



Archaeozoology, Genetics, Proteomics & Morphometrics

**Carl Friedrich von Siemens Stiftung,
Munich, 2023
October 11-13th**

Sponsored by:



Carl Friedrich von Siemens Stiftung

10th ICAZ AGPM Working Group Meeting
11-13th October, Carl Friedrich von Siemens Stiftung, Munich



Organising committee:

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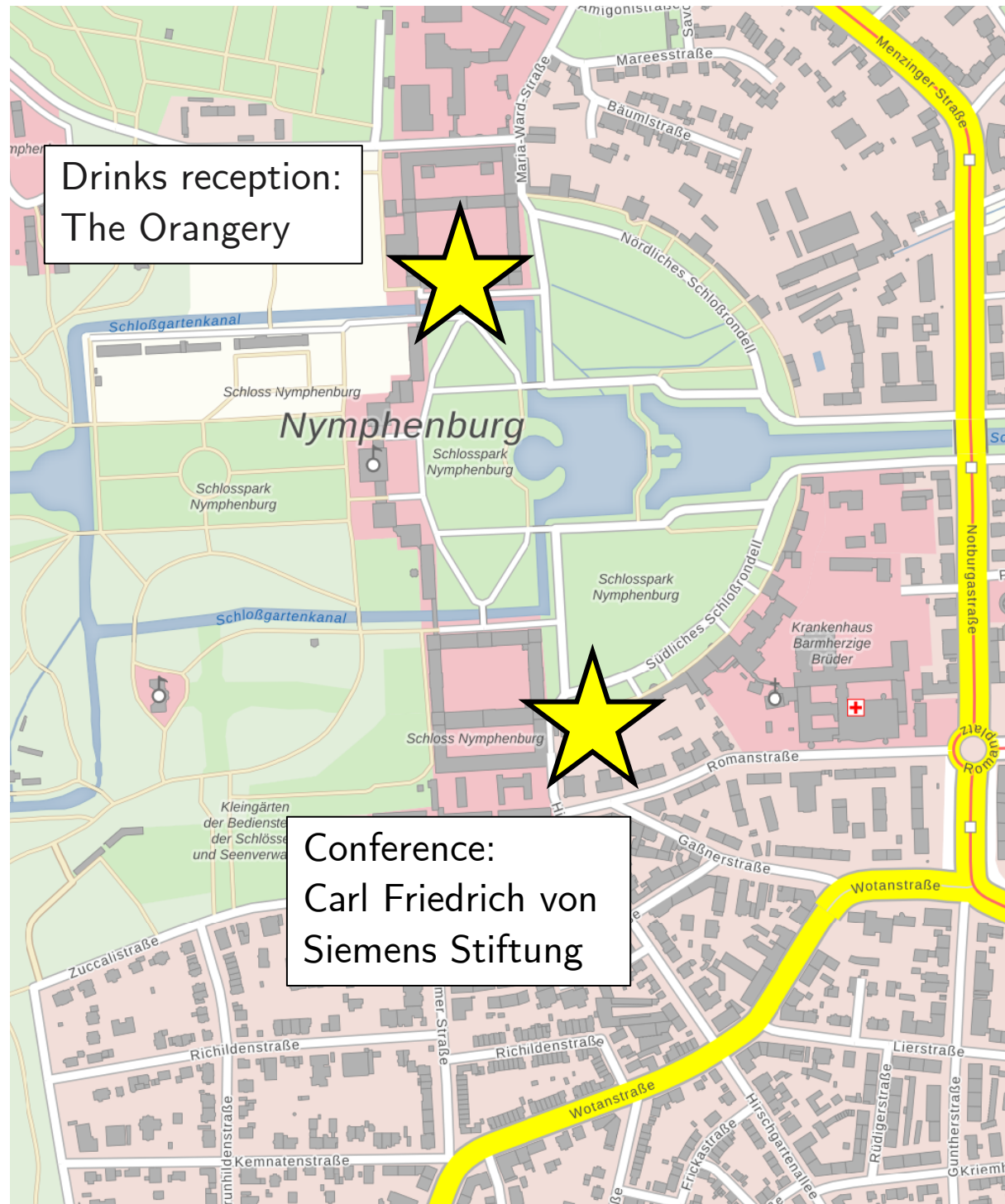
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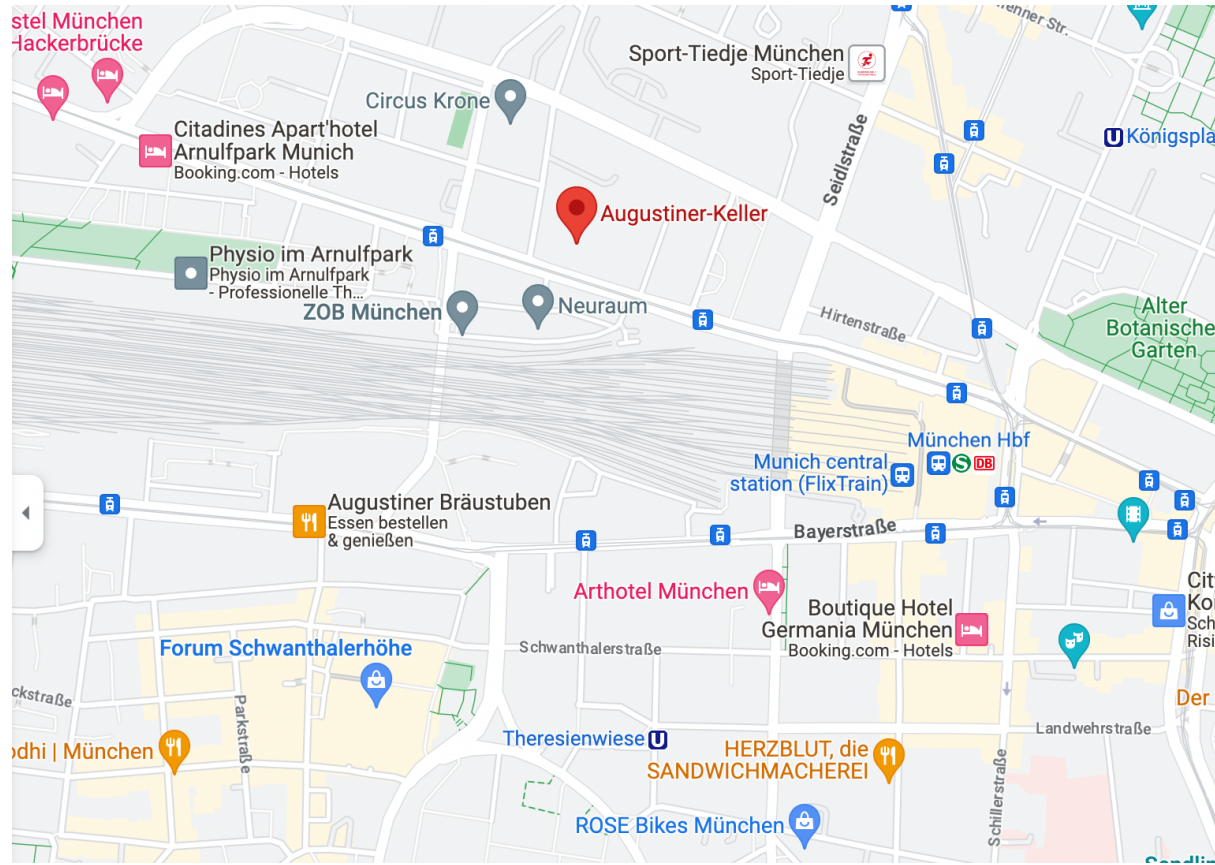
Conference and reception venues:





Dinner venue:

The dinner venue is 5mins walk from the train station (Munich Hbf):





Day One		
08:30 - 09:15	REGISTRATION /COFFEE	
09:15 - 09:30	Opening talk/Housekeeping	
Session 1		
09:30 - 10:00	Allowen Evin	Plenary: Long-term evolution of domestic species: from regional to large-scale morphometric variation
10:00 - 10:20	Ashleigh Haruda	On the wing: Morphological variation in the osteology of Anatidae of the Levant
10:20 - 10:40	Ophelie Lebrasseur	Why did the chicken cross the oceans? A zooarchaeological and palaeogenomics approach to Neotropical American chickens
10:40 - 11:00	COFFEE	
Session 2		
11:00 - 11:20	Eva-Maria Geigl	Paleogenomics of archaeological cats elucidate landmarks of their domestication process
11:20 - 11:40	Danijela Popović	The history of the domestic cat in Central Europe: human-induced dispersal or natural introgression?
11:40 - 12:00	Sean Doherty	Bioarchaeological approaches reveal waves of domestic cat introductions to Europe and the temporal decline of the European wildcat
12:00 - 13:30	LUNCH	
Session 3		
13:30 - 13:50	Lachie Scarsbrook	Ancient genomes reveal the evolutionary history of Australian dingoes
13:50 - 14:10	Sophie Montuire	The necessity of accurate identification of highly variable morphologically close species: illustration with voles and lemmings (rodentia)
14:10 - 14:30	Alice Dobinson	Revealing the Intertwined History of Ferrets and Rabbits
14:30 - 15:30	POSTERS	
Session 4		
15:30 - 15:50	Marie-Pauline Vignes	Multiproxy approach to the Biache-St-Vaast site (Pas-de-Calais, MIS 7): paleoproteomics, taphonomy, zooarchaeology, traceology and experimental archeology
15:50 - 16:10	Marine Jeanjean	Pig, sheep and goat's evolution over the last 8 millennia in the north-western Mediterranean basin: a geometric morphometric perspective
16:10 - 16:30	Jakob Hansen	Assessing species selection of bone artefacts from the NE Iberian Peninsula dated to the Early Neolithic using ZooMS
16:30 - 16:50	Kuldeep More	sedaDNA: Tool to map animal domestication through sediments
16:50 - 17:00	Wrap Up	
18:00 - 22:00	Evening Toast	
	Location: Orangerietrakt, Schloss Nymphenburg, 80638.	
Day Two		

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09:15 - 09:30	COFFEE	
Session 5		
09:30 - 10:00	Naomi Sykes	Deep-time HumAnE (Human-Animal-Environment) approaches to biodiversity
10:00 - 10:20	Thierry Grange	Paleogenomic step stones to shed light on cattle domestication
10:20 - 10:40	Conor Rossi	Population structure and genetic legacy of the extinct Eurasian aurochs
10:40 - 11:00	COFFEE	
Session 6		
11:00 - 11:20	Özlem Sarıtaş	Investigating the morphological changes of suids in the Southwest Asia from Pleistocene to the Late Neolithic
11:20 - 11:40	David Stanton	Pig colonisation in the Pacific: A population genomic study
11:40 - 12:00	Thomas Cucchi	4500 years of morphological diversification in wild boars (<i>Sus scrofa</i>) and the Neolithic transition in Western Europe
12:00 - 13:30	LUNCH	
Session 7		
13:30 - 13:50	Victoria Mullin	Ancient genomics sheds light on the interactions of cattle and humans
13:50 - 14:10	Catarina Ginja	Iron Age genomes from Althiburos - Tunisia elucidate on the origins of African cattle
14:10 - 14:30	Konstantina Saliari	Imports from the South? Mitochondrial DNA and morphometric characterization of cattle from the Iron Age and Roman period north of the Alps.
14:30 - 14:50	Felix Sadebeck	Irregular Chewing, Morphologic Anomalies, and Other Nuisances - Differentiating Cattle Populations Through Geometric Morphometrics
14:50 - 15:30	POSTERS	
Session 8		
15:30 - 15:50	Matthew Collins	A systematic review of database research engines using a controlled, degraded single protein
15:50 - 16:10	Vlatka Cubric-Curik	Smart integration of Genetics with Sciences of the Past in Croatia: where are we now
16:10 - 16:30	Bhararth Nair	Modelling protein degradation: A case study with Beta-lactoglobulin
16:30 - 16:50	Laura Viñas Caron	Fashioning Sudan: proteomic identification of animal species used for garment production
16:50 - 17:00	Wrap Up	

Day Three		
09:15 - 09:30	COFFEE	
Session 9		
09:30 - 10:00	Mustafa Ozkan	Archaeogenomics and the First Nuclear Genomes of Extinct European Wild Ass

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10:00 - 10:20	Arianna Weingarten	Horse mitochondrial genomes from the Middle Pleistocene site of Schöningen
10:20 - 10:40	Ludovic Orlando	The emergence of modern domestic horses
10:40 - 11:00	COFFEE	
Session 10		
11:00 - 11:20	Sierra Harding	Shape analysis of Iron Age sheep astragali suggests west-to-east morphotype diffusion in the southern Levant.
11:20 - 11:40	Kevin Daly	Paleogenomic insights of the origin and trajectory of domestic sheep
11:40 - 12:00	Louise Le Meillour	Identifying the constraints: looking for subsistence adaptations in regards to climatic events in arid environments
12:00 - 12:20	Kaptan Damla	Archaeogenetic analysis of Neolithic sheep from Anatolia
12:20 - 13:50	LUNCH	
Session 11		
13:50 - 14:10	Christine Conlan	Turtles all the way down: Tracking past sea turtle abundance in the Southern Caribbean and its application for sustainable management.
14:10 - 14:30	Shevan Wilkin	Proteomics of novel materials in archaeology
14:30 - 14:50	Moderators: Ashleigh Haruda and Lachie Scarsbrook	"SPECS (Standardisation, Protocols, Ethics, Communication and Sharing)"
14:50 - 15:10	Greger Larson	Plenary
15:10 - 15:30		
18:00 - 22:00	Conference Dinner	
	Location: Augustiner-Keller München Arnulfstraße 52, 80335 München	



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Inquiring into the origins of wolf domestication: paleogenomic analysis of the remains from the Basque Country.

Aloña Aldasoro Zabala * ¹, Asier San-Juan-Nó ¹, Conchi De-La-Rua ¹,
Montse Hervella ¹

¹ University of the Basque Country (UPV/EHU) – Spain

Wolf domestication occurred during the Upper Paleolithic, but the date and origin place(s) are still under debate. Among the causes, current proposals point to the generation of a domestication niche that included several factors (climatic, ecological, anthropic...) that boosted the beginning of this process. The human populations from the Southern refuges of Europe during the LGM would have experienced demographic, social and cultural changes, resulting in a greater interaction with other species (e.g. wolf); interactions that could also be a reflection of behavioral changes of both, wolves and humans. These climatic and social contexts would be close in location and chronology to the recently described Magdalenian dog in Erralla site (Basque Country, Spain). In this regard, we tend to analyze the implication of some factors that favored the inter-species human-wolf-interaction by means of: (i) The paleogenomic study of dog and wolf fossils out of ~20 sites from Franco-Cantabrian region, in order to characterize the mitochondrial lineage and identify possible prosociability associated SNPs of the canids in areas from the Upper Paleolithic to the Neolithic; ii) The contextualization of the paleogenomic results in the sociocultural framework of prehistoric human populations, through the analysis of the variability of the most singular symbolic and artistic elaborations recovered in the same sites. Via several multivariate analyses of both paleogenomic and sociocultural data, we aim to detect possible joint variation trends that could allow us to make some approaches about the possible anthropic factor participating in wolf domestication.

*Speaker

Livestock remains as a boundary object to unite the two cultures?

Matthew Collins ^{*} ^{1,2}, Rune Rattenborg ^{*}

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¹ GeoBiology Section, Globe Institute, University of Copenhagen – Denmark

² University of Cambridge [UK] – United Kingdom

³ Uppsala University – Sweden

New forces are transforming the essential epistemological conflict between material culture (archaeology) and text (history). Technological developments in genomics, proteomics and metabolomics have revealed a degraded but fantastically rich biomolecular record, recovered on, in and buried with material culture. The study of text is intrinsically linked to the development of Large Language Models - which when combined with image processing and data integration profoundly impact access to ancient texts. Used in modern architectures these models are at the heart of the AI revolution in language processing tasks, but are also proving remarkably powerful in biology in solving the structure of proteins, and for me the *de novo* sequencing of peptides. In the study of ancient proteins, it is as if a light switch had been thrown and data hiding in the shadows are suddenly revealed. I want to explore the potential new ground that is being created at the interface of material culture and historical texts by using Livestock Remains as the boundary object to unite Snow's two cultures. Contrasting texts from the Dawn of History and the last manuscript cultures in Western Europe I will explore the new research opportunities for collaboration within and outside ICAZ.

^{*}Speaker

Turtles all the way down: Tracking past sea turtle abundance in the Southern Caribbean and its application for sustainable management.

Christine Conlan * ¹, Lindsey Paskulin ², Jennifer Zhu ², Camilla Speller ², Claudia Kraan ³, Christina Giovas ¹

¹ Department of Archaeology, Simon Fraser University – Canada

² ADPT Laboratories, Department of Anthropology, University of British Columbia – Canada

³ National Archaeological Anthropological Memory Management – Curaçao

Our planet is facing a global biodiversity crisis, with many experts believing we are experiencing Earth's sixth major mass extinction event. Currently, extinction threatens more than 41,000 species worldwide. Among these are hawksbill (*Eretmochelys imbricata*), loggerhead (*Caretta caretta*), green (*Chelonia mydas*), and leatherback (*Dermochelys coriacea*) turtles that frequent Curaçao and Bonaire's shore. The decline of turtle populations in the southern Caribbean may have unpredictable consequences on the entire ecological unit, resulting in the replacement and potential erasure of these cultural keystone species. To support turtle recovery, we must go back past benchmarks associated with industrialization and European arrival to account for the activities that impacted turtle populations prior to modern baselines. If early impacts are not considered we risk misdiagnosing causes for decline resulting in inappropriate management policies. Sea turtle histories in the Caribbean are deeply intertwined with past human activities which have shaped modern populations. However, processing turtles for consumption renders skeletal remains fragmented and morphologically unidentifiable limiting zooarchaeological assessments. We apply Zooarchaeology by Mass Spectrometry (ZooMS) to highly fragmented turtle remains from NAAM's archaeological collections from Curaçao and Bonaire to gain insight into spatial and temporal change in species abundance, diversity, and evenness. Data will be contextualized by known regional events to identify potential cause for differing abundances providing insight into species resilience/vulnerability to human activities and habitat change. Results will complement preliminary aDNA analysis offering long-term biomolecular data that enrich conservation management strategies and support the restoration and maintenance of sea turtle biodiversity in the Southern Caribbean.

*Speaker

Smart integration of Genetics with Sciences of the Past in Croatia: where are we now

Vlatka Cubric-Curik * ¹, Vladimir Brajkovic ², Drzaic Ivana ³, Radovic Sinisa ⁴, Giovanni Boschian ⁵, Ino Curik ⁶, Preston T Miracle ⁷

¹ Vlatka Cubric-Curik – Croatia

² Vladimir Brajkovic – Croatia

³ Ivana Drzaic – Croatia

⁴ Sinisa Radovic – Croatia

⁵ Giovanni Boschian – Italy

⁶ Ino Curik – Croatia

⁷ Preston T Miracle – United Kingdom

An important task of the H2020-TWINN-2015 Project MendTheGap (2016-2019) was to build a multi-inter-trans- disciplinary (MIT) team capable of conducting archaeogenetic research on ancient faunal remains from Croatia and its surroundings. The aim of this presentation is to introduce our MIT research team to a wider scientific community in the field of archaeozoology and to expand our collaborative network. We describe what we have done so far, the problems we have faced, and anticipated our future challenges. First, we report on the improvement of infrastructure, more specifically on the construction of a laboratory for archaeogenetics at the Faculty of Agriculture in Zagreb. Second, we describe our current team and the construction of a MIT research network, for example, how we envision collaboration among geneticists, archaeozoologists, and other scientists of the past. Third, we critically analyse problems and issues that we have faced in recent years. Finally, we present some of our current work and ongoing projects.

*Speaker

4500 years of morphological diversification in wild boars (*Sus scrofa*) and the Neolithic transition in Western Europe

Thomas Cucchi ^{*} ¹, Harbers Hugo ¹, Dimitri Neaux ¹, Marie Balasse ¹,
Clement Zanolli ², Raphaël Cornette ³, Rose-Marie Arbogast ⁴, Stéphanie
Bréhard ¹, Anne Bridault ⁵, Lionel Gourichon ⁶, Jean-Denis Vigne ¹,
Anthony Herrel ⁷

¹ Archéozoologie, archéobotanique : sociétés, pratiques et environnements – Museum National d'Histoire Naturelle, Centre National de la Recherche Scientifique : UMR7209, Centre National de la Recherche Scientifique – France

² De la Préhistoire à l'Actuel : Culture, Environnement et Anthropologie – Université de Bordeaux, Centre National de la Recherche Scientifique – France

³ Institut de Systématique, Evolution, Biodiversité – Museum National d'Histoire Naturelle, Ecole Pratique des Hautes Etudes, Sorbonne Université, Centre National de la Recherche Scientifique, Université des Antilles – France

⁴ Maison Interuniversitaire des Sciences de l'Homme - Alsace – université de Strasbourg, Centre National de la Recherche Scientifique – France

⁵ Archéologies et Sciences de l'Antiquité – Université Paris 1 Panthéon-Sorbonne, Université Paris 8 Vincennes-Saint-Denis, Université Paris Nanterre, Ministère de la Culture et de la Communication, Centre National de la Recherche Scientifique – France

⁶ Culture et Environnements, Préhistoire, Antiquité, Moyen-Age – Université Nice Sophia Antipolis (1965 - 2019), Centre National de la Recherche Scientifique, Université Côte d'Azur, Centre National de la Recherche Scientifique : UMR7264, Université Côte d'Azur : UMR7264 – France

⁷ Mécanismes Adaptatifs et Evolution – Museum National d'Histoire Naturelle, Centre National de la Recherche Scientifique – France

Evolutionary biologists have solicited archaeologists to help document and understand the morphological evolution of animals in response to human activities and, more generally, to help reconstruct the history and significance of the anthropogenic impact on worldwide ecosystems. Artificial selection associated with domestication is the best-known example of a major anthropogenic morphological evolution preserved in the archaeological record. However, the impact of the domestication process and dispersal on the morphological evolution of animals has been far less explored. To fill this gap, we explore how, and in response to which cultural drivers, the Neolithic niche construction has influenced the morphological evolution of Western European wild boars (*Sus scrofa scrofa*) over 4500 years of archaeological record. We used 3D geometric morphometrics of mandibles and calcaneum and 3D morphometric mapping of the humeral shaft to be able to disentangle plastic responses to environmental change from phenotypic change due to directional selection, along with isotopic studies for one key site. The decoupling of size and shape components from bone morphological variation has facilitated the identification of several processes of phenotypic diversification of *Sus s. scrofa* in response to human behaviour during the Neolithic transition in Western Europe.

*Speaker

Paleogenomic insights of the origin and trajectory of domestic sheep

Kevin Daly * ¹

¹ Smurfit Institute of Genetics, Trinity College Dublin – Ireland

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

*Speaker

Ancient taurine cattle genomics: impact of human migrations and introgression from wild animals or Asian indicine cattle

Deborah Diquelou * ¹

¹ Trinity College of Dublin – Ireland

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

*Speaker

Revealing the Intertwined History of Ferrets and Rabbits

Alice Dobinson * ¹

¹ University of Oxford, Palaeogenomics and Bioarchaeology Research Network (PalaeoBARN) – United Kingdom

The evolutionary history of ferrets is widely uncertain, hindered by a scarcity of archaeological evidence, ambiguities within the historic record, and non-specific/unreliable zooarchaeological species identification. Yet, the story of ferret domestication appears unique in the history of human-animal relationships due to their apparently intrinsic connection with another domesticate, the rabbit. During the Medieval period, rabbits expand rapidly across Europe, coinciding with the earliest depictions of harnessed albino ferrets driving rabbits from their burrows. This raises the possibility that growing demand for rabbit hunting and management triggered ferret domestication. If correct, ferrets may be unique in having entered the human niche for the direct purpose of hunting and managing another specific species. The evolutionary history of ferrets and rabbits therefore has implications not only for our limited understanding of their domestication but also the dynamic history of the process more generally. Here, we test the degree of connection by weaving together the historic, archaeological, and genomic record to create a high-definition, tandem history of the two species through time. Ancient genomes of ferrets/polecats across Europe will be generated and analysed in combination with modern genome sequencing data. We intend to identify which wild population(s) of polecats first gave rise to ferrets and reconstruct the spread of lineages through time and space. These results will be analysed in parallel with a concurrent investigation into the origin of rabbit domestication and expansion across Europe. I will present the background, aims, latest results, and the future of the project as an ongoing study.

*Speaker

Bioarchaeological approaches reveal waves of domestic cat introductions to Europe and the temporal decline of the European wildcat

Sean Doherty ^{*} ¹, Alex Jamieson ², Alberto Carmagnini ^{3,4}, Laurent Frantz ^{3,4}, Greger Larson ², Naomi Sykes ¹

¹ University of Exeter – United Kingdom

² University of Oxford – United Kingdom

³ Ludwig Maximilian University [Munich] – Germany

⁴ Queen Mary University of London – United Kingdom

Though the global domestic cat (*Felis catus*) population likely exceeds 400 million, the European wildcat (*Felis silvestris*) exists in a fraction of its former distribution and is increasingly vulnerable. In order to establish the temporal context and cultural circumstances of the arrival and spread of domestic cats and the decrease in wildcat populations, we combined radiocarbon dating with analyses of zooarchaeological, genetic, isotopic and historical evidence. This integrated approach firstly allowed us to discriminate between archaeological remains of *F. silvestris* and *F. lybica/catus*. Our results show that domestic cats derived from *F. lybica* first arrived into Europe during the Iron Age and that successive populations of domestic cats with unique mitochondrial signatures were subsequently introduced during the Roman and Viking Ages. In addition, by characterizing the spatiotemporal representations of both species, we show that the geographic range of European wildcats likely extended across Europe and that their distribution had significantly contracted by the Medieval era.

^{*}Speaker

Getting to know ancient dogs through a genomic approach

Mahaut Goor ^{* 1}, Ludmilla Blaschikoff ², Guimaraes Silvia ², Octavio Serra ³, Fernanda Simoes ³, Cleia Detry ⁴, Macarena Bustamante-Álvarez ^{4,5}, Stéphanie Bréhard ⁶, Adrien Balasescu ^{7,8}, Hossein Davoudi ⁹, Marjan Mashkour ⁶, Régis Debruyne ⁶, Catarina Ginja ¹⁰, Ana Elisabete Pires ^{*}

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Studying ancient dog genomes offers valuable information about past populations, genetic ancestries, and evolution. We investigated nuclear genomic signatures of morphological variation in past dog populations, as well as their mitogenomes. We conducted nuclear and mitochondrial target enrichment assays coupled with high-throughput sequencing on 249 ancient European and Middle Eastern dogs and wolves, dated to the Palaeolithic through the Middle Ages (~33k-600 yBP). We included previously published ancient genomes, present-day breed and village dogs, and wild canids. Seventy-four samples with over 2% of the targeted SNPs (3x), and 133 mitogenomes (90%, 3x depth) were analyzed. The mitogenomic phylogeny revealed HgA's presence in southeastern Europe since the early Neolithic, with two distinct lineages of Eastern and Middle-eastern origin. Additionally, 62 samples with genotype results for at least one specific marker among 24 morphologically-linked SNPs (16 genes) displayed presence of derived alleles for fur aspect, coat color, or body size/weight. For instance, we identified alleles related to intensity of hair shedding (gene MC5R), length (FGF5) and texture (KRT71-KRT74). The apparent diversity in the ASIP alleles suggests coat color heterogeneity. Regarding body size (IGF1, GHR-1,2), the detected genotypes indicate small-sized dogs in Chalcolithic Romania and big sized dogs in Roman Spain, consistently with morphological studies. Mitochondrial and nuclear phylogenies, together with these morphological data provide clues about the emergence and diffusion of some genomic variation in past dog populations. Ultimately, it will provide insights into human-canid relationships throughout chrono-cultural periods.

*Speaker

An archaeogenetics study of Iberian sheep from the Roman Period

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The earliest known sheep in Portugal are dated to c. 5450 cal BC, from the Neolithic site of Lameiras, near Sintra, and c. 5500-5250 BC, from Caldeirão cave, near Tomar. They were probably introduced from the Near East, at least in part by boat. Genetic data for present-day Iberian native breeds support an additional influx of stock from overseas at an unknown time. Osteometric studies show that Iberian sheep increased in size in the Islamic period, while bone shape remained constant after Roman times. Whether the Muslims improved local sheep or imported stock from neighbouring Mediterranean regions is unknown. Moreover, written sources indicate that Romans experimented with sheep breeding to obtain better wool. Ancient DNA analysis is a powerful tool for reconstructing past events, and we obtained shotgun sequencing data for ten sheep remains from the Roman Period collected from five archaeological sites: Coimbra-Criptopórtico (1 sample), Odrinhas (1), Chibanes (3), Santarém (1), Portugal; and Mérida (4), Spain. Endogenous DNA and coverage depths varied between 1.84% to 27.07% and 0.07X and 1.33X, respectively. Phylogenetic analysis of mitogenomes (> 80% covered at > 3X) showed that they belong to haplogroup-B, which is common worldwide in sheep including Iberian fine and coarse wool breeds. Contrasting SNPs data from ancient and modern sheep will introduce a temporal dimension into our demographic inferences and allow us to test for

*Speaker

continuity/discontinuity through time and across space. We plan to examine the variability of nuclear genes for sex determination and investigate the improvement for wool quality by the Romans.

Paleogenomics of archaeological cats elucidate landmarks of their domestication process

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While a great deal of the dispersal of the cat as companions of humans is known through the paleogenetic analysis of archaeological cat remains throughout the Holocene¹, most of the domestication process of cats is still elusive. The reasons for this lack of knowledge are numerous, from scarcity of archaeological cat remains, poor DNA preservation in the presumed domestication centers, propensity to hybridization between cats belonging to different populations/subspecies and, last but not least, strong selection of physical traits not being prerequisite for cats to be a useful member of ancient human societies. These factors have rendered the domestication process of the cat difficult to decipher. We will present the paleogenomic analysis of a few cases that clarify some features of this process. ¹Ottoni et al., 2017, The paleogenetics of cat dispersal in the ancient world. *Nature Ecology & Evolution* 1, 0139.

*Speaker

Iron Age genomes from Althiburos - Tunisia elucidate on the origins of African cattle

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The Maghreb is a key region for understanding cattle dispersal and admixture with local aurochs following their domestication in the Fertile Crescent more than 10,000 years ago. Genomic data collected for Iron Age cattle from Althiburos, El Kef, Tunisia, were used to: i) identify maternal haplogroups; ii) determine the biological sex; iii) infer the proportions of European taurine, African taurine and Indicine autosomal ancestry; and ultimately, iv) investigate genetic affinities with the distinct Moroccan aurochs, past Levantine cattle and present-day breeds. We obtained genome-wide high-throughput sequence data and mitogenomes for four domestic cattle specimens. PCR-based sequence data was also retrieved in these and a further eight samples for a mitochondrial D-loop fragment of 222 base pairs. Five specimens were radiocarbon dated to ~2,877–2,003 calibrated years before present. Four of these yielded sufficient autosomal genome coverages (0.01X to 0.10X) for population genomic analyses. The number of reads mapping to

*Speaker

the Y and X chromosomes were used to determine the biological sex of nine specimens. Principal component analysis and model-based clustering of autosomal data showed Althiburos cattle were close to the pre-domestic Northwest African aurochs and shared ancestry with present-day N'Dama taurine cattle. Maternal lineages were assigned to the R and T1 haplogroups found in two and ten Althiburos specimens, respectively. These are the oldest R-mitogenomes described so far in domestic cattle. Our results can be explained by post-domestication hybridization of Althiburos cattle with local aurochs. However, we cannot rule out an independent domestication event of taurine cattle in North Africa.

Paleogenomic step stones to shed light on cattle domestication

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Archaeozoological data suggest that cattle were domesticated in northern Mesopotamia at the beginning of the Neolithic. Paleogenomic data are in support of this conclusion 1. Nevertheless, little is known about the evolution of the ancestor of domesticated cattle, the aurochs, about its distribution and diversity. Similarly, the evolution of early domestic cattle is still poorly understood. We only appreciate today that it must have been a multi-faceted process. We will present some paleogenomic data as step stones that will shed light on some of the open questions, thus contributing to a better understanding of these processes. 1Pereira Verdugo, M. et al., 2019, Ancient cattle genomics, origins, and rapid turnover in the Fertile Crescent, *Science* 365, 173–176.

*Speaker

Genomic analysis of Neolithic and Bronze Age sheep populations in eastern Europe and southwest Asia

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

*Speaker

Assessing species selection of bone artefacts from the NE Iberian Peninsula dated to the Early Neolithic using ZooMS

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Bone artefacts have, as an archaeological material group, provided an important basis for discussions on, among others, technological advancements, workflows in bone object manufacture, modes of cultural transmission, typologies and chronologies, and material selection and utilisation on a spatiotemporal scale. Though study of raw material selection has given insight into general material preferences and utilisation in past societies, the specificities of taxonomic preferences in bone material selection are less well understood. The surface modifications involved in bone artefact production and usage partially or fully remove diagnostic features, often preventing morphological taxonomic identification. The species composition of bone object assemblages is therefore generally unknown. This issue can be resolved via peptide mass fingerprinting of type 1 collagen (COL1), known as Zooarchaeology by Mass Spectrometry (ZooMS), which enables the taxonomic identification of collagen-based faunal remains. Here we present ZooMS analysis of approximately 600 bone artefacts from one Late Magdalenian and four Early Neolithic sites from across the Iberian Peninsula, using a minimally invasive sampling approach. The results show inter-site variation in the taxonomic composition of the bone object assemblages. Furthermore, specific distributions of species seem to be related to certain artefact types. It therefore appears that inter-group variation occurred on at least a spatial scale in regards to the taxonomic selection for bone object manufacture.

*Speaker

Shape analysis of Iron Age sheep astragali suggests west-to-east morphotype diffusion in the southern Levant.

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¹ University of Haifa – Israel

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The mobility of domesticated animals has often been studied from an expansive point-of-view, while fewer zooarchaeological studies have considered the continuous translocation of domesticates around the premodern Mediterranean Basin. Some osteometric and geometric morphometric studies have shown important results in terms of mobility, non-local introductions, and improvements of domesticates at nodes along ancient trade routes and between settlements in the region. Among these, a recent biometric study conducted on domestic sheep in the Iron Age southern Levant revealed a statistically significant increase in mean body size in Persian period seaside settlements, as well as proportional differences in astragali between coastal and inland zones. These results suggested that coastal herds may have been improved through the introduction of new breeding stock, while also hinting at some translocational exchange between zones based on the spectrum of astragalar proportions. The present study seeks to further understand this previously observed ‘morphocline’, and tease out possible origins of influx. We applied 2D geometric morphometric methods to samples of Iron Age domestic sheep astragali from the island of Cyprus (Rantidi), a port settlement on the Carmel coast (Tel Dor), a coastal settlement on the Akko plain (Tel Keisan), and an inland urban settlement in the Hula Valley (Tel Abel Beit Maacah). Preliminary results of the principal component and disparity analyses suggest a west-to-east diffusion of astragalar morphologies. We interpret these findings to support the possibility of maritime importation and consequent overland trade of non-local sheep variants in the southern Levant during the heyday of ‘Phoenician’ trade.

^{*}Speaker

On the wing: Morphological variation in the osteology of Anatidae of the Levant

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Accurate identification of waterfowl in archaeological assemblages of the Levant has potential to unlock new methods of environmental reconstruction since each species has different preferred habitats and migration patterns influenced by environmental shifts. Additionally, understanding the changing seasonal abundance of avian resources exploited by people in the past is key to addressing how people responded to climatic and environmental realignments. However, the identification of osteological remains of ducks is notoriously challenging, even to tribal level. We present here new geometric morphometric protocols on wing elements from over twenty Palaeoartic species that migrate across Europe, the Levant and Africa to improve the identification of waterfowl. This is an ideal starting point to expand utilisation of GMM in avifaunal research and test applicability to a notoriously difficult taxonomic group.

^{*}Speaker

Pig, sheep and goat's evolution over the last 8 millennia in the north-western Mediterranean basin: a geometric morphometric perspective

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Since their first occurrence in the North-Western Mediterranean basin (Catalonia and South of France) ~8000y ago, domestic animals have evolved in a local environmental and socio-economical context. Many studies have explored the evolution of domestic animals for some chrono-cultural periods or transitions, but only few have studied their evolution over the long term, from their arrival in a specific area to the local modern breeds. We therefore propose to study the agrobiodiversity and its evolution of caprines (sheep and goat) and pigs over 8000 years, and to compare these evolutions with different factors, such as geography, topography, climate, archaeological and socio-economic context. To do so, 2D geometric morphometrics was applied to third lower molar of caprines and pigs, using both landmarks and slidings semi-landmarks. A total of 210 archaeological sites was considered, allowing the study of more than 2500 teeth of sheep and goat and 700 of pigs. These results are part of the ERC-DEMETER project "Eight

*Speaker

millennia of changes in domestic plants and animals: understanding local adaptation under socio-economic and climatic fluctuation”. This work was carried out in collaboration with the various directors of excavation and specialists who studied the archaeological sites.

Archaeogenetic analysis of Neolithic sheep from Anatolia

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Sheep is among the first farm animals domesticated about 12 000 years ago. The zooarchaeological record suggests that domestication may have taken place within central to east Anatolia, although the exact location and timing is unknown. Previous studies suggested the Asian mouflon (*Ovis gmelinii*) as the wild ancestor of sheep, which was distributed from East Iran to West Anatolia by the early Holocene. Two major patterns are noticeable based on genetic studies on present-day breeds. First, high levels of nuclear and mitochondrial DNA diversity are observed. This may indicate that domestication involved multiple centers, or alternatively, a large, heterogeneous wild population. Secondly, present-day domestic sheep clusters into two groups; west (Europe) and east (Asia, Africa and Mediterranean Islands) based on genome-wide polymorphism data and proportions of mitochondrial haplogroups. However, we still do not have a good understanding of when and how these patterns emerged. To address this, we used a total of 21 number of ancient genomes produced from 238 individuals of early Holocene sheep bones from central and west Anatolia and analyzed these genomes comparatively. Comparing these profiles with published modern breeds and ancient genomes from Neolithic and Bronze Age Kyrgyzstan sheep, we show that divergence between West and East appeared in early Neolithic, and that the European and Anatolian sheep gene pools changed significantly since the Neolithic period.

*Speaker

Tracking ancient livestock pathogens across the domestication process

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1

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The Neolithic era in Southwest Asia was marked by the domestication of livestock, which facilitated increased human-animal interactions and amplified the risk of zoonotic disease transmission both within and between animal herds and humans.

Despite the successful recovery of numerous ancient human pathogen genomes through high-throughput sequencing techniques, the number of livestock pathogen genomes retrieved remains limited. Our research is directed towards acquiring pathogen and animal metagenomic aDNA from various livestock species and timelines. Specifically, we are interested in obtaining aDNA from 10,000-year-old sheep and goat material from the Zagros Mountains in Iran, a region with some of the earliest evidence of goat herding and the zoonotic brucellosis in humans.

The objective of this project is to recover livestock pathogens from the earliest phases of domestication, to understand its impact on the evolution and spread of zoonoses within livestock populations and across species barriers.

Additionally, we are exploring the genetic health of ancient ovicaprids by examining patterns of inbreeding and genetic diversity at the immune gene and genome levels.

*Speaker

Identifying the constraints: looking for subsistence adaptations in regards to climatic events in arid environments

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Studying past human-animal relationships does not only reflect on subsistence strategies, but covers a wide range of ancient human behaviours, from culinary practices to ecological constraints. In response to climatic changes, past populations had to integrate new subsistence strategies based on the domestication of species, along with the already hunted wild species. In the Zagros mountains and Northern Levant, the domestication of *Ovis orientalis* and *Capra aegagrus* lead to some of the most herded species: sheep, *O. aries*, and goat, *C. hircus*. The incorporation of domesticated caprines into dietary behaviour, and their relative contributions within this, is difficult to assess in archaeological assemblages of arid environments due to high fragmentation of skeletal remains and to harsh burial conditions. We present the combination of zooarchaeological, palaeoclimatic and palaeoproteomics data to assess the subsistence strategies of past human populations in response to intense climatic events. We focused on faunal remains from four archaeological sites: Shubayqa 1 and 6 and Shaqarat Masiad, Jordan, and SJE170, Sudan. Using a combination of palaeoproteomics and zooarchaeology to assign the skeletal remains to genus or species level, we carefully selected and sampled medium sized-bovids from each phase or layer within a site, preserved proteins extracted, proteolytically digested, and characterised using LC-MS/MS. Molecular species identification was then carried out using a custom proteins sequence database containing all possible species of bovids in existence in the studied regions. This data allows us, coupled with paleoenvironmental data, to document the changes in the dietary behaviour of past human populations.

*Speaker

Why did the chicken cross the oceans? A zooarchaeological and palaeogenomics approach to Neotropical American chickens

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Chickens reached Neotropical America ~500 years ago through human-mediated means and have grown to acquire a socio-economic status of particular importance. Yet the nature and timing of their introduction(s) as well as their cultural history on the continent remain for the most part unknown. The ARAUCANA project is a stepping-stone towards remediating this knowledge gap. Through international and interdisciplinary collaborations, we collected an assemblage of nearly 600 bird bones from 15 archaeological sites located in Argentina, Brazil, Mexico, and Peru, and dating from the early 16th to the 19th century. Following a comprehensive zooarchaeological study conducted on the entire assemblage, 80 chicken bones were sampled for palaeogenomic investigations. We here present the results of our full suite of investigations which address the issues surrounding bird species identification, and hint on the roles of chickens within local societies. Furthermore, when placed within a comprehensive ancient and modern European, and modern Asian genomic dataset, our sequenced data also offers an insight into the genomic ancestry of selected ancient South American populations, hence informing on their likely introduction(s). Overall, our findings provide an understanding of how these non-native birds have reached the continent and grown to become essential to its economy in the span of half a millennia, ultimately informing upon the cultural and biological heritage of South American chicken populations.

*Speaker

Combining geometric morphometrics and mtDNA to study cryptic species: illustration with voles (Rodentia)

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Environmental changes that occurred during the last glacial periods offer the opportunities to study how extant species have responded and understand how they have spread to reach their current geographical distribution. The identification of numerous cryptic molecular lineages in western Europe through several taxonomic groups suggest non-adaptive radiations linked to these climatic events.

In voles, *Microtus agrestis* and *Microtus lavernedii* represent two cryptic species identified recently as such. These two species have probably separated during the Younger Dryas cold event (12ky). Their identification remains difficult and the way they are separated raises questions. Our study combines genetics (mtDNA, palaeogenomics) and geometric morphometrics to a better understanding of the mechanisms leading to their divergence and a fast speciation event. The use of teeth from actual owl pellets, fossils from palaeontological sites and also soft tissues from living animals allows to extract mtDNA and the results will be combined to molar shape characterizations. We are thus able to detect potential hybrid populations of the two species in order to sample a reduced set of individuals along the contact zones which will be whole genome sequenced. Indeed, contact zones remain poorly studied, and a better characterization of the population structure of the different species and the dynamics of the hybrid zones is required. The main goal is to analyze how *M.agrestis* and *M.lavernedii* differ or coexist and behave in western Europe, and then to reassess their geographical distribution in the context of recent climate change.

*Speaker

Biomes and teeth: A 2D GM model of the lower third molar of the white-tailed deer

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White-tailed deer (*Odocoileus virginianus* Zimmermann 1780) is an important species across America, both in pre-Columbian and modern times. This species is distributed in southern Canada and Brazil. It is a polytypic species that has become well adapted to a wide range of habitats, from temperate to subtropical and semi-arid environments to rainforests and savannas. The lower third molar (m3) is considered a significant phenotypic marker for adaptation to natural or anthropogenic environments. It is the last tooth in the tooth row, and hence, is posteriorly less constrained in comparison with teeth at intra-row positions. Therefore, I used a morphological line of evidence and performed a two-dimensional geometric morphometric (2D-GM) model of the lower third molar of white-tailed deer to study shape variations across different biomes in America. I sampled 100 teeth housed in natural science museums and compared them with an archaeological sample from Panama (n=25) to test whether it was possible to predict the biome in which the animal lived in the past. As a result, it was observed that the shape of the lower m3 in extant white-tailed deer is different across biomes, and the archaeological lower m3 could also be placed into a biome category.

*Speaker

THE NECESSITY OF ACCURATE IDENTIFICATION OF HIGHLY VARIABLE MORPHOLOGICALLY CLOSE SPECIES: ILLUSTRATION WITH VOLES AND LEMMINGS (RODENTIA)

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Accurate species identification is a complex task but essential to better understand the evolutionary history of species. During the Quaternary, voles and lemmings were abundant and are considered as good climatic markers. A lot of species are genetically and ecologically divergent, but their molars, on which most of identifications are made, exhibit a large morphological variation that can lead to some confusion. The systematic attribution is usually based on the first lower or third upper molars, and in the case of morphologically close, but highly variable, species, decision making can be subjective. This is the case between *Microtus arvalis* and *Microtus agrestis*. Moreover, at an intra-specific level, recent molecular data suggest that *M. agrestis* populations are a complex of divergent lineages, some of them being recognized as valid species. The same kind of observation can be made about lemmings and in particular for the identification, in the fossil material, of *Myopus*, a bryophagy specialist, which has often been mixed up with the tundra lemming (*Lemmus* spp.). Based on extant populations, this study presents a morphometrical approach to statistically differentiate these species complexes. This method is then applied on fossils. A better knowledge of the intra-specific variation, and a better taking it into account, allow for more correct identifications of both present-day and fossil species. Applied on fossils, some discrepancies with previous classification suggest that revisions could be necessary. Our study attests the contribution of geometric morphometrics to a better understanding of small mammal communities and its implication in paleoenvironmental reconstructions.

*Speaker

sedaDNA: Tool to map animal domestication through sediments

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Animal domestication has had a significant impact on the early human ancestors, affecting their quality of life and economy. Therefore, it's important to better understand the progress of domestication process and its consequences throughout the time. However, the lack of reliable well-preserved archaeological records remains a major challenge in investigating past animal domestication. Fortunately, use of seda-DNA as a tool for paleogenomic investigation in diverse settings such as archaeological sites, permafrost, and sediments has bypassed this problem. Unlike traditional methods relying on fossilization, seda-DNA expands the scope of paleogenomics beyond fossils. By leveraging this technique, we developed a globally applicable tool for screening environmental samples to identify wild and domesticated haplogroups of nine different domesticated animals. This tool uses mitochondrial DNA probes that target haplogroup-defining single nucleotide polymorphisms (SNPs). Currently, the tool is undergoing testing on DNA libraries constructed from fossil-derived DNA to assess its effectiveness. Subsequently, it will be applied to sediments collected from the rock shelter Abrigo de la Malia, situated in the Iberian Peninsula, Spain. This site has yielded exceptionally well-preserved fossils originating from various animals ranging from the pre-Last-Glacial-Maximum (pre-LGM) to the Holocene. The implementation of these probes will elucidate the presence, continuity, and succession of different animal species that either were introduced by humans or sought refuge within the cave. By using this tool on environmental samples, especially, from the period from where the fossils are missing, will help the holistic reconstruction of animal domestication process throughout history.

*Speaker

Ancient genomics sheds light on the interactions of cattle and humans

Victoria Mullin * ¹

¹ Trinity College – Ireland

The domestication of *Bos taurus* ~10.5kya in Southwest Asia was a significant period in human prehistory. For millennia cattle have been an integral source of meat, milk, hide and traction for human societies and subsequently both species have been shaped by one another. One route to explore and further understand the cattle/human relationship is the sequencing of ancient cattle genomes. Utilising a spatio-temporal dataset of > 150 ancient cattle genomes, spanning Anatolia to Ireland, we explore cattle populations over time and space to identify migration events, genetic replacement and admixture with wild aurochs. This time series dataset further facilitates exploration of the intertwined histories of cattle and humans, highlighting possible animal management strategies and timing the selection of present day cattle production traits.

*Speaker

Modelling protein degradation: A case study with Beta-lactoglobulin

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

^{*}Speaker

The Epigenomics of Ancient Cattle and Aurochs

Ciarán O’connor * ¹, Daniel Bradley ¹

¹ Trinity College Dublin – Ireland

The fields of bioarchaeology and ancient DNA (aDNA) have developed rapidly in recent years, greatly advancing our understanding of early animal domestication events and the effects of human interference on the biology of domesticates. However, the focus has primarily been on sequence-specific changes, with a lack of research in the epigenomics of ancient domesticates. Ancient epigenomics is a powerful tool that can leverage the difference in post-mortem cytosine deamination rates of methylated and unmethylated CpG sites in aDNA, enabling the reconstruction of ancient methylomes. Key information such as the sex, castration status, and age-at-death of individuals can be deduced from methylation profiles. Using high-coverage ancient genomes from sites across Europe and Asia, we have generated methylation data for ancient aurochs and domestic cattle. We have developed an elastic net regression model trained on these methylation patterns, selecting for genomic windows centred on CpG sites that are the most predictive of sex. Here we present the preliminary results of this machine learning model, utilising the fraction of methylated CpG sites within informative windows to infer the sex of ancient bovines.

*Speaker

The emergence of modern domestic horses

Pablo Librado , . The Erc Pegasus Consortium , Ludovic Orlando * ¹

¹ Centre d'Anthropobiologie et de Génomique de Toulouse (CAGT) – Université Toulouse III - Paul Sabatier, Centre National de la Recherche Scientifique – France

The horse is one of the last mega-herbivores to have been domesticated but certainly represents the one that most impacted human history. It provided past societies with fast mobility, new ways to make war, and facilitated pastoralism and farming. Recent paleogenomic work revealed the original homeland of modern domestic horses in the steppes of the lower Don-Volga, approximately 4200 years ago. The management practices underlying the transformation and spread of what was a once local genetic lineage into a global resource remain, however, poorly understood. We generated new paleogenomic and functional data, more than doubling the number of ancient horse genomes ever characterized, to better characterize the demographic trajectory, mobility patterns and selection targets accompanying the emergence and further spread of modern domestic horses across Eurasia. Our work documents early selective breeding and sudden shifts in husbandry techniques facilitating the control of horse reproduction within the few centuries preceding the expansion of spoke-wheeled war chariots. The identification of similar features in the Botai assemblage provides further evidence for horse management of an independent horse genetic lineage in Eneolithic Central Asia.

*Speaker

The history of the domestic cat in Central Europe: human-induced dispersal or natural introgression?

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Advances in paleogenomic research have provided new information about domesticated animals, but we still know little about the history of cats. Until now, only one subspecies, the Near Eastern wildcat (*Felis silvestris lybica*), was known to have been domesticated. The domestication areas were assumed to be the Near East and Egypt. From this region, cats spread to the Mediterranean and beyond. It has been accepted that the Roman legions played the primary role in the expansion of cats through northern Europe. However, we found that cats that carried mitochondrial DNA (mtDNA) haplotypes of wildcats from the Near East were present in Central Europe as early as the Neolithic, well before Roman times, and may have been associated with Neolithic expansion. Our new results reveal the presence of the mtDNA haplotypes of the Near Eastern wildcats in Poland even in the pre-Neolithic period. This may suggest that the Near Eastern wildcats could have spread across Europe independently of agricultural expansion. Consequently, the natural range of Near Eastern wildcats may have been much broader than previously assumed. To understand how and when domestic cats appeared in Central Europe, we performed a target enrichment of ca. 57,000 genomic SNPs. We believe that this will allow us to definitively determine whether the appearance of the Near Eastern wildcat mtDNA in Central Europe was a natural admixture between the two subspecies or whether it was a human-induced dispersal of tame/domestic cats. The study is supported by the National Science Centre, Poland, grant no. 2019/35/B/HS3/02923.

*Speaker

Population structure and genetic legacy of the extinct Eurasian aurochs

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Taurine cattle (*Bos taurus*) were domesticated from a small group of their wild progenitors, the aurochs (*Bos primigenius*), in the Near East approximately 10.5 KYA. During the Holocene, domestic cattle spread with farming from the Near East across Europe, Asia, and Africa while the wild species dwindled and eventually went extinct. Cattle remain among the most important livestock animals today but relatively little is known about the genetic diversity and structure of the extinct wild population.

Here, we present whole-genome data from a range of Eurasian aurochs spanning the Late Pleistocene through to the Holocene. These geographically and temporally diverse ancient genomes allow us to explore the diversity of Eurasian aurochs during the Last Glacial Period, when populations were highly structured. We investigate how wild populations reacted to climatic fluctuations during this period, which ultimately resulted in a dramatic collapse of genetic isolation in the Holocene. While the last aurochs cow died in 1627, wild and domestic cattle co-existed for thousands of years and there has been genetic evidence of wild introgression. We examine the genetic legacy of these extinct populations in modern cattle and the implications for the domestication process.

*Speaker

Imports from the South? Mitochondrial DNA and morphometric characterization of cattle from the Iron Age and Roman period north of the Alps.

Konstantina Saliari * ¹, Christina Amory , Erich Draganits , Peter Ramsel , Bendeguz Tobias , Erich Pucher , Walther Parson

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Morphometric examinations on cattle bones from Roman period sites in present-day Austria suggest the arrival of a new large-sized cattle population, which has been connected with the Roman conquest and related imports of cattle from the South. However, recent finds of cattle remains similar to those found in the Roman period, in two Iron Age sites suggest import of cattle from the Mediterranean already long before the arrival of the Romans. Ancient mitochondrial DNA analysis on fourteen Iron Age and Roman period cattle teeth and bones provide for first time evidence on cattle mobility from the Mediterranean to areas north of the Alps through the documentation of haplogroups T1 and T5. Our results offer new archaeogenetic data, help evaluating established morphometric criteria used for the study of the various Iron Age and Roman period cattle morphotypes, offer insights into the origins and evolution of local cattle populations in present-day Austria and suggest contacts and complex mechanisms of livestock exchange before the arrival of the Romans.

*Speaker

Irregular Chewing, Morphologic Anomalies, and Other Nuisances - Differentiating Cattle Populations Through Geometric Morphometrics

Felix Sadebeck * ¹

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Geometric Morphometrics has enabled us to approach questions around domestication and the emergence of new morphotypes of all kinds of animals. Developing an appropriate landmarking protocol and finding the right dataset for each question pursued remain the most important and all too often problematic prerequisites. In an archaeological context, this becomes especially relevant when we want to differentiate not only wild vs domestic or some closely related yet distinct animals (like different equids) but venture forward to intraspecific variation. Using Cucchi et al.'s (2019) paper *Taxonomic and phylogenetic signals in bovine cheek teeth: Towards new biosystematic markers to explore the history of wild and domestic cattle* as a starting point, the author has tried to develop a geometric morphometrics approach that allows distinguishing different cattle populations, motivated by research questions about changing cattle husbandry practices during the Roman period. Mandibular M3 teeth have been chosen as the most promising skeletal part for venturing on this journey, which was everything but straightforward: repeated drawbacks have led the way to what the author thinks of as the yet most appropriate landmarking protocol developed for pursuing the goal of identifying cattle intraspecific variation on mandibular M3s. This protocol was tested on a reference dataset compiled from the two largest reference collections of 20th-century rural European cattle breeds, the Julius-Kühn-Collection in Halle, Germany, and the Adametz-Collection in Vienna, Austria. The present paper will outline the journey that this project took and briefly discuss some of the results.

*Speaker

INVESTIGATING THE MORPHOLOGICAL CHANGES OF SUIDS IN THE SOUTHWEST ASIA FROM PLEISTOCENE TO THE LATE NEOLITHIC

Dr Özlem Sarıtaş * ^{1,2}, Dr Ardern Beaman-Hulme ³, Prof Louise Martin ⁴

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It is well established that a complex of domesticated animals and plants originated in the 'Fertile Crescent' of Southwest Asia. However, the initial spread of domesticated pigs out of the Levantine zone and across Central Anatolia is relatively poorly understood, and evidence of pig management is equally limited. Moreover, in some regions, this taxa were never incorporated into the Neolithic agro-pastoral economies. This indicates that Central Anatolia is a complex region with no evidence of pig management despite the early development of caprine husbandry in the Neolithic of this region. This paper will focus on the Neolithic settlement in Central Anatolia, Boncuklu Höyük (c. 9200- 7800 cal. BC), compared with the sites from the Pleistocene to the Late Neolithic in Southwest Asia. We compare Southwest Asia's archaeological and modern populations to explore their morphological change and status using 2D geometric morphometrics, biometrics and metric data from molar teeth. We observed that the metric/biometric analysis from dental remains and geometric morphometric analysis suggests the presence of small-size pig groups in the 9th-8th Millenium Late period.

Ancient genomes reveal the evolutionary history of Australian dingoes

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The tandem expansion of humans and domestic animals has produced complex evolutionary histories, especially in island ecosystems. In Australia, widespread populations of specialised, free-ranging domestic dogs (dingoes) were established over 3,300 years ago, following their introduction by either maritime hunter-gatherers, or Austronesian agriculturalists. Today, dingoes are highly geographically-structured, and retain basal ancestry, shared with the closely-related New Guinea Singing Dogs. The extent to which these signals, however, have been confounded by ancient population demographics (e.g. bottlenecks) and recent gene-flow with European dogs is not known. To reconstruct temporal patterns of genomic diversity in Australian dingoes, we directly-dated, and screened 58 ancient dingoes from the Nullarbor Plain in southern Australia. Here, we analysed 20 newly generated, low-coverage (1–2X) nuclear genomes spanning the last ~2,250 years alongside over 1,000 modern dog genomes, including 32 dingoes and 17 New Guinea Singing Dogs. We reconstructed the long-term population structure of Australian dingoes; estimated their divergence from other southeast Asian dogs (using time-calibrated Bayesian trees); and assessed the degree to which they interbred with European dogs in colonial periods.

^{*}Speaker

Pig colonisation in the Pacific: A population genomic study

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

*Speaker

Multiproxy approach to the Biache-St-Vaast site (Pas-de-Calais, MIS 7): paleoproteomics, taphonomy, zooarchaeology, traceology and experimental archeology

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The Biache-Saint-Vaast site (BSV, Pas-de-Calais, MIS 7) has yielded three levels rich in bone remains of large terrestrial mammals. In these assemblages, remains called "retouchers" were identified that included impression patches, related to percussion on lithic material. With over 300 such remains currently identified, BSV constitutes one of the largest known assemblages, with exceptional preservation for an open-air site, raising many questions about the use of faunal remains as tools by Neanderthal populations. Was there any intentionality in the choice of the raw material used? Is there a particular preparation of the bone? Is it possible to highlight specific behaviors related to the "making" of such tools?

The detailed study, following multi-proxy approaches of this "retouchers", is still underdeveloped. Non-invasive zooarchaeological, taphonomical and traceological studies are used to understand the acquisition and use of the remains. Paleoproteomics analyses overcome the limitations of classical taxonomic assignments and allow minimally invasive techniques.

The first results obtained seem to indicate that the remains of the three species most represented in the faunal procession identified at BSV were used as "retouchers": *Bos primigenius*, *Ursus arctos* and *Stephanorhinus hemitoechus*. These results demonstrate the interest of the joint application of different approaches and methods for the knowledge of the use of this type of bone tool and more generally of the management of large herbivore fauna by Neanderthal populations. Analyses on a wider spectrum of bone remains will attempt to characterize the entire BSV assemblage and to relate it to other sites of the region.

*Speaker

Fashioning Sudan: proteomic identification of animal species used for garment production

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Cloth garments are sophisticated products that require a chain of specific and elaborate processes in order to be produced, beginning with the acquisition and preparation of the raw materials. In particular, skin and wool textiles derive from a wide variety of different animal species. Thus, their correct identification is essential to understand which species were selected and bred to answer the demands of garment production and assess how they were managed within the whole animal husbandry system. In ancient Sudan, there has been a long-lasting debate surrounding the usage of domesticated versus wild animals (e.g. sheep, goat, cattle, dromedary/camel, gazelle, giraffe and leopard) to produce cloth garments. To elucidate this question, the ERC project "Fashioning Sudan. Archaeology of Dress along the Middle Nile" (101039416) is investigating cloth garments made of textiles and animal skins preserved in graves from Sudan and Nubia and ranging from the Bronze Age to the Late Medieval Period (c. 1500 BCE to 1500 CE). In addition, we use new developments in ZooMS and palaeoproteomics to identify the animal species used across time and space and place the results within the available (zoo)archaeological, iconographic, and textual evidence. Here, we will present the overall project and preliminary proteomic results to shed new light on the economy of ancient Sudan and the use of animal resources beyond food production, an aspect that has been often overlooked.

*Speaker

Horse mitochondrial genomes from the Middle Pleistocene site of Schöningen

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Paleogenetic research on mammalian taxa has focused on the process and history of horse domestication. The role horses played in transportation and warfare has had major consequences in shaping the social and political foundations of ancient populations. However, the human-horse relationship has deep roots in prehistory when horses were significant for hominin subsistence. One of the earliest insights into this relationship comes from the Middle Pleistocene open-air site of Schöningen (Lower Saxony, Germany). The site is well known for the discovery of wooden spears found among butchered horse remains dated to ~300 kya. Despite the exceptional preservation, genetic data from Schöningen has never been reported.

In this study, we analyze the largely complete mitochondrial genomes (mtDNA) of two morphologically determined *Equus mosbachensis* horses. This data fills a large temporal and geographic gap in the paleogenetic record of horses between a Middle Pleistocene genome from North America and Late Pleistocene specimens from across Eurasia. In phylogenetic analyses, we find the Schöningen Middle Pleistocene horses to be located on a deeply divergent mtDNA lineage, distinct from any ancient Eurasian horse sequenced thus far. Moreover, the newly reconstructed mtDNA sequences are basal to all mtDNA diversity found in extant horses. Our data also provides a crucial temporal reference point to improve the horse mtDNA molecular clock, by pinpointing major divergence events in the evolutionary history of equids. By extending the age range of mtDNA retrieval into the Middle Pleistocene, we can gain valuable insight into the genetic origins of modern-day horses.

*Speaker

Proteomics of novel materials in archaeology

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In archaeology, zooarchaeological findings, as well as indirect proxy information that can be used to identify human-animal interactions, are of paramount interest. As recovered amino acid sequences can reveal information about the taxonomic classification and tissues recovered proteins derived from, successful proteomic analyses can provide critical insights into the types of animal products people used that would otherwise remain invisible. While shotgun proteomics has been widely applied to human dental calculus to explore dietary intake through the recovery and identification of plant and animal proteins, it has rarely been applied to novel types of archaeological materials. Metaproteomic analysis can be used to investigate many types of ancient and historic artifacts, however, organic preservation is often a limiting factor. Identifying materials or contexts that function as preservational reservoirs has the potential to extend how far back into the past we can apply biomolecular methods to these questions in the past. This presentation will detail recent findings from three studies that investigate examples of archaeological residue proteomes via liquid chromatography, tandem mass spectrometry. From copper alloy cooking vessels from the eastern steppe, to bronze vessels from Mongolia, and residues from symbolic objects from southern Africa we identified unique animal products in each instance, demonstrating the diverse uses of animal products across time and space.

*Speaker

Archaeogenomics and the First Nuclear Genomes of Extinct European Wild Ass

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Equus hydruntinus, also known as European wild ass, puzzled zooarchaeologists and taxonomists since their first discovery for displaying a mixture of characteristics found in other equids. This study presents ancient genomes of three morphologically unidentified Anatolian equids dating 1st millennium BCE, sequenced to nuclear coverages ranging from 0.6-6.4X. Mitochondrial DNA haplotypes of the Anatolian individuals clustered with those of the extinct European wild ass. Moreover, the Anatolian wild ass whole genome profiles fell outside the genomic diversity of the Asian wild ass (*E. hemionus*) lineages, suggesting that the three Anatolian wild asses represent the latest recorded survivors of *E. hydruntinus*. Comparative genomic analyses indicate that *E. hydruntinus* was a sister clade to the Asian *E. hemionus* and complex population histories and low levels of gene flow between wild-ass groups. Finally, runs of homozygosity and genomic heterozygosity analyses indicate a stark population decline in Anatolian wild asses by the mid-1st millennium BCE, consistent with their recent loss from the zooarchaeological record.

*Speaker