very old sample amounts of ceramic potsherds for molecular analysis by Gas Chromatography-Mass Spectrometry (GC-MS) and single compound (*Talk*)
- Parker, Cody** (Max Planck Institute for the Science of Human History, DE). Abstract submitted: 90 - Expanding the oral microbiome reference set (*Poster*)
- Pecnerová, Patrícia** (Swedish Museum of Natural History, SE). Abstract submitted: 69 - The genetic processes leading up to the woolly mammoth's extinction (*Talk*)
- Pederzani, Sarah** (). Abstract submitted: 136 - Pasteurization, Processing, Palaeoenvironment – Applicability of modern dairy reference fats in archaeological lipid residue analysis using $\delta^{13}\text{C}$ of single fatty acids (*Talk*)
- Pellegrini, Maura** (University of Oxford, Italy). Abstract submitted: 133 - Understanding the faunal response to climate in the Mediterranean area (*Talk*)
- Perry-Gal, Lee** (University of Haifa).
- Pfrenge, Saskia** (University of Tübingen, DE).
- Posth, Cosimo** (Max Planck Institute for the Science of Human History, DE). Abstract submitted: 10 - Pre-Neolithic mitogenomes suggest a single major dispersal of non-Africans and a Late Glacial population turnover in Europe (*Talk*)
- Przelomska, Natalia** (University of Cambridge, UK).
- Ramos Madrigal, Jazmin** (University of Copenhagen, DK). Abstract submitted: 119 - Genome sequence of a 5310-year-old maize cob provides insights into the early stages of maize domestication (*Talk*)
- Reade, Hazel** (University College London, GB).
- Rey de la Iglesia, Alba** (Natural History Museum of Denmark, DK).
- Reynard, Linda** (Harvard University, US). Abstract submitted: 15 - Phosphate, carbonate, and Selected Ion Monitoring (SIM) oxygen isotope ratios in enamel apatite from Kromdraai Cave, South Africa: documenting diet, diagenesis and source water variation. (*Talk*)
- Reynolds, Luke** (Liverpool John Moores University, GB). Abstract submitted: 120 - Mitochondrial DNA analysis of first Neolithic farmers from Anatolia and Syria: implications for the Neolithisation of Europe (*Poster*)
- Richards, Michael** (Simon Fraser University).
- Rinaldo, Natascia** (University of Ferrara, IT).
- Roberts, Patrick** (Max Planck Institute for the Science of Human History, Germany).
- Robson, Harry** (University of York, UK). Abstract submitted: 149 - Illuminating the prehistory of northern Europe through lipid residue analysis of putative oil lamps. (*Talk*)
- Roffet-Salque, Melanie** (University of Bristol, GB). Abstract submitted: 56 - Impact of modern cattle feeding practices on milk fatty acid stable carbon isotope compositions emphasise the need for caution in selecting reference animal tissues and products for archaeological investigations; and 165 - Integrated approaches to an (*Talk*)
- Rogers, Bryony** (Durham University, GB). Abstract submitted: 110 - Stable Isotope Analysis of the Blick Mead Dog: A proxy for dietary reconstruction of Mesolithic Hunter-Gatherers (*Poster*)
- Rolandsen, Guro** (Archaeological Museum of Stavanger, NO).
- Rowell, Keri** (University of York, GB).
- Ryan, Hannah** (University of Oxford).
- Sabin, Susanna** (Max Planck Institute for the Science of Human History, DE). Abstract submitted: 67 - A comparative dataset of dentine and dental calculus from medieval Ireland (*Poster*)
- Sánchez Barreiro, Fátima** (Natural History Museum of Denmark, DK). Abstract submitted: 16 - REALbaits capture on degraded DNA. Population genomics without a reference genome (*Talk*)
- Sandoval Velasco, Marcela** (Natural History Museum of Denmark, DK). Abstract submitted: 117 - Tracing the origins of 19th century enslaved Africans from the island of Saint Helena (*Talk*)
- Santana-Sagredo, Francisca** (University of Oxford, UK). Abstract submitted: 145 - Paired radiocarbon dating on human samples and camelid textiles from Pica 8, northern Chile (*Talk*)
- Santana-Sagredo, Francisca** (University of Oxford, UK). Abstract submitted: 145 - Paired radiocarbon dating on human samples and camelid textiles from Pica 8, northern Chile (*Talk*)

- Scheib, Christiana** (University of Cambridge, GB). Abstract submitted: 4 - Bringing it all together: ancient DNA provides biological foundation for hypothesized population replacement in the California Channel Islands. (Talk)
- Schlumbaum, Angela** (University of Basel, CH).
- Schraiber, Joshua** (Temple University). Abstract submitted: 169 - Testing continuity of ancient samples using SNP data (Talk)
- Schreiber, Mona** (IPK Gatersleben, DE). Abstract submitted: 12 - Geo-genetic population structure and gene flow in Eurasian barley populations (Talk)
- Schuenemann, Verena** (University of Tübingen, DE). Abstract submitted: 101 - Genome sequences of 6000-year old barley provide new insights into the history of crop domestication (Talk)
- Shang, Xue** (UCAS, CN). Abstract submitted: 1 - Point count estimation of articulated husk phytoliths of foxtail millet and its prospective use in agricultural archaeology (Talk)
- Sinding, Mikkel** (DK). Abstract submitted: 8 - Population Genomics of Greenlandic polar wolves (Talk)
- Skerry, Katherine** (, US).
- Skoglund, Pontus** (Harvard Medical School, US). Abstract submitted: 105 - Origins and genetic legacy of the first people in Remote Oceania (Talk)
- Smith, Oliver** (University of Warwick, GB). Abstract submitted: 45 - 3,000 years of genome evolution in sorghum (Talk)
- Solazzo, Caroline** (Smithsonian Institution, US). Abstract submitted: 82 - Molecular markers in keratins from Mysticeti whales for species identification of baleen in museum and archaeological collections (Poster)
- Speller, Camilla** (University of York, GB). Abstract submitted: 11 - Proteomic evidence for dietary biomolecules entrapped in dental calculus (Talk)
- Spyrou, Maria** (Max Planck Institute for the Science of Human History, DE). Abstract submitted: 57 - A demographic history of plague revealed through historical *Y. pestis* genomes (Talk)
- Star, Bastiaan** (University of Oslo, NO). Abstract submitted: 138 - Investigating Viking Age trade of Atlantic cod using ancient DNA (Poster)
- Stevens, Rhiannon** (University College London, UK).
- Stone, Anne** (Arizona State University, US). Abstract submitted: 106 - The preservation of DNA from bone, dentin, and calculus from Gombe National Park and Pinnacle Point in Africa. (Poster)
- Styring, Amy** (University of Oxford, GB). Abstract submitted: 92 - The trials and tribulations of strontium isotope analysis of ancient charred grains (Talk)
- Suryanarayan, Akshyeta** (University of Cambridge). Abstract submitted: 173 - Investigating vessel-usage in the Indus Civilisation using ceramic lipid analysis (Poster)
- Sykes, Naomi** (University of Nottingham, GB).
- Szecsényi-Nagy, Anna** (Hungarian Academy of Sciences, HU). Abstract submitted: 95 - Maternal Genetic Ancestry and Legacy of 10th Century AD Hungarians (Poster)
- Thomas, Mark** (University College London).
- Tong, Jun** (University of Sydney, AU). Abstract submitted: 27 - A comparison of methods for estimating evolutionary timescales using ancient DNA (Talk)
- Tornero, Carlos** (Fundació Institut Català de Paleoecologia Humana i Evolució Social, ES). Abstract submitted: 66 - Investigating early Neolithic vertical pastoralism movements of sheep in the Central Pyrenees by stable isotope analyses: data from a modern reference sample and archaeological specimens from Els Trocs (late VIth millennium cal BC; Spain) (Talk)
- Toso, Alice** (University of York, GB). Abstract submitted: 114 - Dietary practices in medieval Islamic Portugal: using stable isotopes to explore food consumption in 11-12th century Lisbon. (Poster)
- Tuross, Noreen** (Harvard University, US). Abstract submitted: 19 - Tomb 7 at Monte Alban: Use, Antiquity and Importance (Talk)
- Vågene, Åshild** (Max Planck Institute for the Science of Human History, DE). Abstract submitted: 72 - Screening for ancient tuberculosis DNA using MALT – a metagenomic approach (Poster)
- van de Loosdrecht, Marieke** (Max Planck Institute for the Science of Human History, DE). Abstract submitted: 13 - In-solution capture assay to screen for preservation and contamination of ancient human DNA (Poster)

- van Dorp, Lucy** (University College London, UK). Abstract submitted: 147 - Exploring the Migration of the World's first Farmers (*Talk*)
- Velsko, Irina** (University of Oxford, UK). Abstract submitted: 170 - Industrialization-associated changes in oral microbiome ecology (*Talk*)
- Venkatakrishnan, Shweta** (University of Tübingen, DE).
- Vieira, Filipe** (Natural History Museum of Denmark, DK).
- Viganó, Claudia** (University of Zurich, CH). Abstract submitted: 62 - B-Thalassemia cod39 mutation found in an individual from a Punic necropolis (VI century BC-II century AD) in Sardinia (*Talk*)
- Wagner, Stefanie** (French National Institute for Agricultural Research, FR). Abstract submitted: 30 - Ancient DNA from waterlogged oak wood provides a new baseline for evolutionary and archeological studies on temperate deciduous tree species (*Talk*)
- Wales, Nathan** (Natural History Museum of Denmark, DK). Abstract submitted: 5 - Ancient viticulture uncorked: nuclear DNA from archaeological seeds sheds light on the history of grape varieties and berry color (*Talk*)
- Walker, Catherine** (University College London, UK). Abstract submitted: 160 - Human Adaptation to Dietary Changes: Are we optimised to an ancient Palaeolithic diet? (*Poster*)
- Wang, Chuanchao** (Max Planck Institute for the Science of Human History, DE). Abstract submitted: 99 - Reconstructing population history in East Asia (*Talk*)
- Wang, Xin** (University of Chinese Academy of Sciences, CN). Abstract submitted: 2 - Botanical and faunal stable isotope analysis at Baishui River valley (Shaanxi, China) to reconstruct crop management, climate change and palaeodietary during late Neolithic (*Poster*)
- Ware, Roselyn** (University of Warwick, GB).
- Werner Alt, Kurt** (Danube Private University, DE).
- Whelton, Helen** (University of Bristol, GB). Abstract submitted: 155 - A multi-proxy approach to diet and animal management in the Neolithic of northern Greece (*Poster*)
- Woods, Roseina** (Natural History Museum, GB). Abstract submitted: 167 - An ancient DNA analysis of the extinct Caribbean primate *Xenothrix mcgregori* (*Talk*)
- Wu, Yan** (Chinese Academy of Sciences, CN). Abstract submitted: 38 - Implications for mid Miocene Diet from Gomphotherium Phytoliths in Tooth Calculus (*Talk*)
- Yang, Melinda** (Chinese Academy of Sciences, CN). Abstract submitted: 37 - Contextualizing the Tianyuan genome within present and ancient human genomic diversity (*Talk*)
- Yang, Yimin** (University of Chinese Academy of Sciences, CN). Abstract submitted: 53 - Characterization of cosmetic sticks at Xiaohe Cemetery in early Bronze Age Xinjiang, China (*Poster*)
- Yau, Bobby** (University of Oxford, GB).
- Zhou, Xinying** (Chinese Academy of Sciences, CN). Abstract submitted: 39 - Wheat yields in ancient China: a study based on the carbon isotope discrimination of charred grains (*Talk*)
- Zhou, Zheming** (University of Warwick, GB). Abstract submitted: 135 - Identify ancient microbial strains with < 100 palaeogenomic reads (*Poster*)
- Zimmermann, Heike** (Alfred Wegener Institute, DE). Abstract submitted: 9 - Origin of plant organic matter in permafrost revealed by ancient DNA and pollen analyses (*Talk*)

