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## Archaeozoology, Genetics, Proteomics & Morphometrics

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Muséum national d'Histoire naturelle  
Paris, France  
October 17<sup>th</sup>-18<sup>th</sup> 2019



A working group part of



International Council  
for Archaeozoology

# Welcome!

Dear delegates,

We are delighted to welcome you for the 8th Meeting of the Archaeozoology, Genetics, Proteomics and Morphometrics working group here in the Natural History Museum of Paris

With this new edition we wanted to extend this working group to Proteomics in order to cover a wider range of innovative and emerging research in the field of zooarchaeology.

We hope you will enjoy these two days of talks and events as much as we will, and that you will have time to explore Paris' treasures as well.

Thank you for joining us!!

The 2018 organizing committee,

Thomas, Céline, Régis, Antoine, Séverine, Anne, Colline, Marine, Hugo, Louise, Manon & Dimitri

## Organising committee

Thomas Cucchi (AASPE/MNHN)  
Céline Bon (Musée de l'homme/MNHN)  
Régis Debruyne (MNHN)  
Antoine Zazzo (AASPE/MNHN)  
Séverine Zirah (MCAM/MNHN)  
Anne Quezel (AASPE/MNHN)  
Colline Brassard (AASPE/MNHN)  
Marine Durocher (AASPE/MNHN)  
Hugo Harbers (AASPE/MNHN)  
Louise Le Meillour (AASPE/MNHN)  
Manon Le Neün (AASPE/MNHN)  
Dimitri Neaux (AASPE/MNHN)

## The working group is promoted by the following institutions

- International Council for Archaeozoology (ICAZ)
- Muséum National d'Histoire Naturelle (MNHN)
- Institut Ecologie et Environnement du Centre National de la Recherche Scientifique (CNRS-InEE)



International Council  
for Archaeozoology



CNRS

Institut Ecologie et Environnement



Muséum national d'Histoire  
naturelle



UMR 7209

Archéozoologie, Archéobotanique : Sociétés,  
Pratiques et Environnements



UMR 7206

Eco-Anthropologie

**8th ICAZ AGPM Working Group meeting**

October 17-18 2019, MNHN, Paris, France

# **PROGRAMME**

## **Thursday, October 17, 2019**

09:00	Registration desk open (Auditorium de la grande galerie de l'évolution) - Registration
09:30	Introductory talk. <b>Jean-Denis Vigne</b>
09:45	<b>Keynote</b> Palaeoproteomics and zooarchaeology, a marriage made in heaven? <b>Matthew Collins</b>
<b>Session 1: Pathogens</b>	
10:20	<b>O1</b> Exploring the evolution of animal diseases in Ethiopia: combining zooarchaeology, ancient genetics and epidemiology to tackle a global challenge. <b>Ophelie Lebrasseur</b>
10:40	<b>O2</b> "The rotte, the pockes and the blode": an interdisciplinary approach to the diagnosis of medieval sheep disease. <b>Annelise Binois</b>
11:00	<b>O3</b> The significance of robustly identifying microbes in archaeological samples of domesticated animals. <b>Evangelos Dimopoulos</b>
11:20	<b>Coffee break</b>
<b>Session 2: Dispersal, mobility &amp; migration</b>	
11:40	<b>O4</b> Wild and domestic, native and translocated; endangered and invasive: the global history of the fallow deer ( <i>Dama dama</i> ). <b>Naomi Sykes</b>
12:00	<b>O5</b> The arrival of the mountain hare to the Western Isles of Scotland: an ancient DNA study. <b>Alex Jamieson</b>
12:20	<b>O6</b> Implementing a multidisciplinary approach to study the introduction of the turkey ( <i>Meleagris gallopavo</i> ) in Europe: when archaeozoology meets biomolecular archaeology. <b>Aurélie Manin</b>
12:40	<b>Lunch &amp; Posters</b> (Grand amphithéâtre d'entomologie)
14:00	<b>O7</b> "Of sheep and men"? How ancient proteins can document African Late Stone Age subsistence strategies. <b>Louise Le Meillour</b>
14:20	<b>O8</b> The Nubian cat ( <i>Felis silvestris lybica</i> ) in Neolithic Poland – identification, chronology and synanthropic behavior. <b>Magdalena Krajcarz</b>
14:40	<b>O9</b> Variation in geographical sources of osseous reindeer craft material in Viking Age town revealed by ancient DNA and stable isotopes. <b>Matti Heino</b>
15:00	<b>Coffee break</b>
<b>Session 3: Methods &amp; approaches</b>	
15:20	<b>O10</b> Geometric morphometrics on astragali: new approaches to studying sheep ( <i>Ovis aries</i> ) phenotypic variability. <b>Lidia Colominas</b>
15:40	<b>O11</b> Capturing mobility control in limbs bones anatomy: an experimental proof of concept. <b>Thomas Cucchi</b>
16:00	<b>O12</b> Captivity and cranial morphology in wild boar ( <i>Sus scrofa</i> ): exploration of new markers of the process of domestication. <b>Dimitri Neaux</b>
16:20	<b>O13</b> Time-dependent molecular evolution in ancient DNA. <b>Audrey Lin</b>
16:40	<b>O14</b> Comparative paleogenomics of the woolly mammoths: genotyping by reduced genomics and target capture. <b>Laetitia Aznar-Cormano</b>
17:00	<b>O15</b> Using proteomics to uncover ancient human-animal interactions. <b>Shevan Wilkin</b>
17:20	<b>O16</b> Domesticated animal products on ancient shipwrecks, searching for DNA. <b>Lisa Briggs</b>

# **PROGRAMME**

## **Friday, October 18, 2019**

<b>Session 4: Pleistocene diversity</b>	
09:00	<b>O17</b> Investigating hominin subsistence strategies at Denisova Cave (Russia) using stable isotopes and peptide mass fingerprinting. <b>Samantha Brown</b>
09:20	<b>O18</b> The challenge of bone fragmentation: Combining ZooMS and Zooarchaeology to assess hominin subsistence behaviour at Fumane (Italy). <b>Virginie Sinet-Mathiot</b>
09:40	<b>O19</b> Paleogenomics and Paleontology reveal two different aspects of the evolution of bison. <b>Thierry Grange &amp; Jean-Philippe Brugal</b>
10:00	<b>O20</b> Characterization of aurochs population dynamics and domestication through their maternal lineages. <b>Wejden Ben Dhafer</b>
10:20	<b>Coffee break</b>
<b>Session 5: Domestication</b>	
10:40	<b>O21</b> Ancient cattle genomics and rapid turnover in the Fertile Crescent. <b>Daniel Bradley</b>
11:00	<b>O22</b> Ancient genomic insights into the goat herds of the earliest phases of domestication. <b>Kevin Daly</b>
11:20	<b>O23</b> Palaeogenomics of ancient dogs. <b>Greger Larson</b>
11:40	<b>O24</b> News from Mesolithic Iberian dogs. <b>Ana Elisabete Pires</b>
12:00	<b>O25</b> Morpho-functional study of extant canids with application to the European Neolithic. <b>Colline Brassard</b>
12:20	<b>Lunch &amp; Posters</b> (Grand amphitéâtre d'entomologie)
13:40	<b>O26</b> Paleogenetics of horse domestication in Anatolia and the Caucasus. <b>Eva-Maria Geigl</b>
14:00	<b>O27</b> Burrowing into the bio-cultural history of Rabbits. <b>Carly Ameen</b>
14:20	<b>O28</b> Identifying the early stages of reindeer domestication by the Sámi in northern Fennoscandia: an exploratory geometric morphometrics approach of forelimb bones. <b>Maxime Pelletier</b>
14:40	<b>O29</b> Tracing reindeer domestication in Fennoscandia: an osteometric study of castrated and full male reindeer bones. <b>Mathilde van den Berg</b>
15:00	<b>Coffee break</b>
<b>Session 6: Husbandry</b>	
15:20	<b>O30</b> The development and diversity of sheep populations in Estonia. <b>Eve Rannamäe</b>
15:40	<b>O31</b> Parchment and animal husbandry strategies in Medieval Scandinavia. <b>Lena Strid</b>
16:00	<b>O32</b> Whole genome sequencing of Viking Sheep from the North Atlantic. <b>Albína Hulda Pálsdóttir</b>
16:20	<b>O33</b> The impact of breeding practices in the genomic composition of Iberian cattle: inferences from Medieval-Moslem vs. Post-Medieval Christian specimens. <b>Catarina Ginja</b>
16:40	<b>O34</b> Sus 100: Geometric morphometric and genetic variation in <i>Sus scrofa</i> associated with intensive human selection pressures. <b>Ashleigh Haruda</b>
17:00	<b>O35</b> Genetic diversity of Slavic horses. <b>Danijela Popović</b>
17:20	<b>O36</b> Ancient DNA and Osteometry of cattle from Iron Age to Medieval times in NW Switzerland. <b>Angela Schlumbaum</b>
17:40	<b>Closing remarks</b> - Next ICAZ AGPM?

## GENERAL MAP OF THE VENUES

- The working group *plenary sessions* will be held at the Auditorium of the Grande Galerie de l'Evolution
- The *lunchs and poster sessions* will be held at the Grand Amphithéâtre d'Entomologie, 43 rue Buffon







## **ABSTRACTS**

### **Oral Communications**



***8th ICAZ AGPM Working Group meeting***

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*October 17-18 2019, MNHN, Paris, France*

## Session 1: Pathogens

### **O1 Exploring the evolution of animal diseases in Ethiopia: combining zooarchaeology, ancient genetics and epidemiology to tackle a global challenge**

Ophelie Lebrasseur, Lisa Cavalerie, Olivier Hanotte, Siobhan Mor, Keith Dobney, Helina Woldekiros

Ethiopia is home to the largest livestock population in Africa, with 80% of Ethiopian households dependent on agriculture and thus in direct contact with domestic animals. This renders the country particularly vulnerable to the spread of zoonotic diseases, directly affecting people's health but also their wealth and nutrition. Since their introduction in the Horn of Africa, domesticates have adapted to the country's endemic diseases by developing resistance (*i.e.* the Sheko cattle breed with its high trypanotolerance). Yet animal diseases remain a serious challenge for the agricultural economy and human-animal health of the country. Our understanding of the evolutionary history of these diseases leaves a lot to be desired (past published research has primarily focused on tuberculosis, brucellosis and the plague), and crossbreeding with European stock and lack of identification, characterisation and conservation of the indigenous gene pool is leading to the erosion and loss of that resilience. We here address these major issues by bringing in a temporal dimension to ongoing veterinary and epidemiological research via the HORN project. Nestled within a One Health framework, our research aims to i) recover ancient genomes of pathogens from zooarchaeological remains and investigate their evolutionary history, and ii) characterise genetic adaptation of cattle to local diseases and the environment through time in relation to productivity. We first provide a general review of published modern and ancient zoonoses studies in the Horn of Africa, highlighting targeted pathogens and those lacking consideration. We also report published work on Ethiopian cattle adaptation to environment and diseases. Knowing ancient DNA preservation is not optimal in Ethiopia due to environmental and climatic conditions, we present and discuss available material types and methodologies. We finish by exploring the ways in which our results can be integrated within policy-making and breed development programs.

### **O2 "The rotte, the pockes and the blode": an interdisciplinary approach to the diagnosis of medieval sheep disease**

Annelise Binois

Sheep farming played an essential part in the medieval European economy, with entire industrial sectors, and most notably the wool and cloth trade, relying solely on the use of sheep products. Major mortality events affecting the ovine population at a regional scale were therefore likely to have had serious and lasting impacts on medieval societies, and the written evidence testifies indeed to the frequency and severity of these events. This evidence does little, however, for the identification of the specific pathogens involved in these deaths. Diagnosis may appear just as difficult on the skeletal remains of the victims. Indeed, most causes for mass mortalities leave no traces on the bones, compromising any lesional diagnostic approach. We contend nonetheless that an interdisciplinary investigation of archaeological mortality deposits, integrating several lines of enquiry in a global diagnostic process - zooarchaeology, paleo-epidemiology, historical investigations, paleoparasitology, ancient DNA analyses... - has the potential to shed light on the specific causes of past sheep mortalities. In this presentation, we will expose our approach through the example of a 13th century sheep deposit from Tétéghem, France, in which this multi-pronged approach ultimately allowed us to identify the physical and molecular remains of past pathogens and, in all likelihood, to determine the cause of death.

### **O3 The significance of robustly identifying microbes in archaeological samples of domesticated animals**

Evangelos Dimopoulos, Irina Velsko, Evan Irving-Pease, Laurent Frantz, Greger Larson

The accurate identification of microbial species from archaeological samples has the potential to provide an unprecedented perspective on the evolutionary history of major diseases that have affected humans and domestic animals. Limited DNA survival and DNA damage, however, have hindered the search for ancient pathogens. Here, we present a novel, hypothesis driven, method for identifying microbes in ancient DNA libraries that complements established metagenomics pipelines. By applying this method to individual libraries constructed on extracts from 1,066 ancient pig and 1,838 ancient dog samples, we identified the causative agents of a range of bacterial and viral diseases including: Kennel cough, Rabies and Salmonellosis. We also interrogated published human metagenomic datasets and we were able to identify microbes that are capable of infecting

both humans and domesticated animal hosts including the causative agents of tuberculosis and diphtheria. This method can therefore be employed to test specific hypotheses related to the role of domesticated animal species as pathogen reservoirs. Since many of the causative agents of these zoonotic diseases became prevalent in a post-industrial context, the results of this approach will be able to offer insights into how human activity has reshaped the landscapes of both the natural environment and animal diseases.

## Session 2: Dispersal, mobility & migration

### **O4 Wild and domestic, native and translocated; endangered and invasive: the global history of the fallow deer (*Dama dama*)**

Naomi Sykes, Holly Miller, Karis Baker

The fallow deer (*Dama dama*) is the most widely distributed cervid on the planet, having been transported around the world by humans over the last 10,000 years. The species is native to the eastern Mediterranean (where today the last 'wild' population is endangered) but was taken to many Aegean and Mediterranean islands during the Neolithic and Bronze Age. Further waves of diffusion, during the Roman and medieval periods, took fallow deer to mainland and northern Europe. Their subsequent spread around the world was result of European colonialism, which saw fallow deer established in South Africa, Australia, New Zealand and the Americas as well as islands in the Fijian group, and the Lesser Antilles. Today, many translocated populations are managed as semi-domesticated, with some being farmed; whereas other feral herds are considered 'invasive' pests. The deep history of human-dama relationships is, therefore, complex and shifting. To unpick such complexity requires more than a single analytical method. This paper will present the results of a project that has employed full-suite analysis of fallow deer remains (traditional zooarchaeological techniques, multi-isotope analysis and genetic analysis) the results of which are presented in combination with historical, linguistic and iconographic evidence. Together these data tell the story of human ideology, population movement and social structure, reflecting the dynamics of culture, economies and attitudes to the natural world. Perhaps most importantly, these data highlight the multiple issues surrounding existing legislation for wildlife management and protection at a global level.

### **O5 The arrival of the mountain hare to the Western Isles of Scotland: an ancient DNA study**

Alex Jamieson, Greger Larson

Mountain hares today can be found from Scandinavia to Eastern Russia with isolated populations in Ireland, Scotland and the Alps. They are a cold adapted species found in mountainous and tundra environments. While their modern distribution is well understood, the extent of their past range and whether humans were responsible for transporting them beyond their natural range remains understudied. The primary aim of my research is to assess the natural and human-aided distribution of mountain hares across their circumpolar region. I am employing an ancient DNA approach to assess the geographic and temporal shifts in mitochondrial haplotypes. The study initially focuses upon the western most edge of their range, the Western Isles of Scotland. Mountain hares are thought to be a non-native species to the islands and their place of origin is unknown. They first appeared in archaeological deposits of the Mesolithic period. I will present here initial results showing where these mountain hares may have originated and how they came to be on the fringe of Europe. This not only informs us more about the species itself. It may even give us insights into the Mesolithic people's trade routes or possibly even the origins of the people themselves.

### **O6 Implementing a multidisciplinary approach to study the introduction of the turkey (*Meleagris gallopavo*) in Europe: when archaeozoology meets biomolecular archaeology**

Aurélie Manin, Michelle Alexander, Jan Bakker, Norbert Benecke, Zora Bielichová, Povilas Blaževičius, Benoît Clavel, Simon Davis, Freydis Ehrlich, Quentin Goffette, Günther Karl Kunst, René Kyselý, Krista Mcgrath, Marta Moreno García, Giedrė Piličiauskienė, Noémie Tomadini, Richard Thomas, Martyna Wiejacka, Camilla Speller

The turkey is a North American domestic bird that took part in the Columbian exchange soon after 1492. According to historical accounts, the first birds were imported to Spain, from Mexico or Central America, in 1512 and it took them only a few decades to reach Northeastern Europe. Eventually, some domestic populations that were selected in Europe were brought back to America. While today the domestic turkey plays a substantial role in meat production worldwide and is a central symbol of festivities in various cultures, in particular in Europe, many questions remain unanswered regarding its spread from North America to Europe and its subsequent adoption. This presentation addresses the challenges in understanding the post-1492 history of the turkey through the implementation of a multidisciplinary study of archaeological bones. A large collaborative effort allowed us to gather ca. 150 turkey remains from 14 European countries and one Caribbean island. Turkey bones

can be difficult to identify due their high similarity with different domestic galliforms (chicken, peacock, Guinea fowl). Thus we used a combination of morphological criteria and biomolecular analyses (archaeogenomics and, to a lesser extent, peptide mass fingerprinting [ZooMS]) to validate species identifications. Sex identification was performed combining morphological criteria, morphometrics and genomic markers to infer husbandry practices and potential biases in sample choice. Finally, we used a genomic approach to explore population dynamics from America to Europe and back.

## **07 "Of sheep and men"? How ancient proteins can document African Late Stone Age subsistence strategies**

Louise Le Meillour, Séverine Zirah, David Pleurdeau, Josephine Lesur, Antoine Zazzo

Among the major shifts that occurred in Holocene African societies, the introduction and diffusion of domestic caprines (sheep and goats) through the continent remains unclear. Henceforth key species in the population's economy, understanding how they were first managed would bring valuable information regarding the transition from a hunter-gatherer-based economy to the first pastoral communities. First introduced in the North by the sixth millennium, they reached Austral Africa at the turning of the era. Very few information has been gathered regarding the modalities of flocks' diffusion and whether a species was preferred over the other. The paucity of data concerning the early steps of caprines introduction can be partly explained by morphological similarities between close related species (wild and domestic) and bone diagenesis that limit morphological attributions of archaeological remains and sometimes lead to misidentifications. This study focuses on the use of proteomics approaches to document this question. Regarding the absence of protein sequences from wild bovids in international databases, we focussed on establishing a new protein referential that could both be useful to archaeologists and biochemists. Skeletal remains of twenty species from the Comparative Anatomy collections of the MNHN were sampled. Bone powders were first decalcified to isolate the organic fraction and the proteins extracted were digested and characterized by UHPLC-MS/MS. The data were treated using a database assisted de novo reconstruction software. Sequences of bone matrix proteins such as collagen type I and 2-HS-glycoprotein are hereby proposed for all the antelope's species. This study allows to construct a completely new referential for species difficult to identify on morphological basis only and propose a protein based phylogenetic repartition of these species. This new database would allow to refine taxonomic identifications of archaeological remains attributed to caprines and thus, to molecularly ascertain the presence of those domestic species on African archaeological sites.

## **08 The Nubian cat (*Felis silvestris lybica*) in Neolithic Poland - identification, chronology and synanthropic behavior**

Magdalena Krajcarz, Maciej T. Krajcarz, Danijela Popović, Mateusz Baca, Daniel Makowiecki, Jan Wiejacki, Hervé Bocherens

The Nubian cat, *Felis silvestris lybica*, is considered to be a wildcat subspecies native to Northern Africa, Near East and Central Asia. Though there are other subspecies, this is the only one which has been domesticated, with the human-cat interactions confirmed for the last 10 000 years. It is also known that the relationship must have started somewhere in the region of the Fertile Crescent. Its appearance in Central Europe is still vague and believed to be connected with introduction by humans. Despite the growing body of knowledge on the history of cat domestication, still little is known about its early dispersal to Europe, its occurrence in subfossil material and its paleoecology. Previous radiocarbon dating and genetic studies have shown that domestic cats have been present in Poland since the Roman Period. However, new discoveries revealed much earlier expansion of the *F. s. lybica* into this region. In this paper we present a multiproxy study of the remains from Poland. We present an archaeological context of finds, their taxonomic identification through mtDNA analysis and their chronology based on direct radiocarbon dating. With use of stable isotopes we explore a role of this species in the Central European ecosystem during the Neolithic period, both in relation to the wild native animals and in the aspect of its possible synanthropic behavior, linked to Neolithic farmers and their agriculture. The study was supported by the National Science Centre, Poland (grant number 2017/27/B/NZ8/00728).

## **09 Variation in geographical sources of osseous reindeer craft material in Viking Age town revealed by ancient DNA and stable isotopes**

Matti Heino, Johnny Karlsson, Markus Fjellström, Jouni Aspi, Love Dalén, Anna-Kaisa Salmi

Data from DNA and stable isotopes can be used to obtain information on the geographical provenances of animal materials found in historical human settlement sites. This information can be used to gain insights into historical

trading routes and networks. We investigated geographical origins of osseous reindeer craft material excavated from a Swedish Viking Age town of Sigtuna, by subjecting bone samples for stable isotope and DNA analyses. Genetic data showed that some of the reindeer were related to modern Norwegian mountain reindeer whereas some were related to modern forest reindeer. This division correlated with stable nitrogen values so that the reindeer that were genetically related to modern forest reindeer had on average higher nitrogen values than those that were genetically related to modern Norwegian mountain reindeer. Our results therefore suggests that the osseous reindeer craft material in Viking Age Sigtuna consisted of two genetically and ecologically different types of reindeer. Although we cannot pinpoint the exact geographical origin of the material of the forest type of reindeer, our results show that the reindeer material was sourced from multiple sources.

## Session 3: Methods & approaches

### **O10 Geometric morphometrics on astragali: new approaches to studying sheep (*Ovis aries*) phenotypic variability**

Lidia Colominas, Ashleigh Haruda, Nadja Pöllath, Allowen Evin

A well-established and useful addition to the archaeozoological toolbox is Geometric Morphometric methods (GMM). It has proven to be a very sensitive method for separating closely related taxa as well as wild and domestic populations. Recent methodological developments have shown that it is also possible to discriminate between populations and breeds of the same domestic species, specifically domestic sheep (*Ovis aries*). Here we present three recent advances in which GMM techniques have been successfully used to study sheep phenotypic variability through the analysis of astragalus morphology. The first study explores morphological divergence of wild and domestic sheep within populations from prehistoric sites in Anatolia and Syria as well as on modern populations from the Middle East and Europe. The second study investigates the connectivity of Final Bronze Age pastoral settlements sites in Central Asia by distinguishing palaeoecological land use of ancient sheep populations. Finally, the third study explores sheep mobility linked with husbandry practices during the Iron Age and Roman period in northeastern Iberia across the Pyrenees mountains and lowlands. We demonstrate with these examples that the astragalus is a very useful element of the skeleton for discriminating between populations of ancient sheep and allows a new approach to address archaeological research related to human selection, landrace and breed development, and mobility and exchange.

### **O11 Capturing mobility control in limbs bones anatomy: an experimental proof of concept**

Thomas Cucchi, Harbers Hugo, Anthony Herrel, Raphaël Cornette, Clement Zanolli, Roberto Macchiarelli, Stéphanie Bréhard

The domestication process remains too elusive to be documented from the domestication syndromes commonly used in zooarchaeology. These morphological syndromes mainly rely on genetically driven morphological markers induced by adaptation and directional selection. They document the occurrence of a domestic animals in the archaeological record but not the domestication process of a wild one. Furthermore, gene flow during the domestication process has likely delayed the expression of these domestication syndromes, preventing the zooarchaeologists to explore the earliest stages of the domestication process. DOMEXP research project explore the imprint of the biomechanics stress induced by the captivity in the skeleton development using an experimental design on an ungulate model: the wild boar (*Sus scrofa*) and a comparative approach with the norm of reaction of wild and domestic populations. We combined both 3D Geometric Morphometrics of bone surfaces and 3D morphometric mapping of the cortical thickness of long bones to capture the biomechanic signal of captivity and explore this signal in the archaeological record of Western European suids from Mesolithic to Late Neolithic context.

### **O12 Captivity and cranial morphology in wild boar (*Sus scrofa*): exploration of new markers of the process of domestication**

Dimitri Neaux, Anthony Herrel, Raphaël Cornette, Vincent Debat, Thomas Cucchi

Domestication effects on animal phenotype combine inherited genetic changes and individual plastic responses to environmental changes in the course of its development. The genetic and developmental background of the domestication syndromes defined by Darwin have been thoroughly explored. However, the plastic responses to the environmental factors of domestication remain poorly understood. To bridge this gap we have investigated the effects of biomechanical stress of captivity on the skeleton of a wild ungulate in the course of its development. We used the wild boar (*Sus scrofa*) as model and for this study, we focused on the skull as a phenotypic marker. We compared the skull size and shape of wild boars populations grown in the wild and in captivity, as well as captive and free ranging pig populations (*Sus scrofa domesticus*) using homologous landmarks and sliding semilandmarks on three-dimensional virtual representations of crania and mandibles. We explored the differences among the populations in their response to captivity using Principal Component Analyses and Partial Least Squares Analyses. Our results underline significant differences between the wild boar populations grown in wild and in captivity. The captive wild boars specimens display morphological features close to those found in domestic pigs (e.g., more concave cranium, reduction of the angle of the mandible). These results



support the hypothesis that captivity has a great impact on the development of bones, and his therefore one of the preminent features acting on the shape changes occurring during the domestication process.

### **O13 Time-dependent molecular evolution in ancient DNA**

Audrey Lin, Simon Ho, Laurent Frantz, Beth Shapiro, Dan Bradley, Ludovic Orlando, Louis Du Plessis, Greger Larson

Estimating rates of molecular evolution is necessary in order to infer demographic dynamics and evolutionary timescales from genetic data that had been sampled at specific points in time. For phylogenetic analysis of time-structured data, ages of the ancient DNA sequences can be drawn from radiocarbon-dated samples to calibrate the molecular clock. The hypothesis of time-dependent molecular evolution states that the rate of observable evolution varies depending on the timeframe over which the rate is measured. Domestic animals and their wild progenitors are an excellent proxy to test the hypothesis of time dependency given their relatively short generation time and their ubiquity in the archaeological record. The hypothesis of time-dependent molecular evolution is tested by comparing the directly-dated mitochondrial genomes of multiple ancient archaeological samples across a balanced temporal distribution. By analysing these data using dated molecular clock analyses, changes in the molecular substitution rate across different time scales can be estimated. In our study, hundreds of samples from vertebrate species (including bison, chicken, goat, horse, and pig) used for analyses were either radiocarbon dated or are associated with archaeological sites with high confidence. We used different phylogenetic methods in estimating the rates from time-structured data, including root-to-tip regression, scalable relaxed clock dating, approximate Maximum Likelihood inference, and Bayesian inference. Preliminary results from some of the taxa show evidence of time-dependent molecular evolution within timeframes spanning between the present day to 128,000 BP. There is a negative relationship between rate and time, where as the sample age increases, there is a corresponding decline in estimated substitution rate. To our knowledge, this study will be the largest analysis yet using ancient DNA in testing the hypothesis of time-dependent molecular evolution. These results may help inform and improve fossil calibration of current molecular clock models.

### **O14 Comparative paleogenomics of the woolly mammoths : genotyping by reduced genomics and target capture**

Laetitia Aznar-Cormano, Jawad Abdelkrim, Véronique Barriel, Régis Debruyne

Reduced comparative genomics has gained popularity during the last decade, facilitating genotyping of non-model species through methods like RADSeq (Restriction-Associated DNA sequencing). However, for paleontological, archeological or museum collection specimens, this type of study is impeded by degradation, ancient DNA being notably too fragmented to successfully apply restriction digest. In contrast, paleogenomics main focus are either the sequencing of complete nuclear genomes, which is cost intensive and can only be applied to a small proportion of well-preserved specimens, or the target capture of smaller genomes (prokaryotes or mitogenomes) on hundreds of individuals. To get the best of both worlds, protocols combining RADSeq data on modern material and target capture enrichment on ancient specimens have been proposed to retrieve nuclear information and thus genotype more easily large sample groups at a lower cost. They can target the totality (HyRAD) or a subsampling (Rapture, RADCap) of a RAD marker catalog, the later requiring an additional step of capture probe selection through bioinformatics. We optimized two protocols to genotype woolly mammoths (*Mammuthus primigenius*) from the Pleistocene. This communication will present their comparison, from the ease of implementation to the efficiency of nuclear enrichment.

### **O15 Using proteomics to uncover ancient human-animal interactions**

Shevan Wilkin

Ancient protein analysis through tandem mass spectrometry (LC-MS/MS) is a developing method used to explore archeological and paleontological materials. It can be especially revealing when exploring questions of diet and economy in the regions that suffer from a dearth of excavated faunal remains and occupation sites. Proteins extracted from materials such as dental calculus (calcified dental plaque) or ceramics (residues and the matrix) are identified by differences in the amino acid sequences, and can confirm the consumption (calculus) or processing (ceramics) of species-specific animal tissues. This paper will detail a recent application of this method to dental calculus in ancient and imperial Mongolia, along with the possibilities and limitations of this method.

## **O16 Domesticated animal products on ancient shipwrecks, searching for DNA**

Lisa Briggs

Ancient shipwrecks can offer unique insights into long-distance trade, agricultural developments, and social transformations in the past. Amphorae, the transport containers par excellence of the ancient world, are generally assumed to have carried wine, olive oil, or fish sauce, but in several instances macro-remains of domesticated animals have been found inside of ancient shipwreck amphorae, included butchered beef remains (Carlson 2003, and butchered pork remains (Bruni 2000). This research has used Next Generation Sequencing and metagenomics to characterise what DNA can be recovered from shipwreck artefacts, seaoor sediment and the water column that surrounds these sunken ships. Several species of domesticated animals have been detected including *Sus scrofa*, *Ovis species*, *Canis familiaris*, and *Felis catus*. The presence of the DNA derived from these species in the deposition environment illustrates the necessity to authenticate what may or may not be genuinely ancient DNA found amongst the cargo items of ancient Mediterranean shipwrecks.

## Session 4: Pleistocene diversity

### **O17 Investigating hominin subsistence strategies at Denisova Cave (Russia) using stable isotopes and peptide mass fingerprinting**

Samantha Brown, Thomas Larsen, Patrick Roberts, Maxim Kozlikin, Michael Shunkov, Anatoly Derevianko, Thomas Higham, Katerina Douka

The hominin remains available for chronometric and biomolecular analysis in the Middle-Late Pleistocene archaeological record are currently highly limited. While Europe is increasingly well covered in this regard, with a number of palaeodietary studies on Neanderthals, for example, the lack of comparable data is starkly felt in eastern Eurasia. This is despite the fact that Neanderthals, Denisovans, and perhaps even *Homo sapiens*, have been contemporaneous in the same landscapes for several millennia. Here, we report on a combined proteomic and stable isotopic approach to the study of bone fragments in the East Gallery of Denisova Cave. Large-scale application of peptide mass fingerprinting (ZooMS) has led to the discovery of several new hominin bone fragments, illuminating in parallel the diversity of local fauna including taxonomic groups which are not represented in the morphological remains. This in turn has enabled the construction of a highly detailed stable carbon and nitrogen isotope palaeoecology associated with hominin behaviour through time. Our results show that many of the mammals present at the site have similar isotopic values to taxa living in Europe. The hominin remains, however, have bulk nitrogen values as much as 3 higher than Neanderthals with the most elevated trophic positions in Europe. The discrepancy between the expected  $\delta^{15}\text{N}$  values for mammals present at Denisova Cave and the unexpectedly elevated values for the hominins highlights the need for a more regional perspective for dietary and ecological behaviours. By creating a detailed isotopic framework from bones identified using peptide mass fingerprinting we expand the current understanding of Middle and Upper Pleistocene hominin adaptations in environments across a greater portion of their geographical range than has been considered to date.

### **O18 The challenge of bone fragmentation: Combining ZooMS and Zooarchaeology to assess hominin subsistence behaviour at Fumane (Italy)**

Virginie Sinet-Mathiot, Geoff M. Smith, Matteo Romandini, Arndt Wilcke, Marco Peresani, Jean-Jacques Hublin, Frido Welker

Bone fragmentation in Pleistocene faunal assemblages can be due to taphonomic or to anthropological processes, preventing any taxonomic identification using traditional morphological attributes (Morin et al. 2017). This constitutes a potential bias in the analysis of hominin behaviour as it excludes a vast quantity of archaeologically valuable data. Up to now, Zooarchaeology by Mass Spectrometry (ZooMS) (Buckley et al. 2009) has focused solely on ecological questions, but its potential to investigate hominin subsistence behavior and faunal carcass processing using the morphologically unidentifiable bone fragments has been, thus far, unexplored. In this study, we provide a novel integration of complementary data sets from both ZooMS and morphologically identified assemblages from the final Mousterian (layer A4) and Uluzzian (layer A3) contexts (Tagliacozzo et al. 2013, Peresani et al. 2016) at the key Late Pleistocene site of Fumane (Italy), in order to study the relationship between faunal composition and bone fragmentation. We have identified a significantly large frequency difference marked by a six fold-increase in the quantity of Bos/Bison remains in the molecularly identified component within the same archaeological unit. Direct comparison of bone surface modifications between both assemblages allowed us to exclude taphonomic and diagenetic drivers (Fisher 1995). High frequencies of percussion marks suggest Bos/Bison remains were intentionally fragmented by human activity, more so than other taxa, to extract marrow from long bones or as a potential fuel source. Our study deals for the first time with the challenging issue of high bone fragmentation through combining approaches at a macroscopic and molecular level, and provides a more informed picture about carcass processing at Fumane that could not be detected through conventional zooarchaeology alone. Such a compilation of data sets has the potential for a more widespread application in the future to other highly fragmented Pleistocene bone assemblages.

### **O19 Paleogenomics and Paleontology reveal two different aspects of the evolution of bison**

Thierry Grange, Jean-Philippe Brugal, Antigone Uzunidis, Eva-Maria Geigl

The Pleistocene was characterized by marked climatic and environmental changes that profoundly impacted on the population dynamics of animals and plants leading to their expansions, retractions and extinctions. These processes have been described based on paleontological and, more recently, on paleogenomic data. While the former ones may be distorted due to gaps in the fossil record, taphonomic loss and degradation, sexual dimorphism, small sample size, insufficient representation of anatomical elements and lack of morphological characteristics of certain skeletal parts (taxinomic bias), the latter ones may be biased by DNA degradation, gaps in the paleontological record, small sample size and insufficient number of genetic markers analyzed. The study of the dynamics of past populations should therefore be carried out by combining approaches to compensate for these mutual deficiencies. We coupled both approaches for our study of the population dynamics of the *bison* in Eurasia during the Late Pleistocene. Through paleogenomics, we retraced the maternal lineages of bison in Europe and Asia over the last 50,000 years and compared the obtained lineages and dates to paleontological data (BMC Biology, 2016,14:93-110). Surprisingly, while paleogenomics of mitogenomes and their Bayesian analysis revealed the existence prior to the MIS2 of a so far unknown lineage of the European bison, its replacement in France by the steppe bison during MIS2, and the replacement of the latter one by the European bison right after the Younger Dryas, paleontological (morphometry) data based on the analysis of metapodials of female individuals did not suggest a population replacement at the transition MIS3 - MIS2. We hypothesize that this discrepancy is the consequence of different behaviors of the two sexes: while females are philopatric and responsible for the population structure, males are migratory, ensuring the reshuffling of the gene pool of the populations (Diversity, 2018, 10: 65).

## **O20 Characterization of aurochs population dynamics and domestication through their maternal lineages**

Wejden Ben Dhafer, Silvia Guimaraes, Diyendo Massilani, Thierry Grange, Eva-Maria Geigl

Paleogenetic and paleogenomic analyses enable us to retrace domestication processes and spread of domesticates. The interpretation of the genetic data obtained in the course of these studies require knowledge of the ancestral wild populations of the corresponding domesticates. In particular, it is essential to acquire a sound understanding of the phylogeographic structure and its dynamics. Paleontological and archeozoological studies have shown that the aurochs, the wild ancestor of cattle, was present during the Upper Pleistocene and the first half of the Holocene in Europe, Asia and Africa, yet were not successful to discover a sound population structure. Nevertheless, the profound climatic and environmental fluctuations taking place during the Pleistocene must have had a deep influence on the dynamics of the various aurochs populations that became the substrate of domestication at the onset of the Holocene, their population expansions, retractions and extinctions. We analyzed aurochs remains from Europe and southwest Asia using a paleogenomic capture approach to produce whole mitogenomes. Their Bayesian analysis allowed us to date the divergence of the various maternal lineages that characterized the aurochs populations during the Upper Pleistocene and the Holocene. We also showed that the population structure at the end of the Pleistocene, which was revealed through our study, later got blurred through the domestication and spread of the domesticated cattle and the gradual disappearance of the wild populations until their extinction.

## Session 5: Domestication

### **O21 Ancient cattle genomics and rapid turnover in the Fertile Crescent**

Daniel Bradley

The genetic origins of domestic cattle have been explored for over two decades by extrapolating patterns from modern genomes. This has had some success, for example in identifying highly divergent eastern and western populations that are consistent with separate wild genomic origins. However, patterns which are observable today result from multiply overlaid processes of migration, admixture, population fluctuations and selection which it can prove impossible to parse, especially within restricted geographical regions such as the Near East. Recent years of investigation of ancient human genetic diversity in Europe has taught us that the genetic past can only be reliably modelled through directly accessing ancient genome variation. Despite the challenge of working with DNA-depleted bones typical of warmer climates, we have built a collection of Near Eastern genome data in cattle by directed sampling of petrous bones and high throughput sequencing. This talk will focus on emerging ancient data and how this adds inference about the nature and geography of recruitment from the wild. Also the imprint of a rapid introgression episode can be observed and interpreted. Invaluable contributions from collaborating investigators will be acknowledged fully within the talk.

### **O22 Ancient genomic insights into the goat herds of the earliest phases of domestication**

Kevin Daly

As one of the first animals domesticated, the domestic goat (*Capra hircus*) has partook in a mutualistic relationship with humans spanning the last 10,000 years. Previous zooarchaeological and ancient DNA analyses have shed light on the dynamics of this long history, but comparatively little is known about the goat populations involved in the initial stages of domestication. We present mitochondrial and nuclear genome data from early Neolithic archaeological sites, including those in the Zagros Mountains of Iran with some of the earliest evidence of goat management. We investigate how these relate to later and modern goat groups, the population dynamics during the initial spread of goat herding, and the role played by gene flow from distinct wild populations in shaping modern goat genetic diversity.

### **O23 Palaeogenomics of Ancient Dogs**

Greger Larson

Despite numerous investigations leveraging both genetic and archaeological evidence, the geographic origins of dogs remain unknown. On the basis of an ancient Irish dog genome and an assessment of the spatiotemporal appearance of dogs in the archaeological record, a recent paper suggested that dogs may have been domesticated independently in Eastern and Western Eurasia from distinct wolf populations. Following those independent origins, a mitochondrial assessment suggested that the Mesolithic dog population in Western Europe may have been replaced by a population from the East. To test this hypothesis, we are generating nuclear genomes of ancient dogs sampled from sites in Europe and Western and Eastern Russia, and mitochondrial genomes from ~400 dogs spanning the last 15,000 years across Eurasia. The results of this analysis will reveal the phylogenetic affinities of dogs that were present across the Old World prior to the introduction of dogs associated with farming communities. This study will also allow us to pinpoint the timing of the European mitochondrial turnover and to assess whether there was a commensurate turnover at the nuclear level, thus directly addressing whether dogs were domesticated from more than one population.

### **O24 News from Mesolithic Iberian Dogs**

Ana Elisabete Pires, Cleia Detry, Lounes Chikhi, Rita Rasteiro, Ludmilla Blaschikoff, Octavio Serra, Silvia Guimarães, Isabel R Amorim, Fernanda Simoes, José Matos, Francisco Petrucci-Fonseca, Morgane Ollivier, Catherine Hänni, Joao Luis Cardoso, Pablo Arias, Mariana Diniz, Ana Cristina Araujo, Nuno Bicho, Ana Catarina Sousa, Marta Moreno-García, Ana Margarida Arruda, Carlos Fernández-Rodríguez, Eduardo Porfírio, José Morais Arnaud, Alexandra Valente, David Miguel Gonçalves, Lara Alves, Anders Götherström, Simon J.m. Davis, Catarina Ginja

Dog genomes from Mesolithic Europe, particularly from peripheral regions such as Iberia, are still little known and their specific ancestry is a mystery. We shed some light into this subject by performing a zooarchaeogenetic

study of six *Canis* remains from Mesolithic Iberia, dated between 7,903-7,570 years (cal BP), including two almost complete skeletons. These remains were statistically identified as dogs using Bayesian analyses to integrate data from different sources – archaeological context, direct dating, osteometry and isotopic composition. We analysed a 181 base pair long mitochondrial DNA (mtDNA) fragment (Dloop) and found an unusual high frequency (83%) of dog Haplogroup (Hg) A in our Mesolithic Iberian dogs. This is the first evidence for a high frequency of dog HgA in pre-Neolithic Europe. We show that, contrary to the current view, HgA did not necessarily arrive in Europe from East-Asia. This phylogeographical difference regarding HgA frequency suggests that prior to domestication there was already genetic structure within the Eurasian population of wolves, or that Mesolithic Iberian dogs have diverged from their European counterparts soon after becoming domesticated. Thus, a pre-Neolithic local domestication process involving the Iberian wolf needs to be considered in the origin of the Iberian dogs. New chronogeographic genomic data from *Canis* addressing the question of Iberian dogs' ancestry will be presented.

## **025 Morpho-functional study of extant canids with application to the European Neolithic**

Colline Brassard, Rose-Marie Arbogast, Adrian Balasescu, Jacques Barrat, Céline Bemilli, Adina Boroneant, Cécile Callou, Fabien Convertini, Raphaël Cornette, Trish Fleming, Muriel Gandelin, Claude Guintard, Elodie Monchatre-Leroy, Anne Tresset, Stéphanie Bréhard, Anthony Herrel

The large number of dog remains in European archaeological sites is an indication of their omnipresence in the daily lives of Neolithic humans, whether as a food source or in symbolic systems. However, the temporal and spatial evolution of their morphological variability – in relation to social and techno-economic changes – remains poorly documented. Yet, the high phenotypic plasticity in dogs may have allowed rapid adaptations to novel selective pressures. Since archaeological mandibles are generally well preserved and have a key role in the animal's chewing ability, they are promising to explore morphological variability and its functional consequences. In order to explore the impact of external constraints such as diet or increased proximity to humans, we developed a biomechanical model for extant domestic dogs, and commensal dingoes and red foxes. Photogrammetry was used to obtain 3D reconstructions of mandibles which are analysed using geometric morphometrics. Extant specimens were dissected to establish a biomechanical model allowing us to estimate bite force of archaeological remains based on the mandible only. The model will ultimately be applied to dogs and foxes who populated Western Europe between the Tardiglacial and the Bronze Age. This should enable to better understand the evolution of dogs under increasing anthropic constraints at the beginning of the Holocene.

## **026 Paleogenetics of horse domestication in Anatolia and the Caucasus**

Eva-Maria Geigl, Silvia Guimaraes, Ben Arbuckle, Sarah Adcock, Hylke Buitenhuis, Hannah Chazin, Joris Peters, Ninna Manaseryan, Hans-Peter Uerpmann, Thierry Grange

Archeozoological and chemical studies have pointed to the eneolithic Botai culture in Central Asia (present-day Kazakhstan) that delivered the earliest evidence for the domestication of the horse during the 5th to 4th millennium BCE. Other hypotheses considered that horses have been domesticated in the Iberian Peninsula, Anatolia and the Pontic-Caspian steppe. Recent paleogenomic studies of horses have convincingly demonstrated that the horses from the Botai culture, as well as the Iberian Peninsula were not the ancestors of present-day domestic horses, a finding that invalidated these areas as centers of horse domestication. We performed a paleogenetic analysis of horses from Anatolia, a region with a long history of horse exploitation and therefore candidate region where horses could have been domesticated. We analyzed mitochondrial and Y-chromosomal DNA as well as autosomal markers associated with the coat color in Holocene horse remains from Anatolia and the Caucasus. This allowed us to follow the dynamics of these genetic markers from the early Chalcolithic to the Iron Age, i.e., before during and after the domestication period. The obtained results enable us to invalidate the hypothesis of Anatolia as an area of autochthonous horse domestication and to show that domestic horses have been imported into the Anatolian plateau during the Late Bronze Age.

## **027 Burrowing into the bio-cultural history of Rabbits**

Sean Paul Doherty, Soa Granja

Rabbits (*Oryctolagus cuniculus*) are one of the most recently domesticated animals. Native to the Iberian peninsular and southwest France, they have been transported by humans to all corners of the globe to live in diverse relationships with people: as pets, pests, sources of food and laboratory animals. The AHRC-funded



project 'Exploring the Easter E.g.' (<http://easterorigins.org/>) is integrating historical and linguistic techniques with traditional zooarchaeological and biomolecular methods (including full-suite osteometric, geometric morphometric, isotope and genetic analysis) to examine the dynamics of varying human-rabbit relationships. In this paper we present our early results of the integration of zooarchaeological, genetic and geometric morphometric data into determining the timing of domestication, as well as exploring their extinction and re-introduction in post-Roman Britain. Here we demonstrate how the combination of these approaches helps us to understand rabbit domestication and husbandry, and unpick this animals complex bio-cultural history.

## **O28 Identifying the early stages of reindeer domestication by the Sámi in northern Fennoscandia: an exploratory geometric morphometrics approach of forelimb bones**

Maxime Pelletier, Sirpa Niinimäki, Antti Kotiaho, Anna-Kaisa Salmi

In Northern Fennoscandia, reindeer domestication may have begun during the Late Iron Age by the indigenous Sami people. Reindeer are considered to still be in the early phases of the domestication process. The traditional morphological markers that are used in zooarchaeology to decipher the domestication syndrome are hardly perceptible in these early stages. Hence, reindeer (*Rangifer tarandus*) provide a valuable opportunity to address this issue. In this work, we focused on the long bones of the forelimb, important to understand the feeding behaviour: during winter wild reindeers dig for lichen from under the snow while domestic individuals may have been provided with supplementary food by herders. These bones might also be affected by load carrying or draught in the case of domestic reindeer. We analysed 116 modern specimens, including both subspecies currently present in Fennoscandia: mountain reindeer (*R. t. tarandus*, including both wild and semi-domesticated reindeer), and wild Finnish forest reindeer (*R. t. fennicus*). We considered both sexes and different lifestyles (i.e., free-ranging, racing, and captive individuals). In order to detect a domestication signal, we used 3D geometric morphometrics to compare the size and shape variables of the long bones from CT scans. We found a good discrimination between the subspecies and both sexes. We found that the individuals that were bred in captivity had smaller bone elements in general and a distinct morphology from free-ranging individuals. This demonstrates that the long bones of the forelimb can provide information on changes in locomotor behaviour prompted by the domestication process, like reducing and/or controlling the mobility of individual reindeer by humans. This also demonstrates that analysis in 3D geometric morphometrics is useful in detecting incipient domestication markers. Our results can be used to trace domestication from fossil reindeer remains, and aid in reconstructing the socio-economic changes of Sami populations over time.

## **O29 Tracing reindeer domestication in Fennoscandia: an osteometric study of castrated and full male reindeer bones**

Mathilde Van Den Berg, Henri Wallen, Anna-Kaisa Salmi

Knowledge of the processes surrounding reindeer (*Rangifer tarandus*) domestication can give insight in the history of many past and contemporary circumpolar cultures. However, the time and origin of reindeer domestication remains hotly debated today. Determining the domestication status of reindeer in archaeological bone assemblages is problematic because wild and semi-domesticated reindeer are morphologically very similar. Many argue that castrated males were probably the key to reindeer domestication. Although the importance of castrates and their part in incipient reindeer domestication is widely recognized, no methods exist that can discern a reindeer gelding from a reindeer bull. Focusing on the use of castrated reindeer and defining the osteological manifestations of reindeer castration is a new approach to document human intervention in the population structure of this species. The premise of this method is that longitudinal growth of bones is linked to epiphyseal fusion. For several studied species (e.g. sheep, goat), castrates show a clear pattern of delayed epiphyseal fusion relative to both males and females, which allows the elongation of the bones, and long-bones in particular. This study focuses on reindeer domestication in Fennoscandia in particular, but the results can gain insight into the reindeer domestication process of other areas also. For this study three ecotypes of reindeer that were extant in Fennoscandia until the 19th century were analyzed. These are wild mountain reindeer (*R.t. tarandus*), wild forest reindeer (*R.t. fennicus*), and semi-domestic reindeer (*R.t. tarandus*). Skeletons of known age, sex, castration status, and subspecies were measured and the measurements were analyzed to plot the osteometric differences between castrates and full males. In this presentation the preliminary results of this study are presented. The outcomes of this research aid in evaluating a novel method of tracing (incipient) domestication also for other species.



## Session 6: Husbandry

### **030 The development and diversity of sheep populations in Estonia**

Eve Rannamäe, Matthew Teasdale, Urmas Saarma, Anneli Ärmpalu-Idvand, Camilla Speller

In Estonia today, sheep husbandry is rather small scale, but still a considerable input to the local animal production. Moreover, Kihnu native sheep are an important addition to the list of native breeds, both on a national level, but also for the Baltic region and Northeastern Europe in general. The history of sheep husbandry in Estonia can be seen for at least three thousand years, and in the past – as seen from the zooarchaeological material – sheep were one of the main livestock resources together with cattle, pigs and goats. Our interest has been the development of local sheep populations from the Late Bronze Age onwards, starting from ca 800 BCE, including patterns of consumption, ancestry, changes in genetic diversity, effects of large-scale breeding, and affinity between the ancient and modern populations. To this aim, we have studied the utilisation of sheep as shown in the faunal remains; with genetic methods we have investigated the position of both ancient individuals and modern Kihnu native sheep among other European breeds; and we have described the importance and value of the native breeds both on local and global scale. The research results so far affirm the continuity in the Estonian sheep lineages from the Late Bronze Age to present-day, and corroborate the opinion that the Kihnu native sheep is one of the preserved northern European native breeds. Additionally, we demonstrate how study on ancient material contributes to the study on extant native populations.

### **031 Parchment and animal husbandry strategies in Medieval Scandinavia**

Lena Strid

Parchment production was extremely important for medieval society; the backbone upon which the bureaucracy of the state, the records of the merchants and the estates, and the religious life of priests, monks/nuns and the laity rested. Despite this, parchment production is an understudied area, possibly related to scarcity of both archaeological finds and historical records indicating parchment workshops. The aim of this project is to explore the use of parchment in Medieval Scandinavia through biochemistry, zooarchaeology and artefact studies. Important topics include how the choice of species for parchment relates to economic decisions regarding animal husbandry strategies, both between regions and over time. The interplay between volume of parchment production, diachronic increase in literacy and the introduction of paper in the late Middle Ages will also be examined. This preliminary report will discuss the results from eZooMS sampling of early 13th-early 16th century charters written in monasteries and towns from western Sweden and eastern Denmark/ southern Sweden, and compare them with animal bone data from these regions as well as to historical sources on trade in animals and animal products from Scandinavia to continental Europe. My study will form an important addition to previous eZooMS studies on parchment from Britain and continental Europe, that have shown spatial and temporal variation in the species used for parchment. For example, sheep and goat are most common in Italy, calf in France, and calf and sheep in England.

### **032 Whole genome sequencing of Viking Sheep from the North Atlantic**

Albína Hulda Pálsdóttir, Heidi Maria Nistelberger, Juha Kantanen, Jón Hallsteinn Hallsson, Sanne Boessenkool

The sails of Viking ships were made of sheep wool and without wool the settlement of the islands of the North Atlantic, the Faroes, Iceland and Greenland, by the Norse would not have been possible. By providing wool, milk and meat sheep were vital to subsistence in the North Atlantic and their bones are frequent finds in archaeological excavations. Despite the importance and ubiquity of sheep in the region where they came from and how people have shaped their genetics is poorly understood. We have sampled over 80 sheep bones from Viking Age to medieval excavations in Iceland, Greenland, the Faroe Islands, Norway and the UK and now have whole genome sequences of 27 ancient sheep. We have also sequenced modern Icelandic, Faroese and Norwegian sheep breeds. By comparing our ancient and modern genome data to published sheep genomes we are studying where the sheep came from and how the local breeds have evolved over the past 1000 years.

### **033 The impact of breeding practices in the genomic composition of Iberian cattle: inferences from Medieval-Moslem vs. Post-Medieval Christian specimens**

Catarina Ginja, Irene Ureña, Sylvia Valenzuela, Sílvia Guimarães, Luciana Simões, Simon Davis, Cleia Detry, Ana Arruda, Catarina Viegas, Andreia Martins, João Pimenta, Ana Caessa, Nuno Mota, Anders Götherström, Ana Elisabete Pires

Iberian cattle exhibit considerable genomic diversity when compared to their European counterparts. Primitive local breeds display significant influences from African taurine cattle, and include mitochondrial and Y-chromosome lineages from multiple origins. A complex demographic history, resulting from a combination of trading traditions and breeding practices in the Mediterranean region, shaped their genomic composition. However, it is not understood if such variability could also derive from recruitment of Iberian aurochs. Osteometric and molecular sex determinations indicated a considerable size increase of cattle in Portugal following the Christian *reconquista* (11th-13th centuries AD). The histograms of the distal widths of cattle metacarpals from Moslem Alcáçova de Santarém (9th-12th century AD) and 15th century Beja (Alentejo) revealed a bimodal distribution of small (female) and large (male) measurements and that there was an improvement, i.e., a size increase, of Post-Medieval cattle. We used an archaeogenetics approach to investigate the impact of breeding practices in the genomic composition of Iberian cattle, i.e. a selection for larger beeves for meat and/or of more robust cattle for power, by contrasting Medieval-Moslem, Post-Medieval Christian and Modern contexts. We sub-sampled well-documented cattle metacarpals collected at key archaeological sites in Portugal, specifically: 8 from Alcáçova de Santarém, 9 from Beja, 3 from the Museu do Neorealismo (Lisbon, 13th-16th century AD) and 6 from Carnide (Lisbon, 17th century AD). We then generated whole-genome resequencing data for these specimens on the Illumina HiSeqX platform. Endogenous DNA content ranged between 1% and 8%, and mitochondrial genome coverages were between 2x and 74x. We shall discuss these data which indicate specific biological properties, including the sex, coat colour and body size of these animals. We shall interpret these data under a population genomics perspective to model genomic variation over time, investigate genetic relationships and test for genetic continuity since the Moslem period.

### **O34 Sus 100: Geometric morphometric and genetic variation in *Sus scrofa* associated with intensive human selection pressures**

Ashleigh Haruda, Emrah Coraman, Henry Reyer, Frieder Mayer, Renate Schafberg

*Sus 100* is an interdisciplinary project that synthesizes the methods of biology, livestock science, and archaeological science within a social framework to evaluate the biological effects of human driven selection pressures upon the modern domesticated pig. Modern and historical specimens dating from the turn of the last century from two key pig breeds, the Deutsches Edelschwein and the Deutsche Landrasse, are compared with wild European boar in order to measure the responsiveness of the osteological frame and genetic code to productive characteristics that are typical of intensive industrial agricultural systems. Variation in skeletal morphology is measured and analysed using three-dimensional geometric morphometric methods while DNA is measured using a modern, cost-effective SNP chip technique to explore these changes and to set a 'rate of change' of response to selective breeding within this 20th century context. This project acts as a modern case study not only to model the responsiveness of *Sus scrofa* to evolutionary pressure but also to evaluate osteological response to intense culturally-driven human selection upon past animal populations.

### **O35 Genetic diversity of Slavic horses**

Danijela Popović, Mateusz Baca, Daniel Makowiecki, Martina Wiejacka, Wojciech Chudziak

During the Early Middle Ages and the formation of the Polish state horses played a significant role in social, economic and military life. They were owned by the higher social group, mainly ruling elites and their military formation. On the other side, there are historical records of symbolic role of horse in the ritual ceremonies of the Slavic's tribes living in the Vistula and Odra basins in that time. Particularly intriguing are information about different coat color preference in some Slavic tribes, special meanings had a black or white color. The rich archaeological and archeozoological evidence of subfossil horse remains emphasize the importance of this species in the Medieval societies. Biometric data showed great diversity of horse subfossil remains excavated on the territory of the present-day Poland. Especially interesting is distribution of height at the withers. In the case of cattle, sheep and pig, the examined feature and other biometric data from all regions indicate identical distributions for each species. This was not true for horses. We found that populations from different regions differs significantly in their height. This morphometric diversity may reflect different populations or even lineages which are not possible to be detect using macroscopic and biometric methods applied in archaeozoology. To better characterize the Medieval horse populations, from the territory of present-day Poland we performed target enrichment and high throughput sequencing of 5,000 genomic SNPs which covered polymorphisms associated with coat color, genetic disorders and functional traits. The research is part of the project "Horse in Poland in the Early Piasts and Internal Fragmentation" (2017/25/B/HS3/01248) financed by the National Science Centre, Poland.

### **O36 Ancient DNA and Osteometry of cattle from Iron Age to Medieval times in NW Switzerland**

Angela Schlumbaum, José Granado, Sabine Deschler-Erb, Barbara Stopp, Elisabeth Marti-Grädel, Jörg Schibler

Phenotypic changes in domestic animals, often indicate changes in the nature of animal husbandry, such as the introduction of new individuals into a population. A classic example of this is the widespread increase in the size of cattle at the transition from the Iron Age to the Roman period, and the subsequent decrease from the Roman to Medieval period. This pattern can be seen at Swiss sites, as well as across many other European areas. We monitored ancient mitochondrial d-loop diversity in cattle from Swiss assemblages from the Iron Age (Basel Gasfabrik, Basel Martinsgasse), Roman (Augst/Kaiseraugst: Theater Nord-Weststecke, Hotel Adler, Kastelen, Insula 23) and Medieval (Reinach Brunngasse, Lausen) periods. Cattle belong to the taurine macro-haplogroup T3, two Roman cattle individuals belong to haplogroup T2 and one Medieval cattle to haplogroup T1, the later has a mainly African distribution today. We find that genetic diversity correlates roughly with size fluctuations. We will discuss the evidence within its archaeological/archaeozoological context.

## **ABSTRACTS**

### **Posters**

***8th ICAZ AGPM Working Group meeting***

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*October 17-18 2019, MNHN, Paris, France*

## **P1 Colonial Cattle on the Frontier: mtDNA Analysis of the Grange Plantation Cows (18th c., Georgia)**

Nicolas Delsol, Elizabeth Reitz, Rob Guralnick, and Kitty Emery

Soon after their introduction to the Americas, cattle became prominent in the economies and cultures in many regions. The breed today known as Criollo is descended from these early Spanish cattle. Recent genetic studies on existing populations of Criollo cattle highlight the diverse genetic makeup of the modern breed and reveal a complex history of successive introductions. A study by Speller and colleagues (2013) in Jamaica confirm the complexity of cattle introductions and suggest that the populations that would constitute the foundations of the Criollo cattle came mainly from Southwestern Europe. Few other studies of ancient genetic material from early American cattle are available to shed light on the migrations and interbreeding processes at work during the first centuries of European colonization. In this study, we present our research on an assemblage of archaeological *Bos taurus* individuals from the Grange Plantation in Georgia, USA. This rural trading post and cow pen was on the southern frontier of the English Carolina colony. The zooarchaeological assemblage contains a high percentage of cattle specimens. We identify the taurine haplogroups using analysis of mtDNA to address three objectives: 1. This study will contribute to the baseline of ancient mtDNA *Bos taurus* genetic information from the Americas. 2. Our assessment of the relative preservation of aDNA in this archaeological context will inform later studies of bovine paleogenomics in the region. 3. Our mtDNA results will add to our knowledge of the phylogeographic history of cattle in the Americas, particularly evaluating the potential introgression of cows originating from Spanish colonies in the Caribbean and Florida into the English stock in southern English colonies such as South Carolina.

## **P2 Domestication in Action – Tracing Archaeological Markers of Human-Reindeer Interaction**

Anna-Kaisa Salmi, Päivi Soppela, Sirpa Niinimäki, Maxime Pelletier, Oula Seitsonen, Markus Fjellström, Matti Heino, Sanna Kynkäänniemi, Henri Wallen, Mathilde Van Den Berg

Reindeer domestication process began in Northern Fennoscandia probably ca. 800-900 AD. Reindeer pastoralism was a major source of livelihood and an important cultural focus for many Sámi groups in the 15th century and it still remains an important part of many northern cultures. Although there is a general agreement on the rough timeline of reindeer domestication, the details and local variation are still poorly understood. This is partly due to the elusive nature of reindeer domestication: in traditional reindeer pastoralism, human intervention into the lives of the reindeer was minimal, complicating the interpretation of traditional domestication markers such as morphological changes associated with domestication syndrome. To address this problem, *Domestication in Action* project was launched at the University of Oulu in 2017. Instead of traditional domestication markers based on the idea of human control over the domesticates, we focus on tracing human-reindeer interactions, such as draught reindeer use, reindeer feeding, reindeer castration, and other daily tasks of the reindeer herders, through the archaeological record. We employ a multidisciplinary methodological package, including physical activity reconstruction, geometric morphometrics, stable isotope analysis, GIS analysis and ancient DNA analysis. We also engage in participatory research with reindeer herders to better understand the effects of working reindeer training and other human-reindeer interactions on human-reindeer relationships in the past and present.

## **P3 Emorph Project: Reconstructing habitat type and mobility patterns of Rangifer tarandus during the Late Pleistocene in Southwestern France: an ecomorphological study**

Ana Belén Galán López, Ariane Burke, Sandrine Costamagno

Reindeer (*Rangifer tarandus*) was one of the most important prey species for human populations in Western and Central Europe during much of the Palaeolithic period, notably during the Glacial periods (Costamagno et al. 2015). As a result, many studies have focused on the role of reindeer in Upper Palaeolithic systems, particularly during the Magdalenian (17,000-12,000 years ago). Modern ethological data indicate that reindeer herds adopt different mobility strategies that correlate with habitat type and topography. The mobility patterns of prehistoric reindeer, therefore, should be predictable since palaeoenvironmental reconstructions allow us to identify whether or not they lived in more open or more wooded environments. Despite numerous attempts to reconstruct the migratory behaviour of Palaeolithic reindeer, however, there is no clear model explaining their movement. An animal's habitat and pattern of mobility hypothetically affect bone density and limb bone morphology, as has been demonstrated in several large vertebrate species (DeGusta and Vrba, 2003; Bignon et

al. 2005; Van Asperen, 2010). This project will identify the impact of habitat type and mobility on bone density and morphology of reindeer living in different habitats using Computer Tomography (CT) and geometric morphometric techniques (GMM). Once the relationship between habitat, mobility and bone structure has been quantified, the information collected will be applied to faunal assemblages from Upper Palaeolithic archaeological sites in Southwestern France and used to reconstruct patterns of prey mobility. Thus, this project proposes an actualistic approach that will allow us to reconstruct migratory patterns of Palaeolithic reindeer and how they affected human hunting strategies and socioeconomic decisions, which will enable us to better understand their behaviour and identify the precise role of reindeer in their economy.

#### **P4 Ancient Sus DNA at the Neolithic site of Cova de Els Trocs, Spain**

Natividad Lupiáñez-Corpas, Jorge H. Calvo, Marta Moreno-García, Pilar Sarto, Magdalena Serrano, Almudena Fernández, Carmen González, Laura P. Iguacel, Cristina Tejedor-Rodríguez, José I. Royo-Guillén, Héctor Arcusa-Magallón, Iñigo García-Martínez De Lagrán, Rafael Garrido-Pena, Manuel Rojo-Guerra

Cova de Els Trocs, situated at above 1500 m.a.s.l., on the Iberian southern slopes of the central Pyrenees, is currently one of the few sites with a fully documented Neolithic stratigraphic sequence spanning from the 6th to the last third of the 4th millennium cal BC. Archaeological campaigns carried out since 2011 have recovered more than 22500 large-sized mammal remains. The abundant number of caprine (particularly sheep) remains clearly shows the high involvement in herding activities by the human groups that spent spring and summer in this territory, while hunting of wild taxa seems marginal and constrained to few species among which wild boar stands out. Here we present preliminary results of DNA variation in mitochondrial, *SRY* and *AMEL* partial sequences on the teeth of five suid specimens related to the three occupation layers of the cave. In this study, we successfully adapted ancient DNA extraction, PCR and SANGER sequencing approaches for the analysis of mitochondrial DNA sequence variation. In addition, fragments of the *SRY* gene and *AMELX* and *AMELY* loci were also amplified to determine the sex of the individuals. Four out of the five samples analysed allowed to determine the partial D-loop sequence of 878 bp, and sex sequences; whereas one only allowed to amplify a fragment of 629 bp for mitochondrial DNA. Four mitochondrial haplotypes were found, showing three of them the higher identity results with other described Iberian haplotypes found in Iberian pig and wild boar. Phylogenetic analyses showed four samples (three haplotypes) located in the European clade. However, one sample (radiocarbon dated between 5208 – 4961 cal BC) grouped within the Near Eastern clade. Such result might indicate domesticated pigs of Near Eastern ancestry could have been introduced in the Iberian Peninsula before the 5th millennium B.C.

#### **P5 Paleogenomics of the evolution of the house cat**

Jeanne Mattei, Thierry Grange, Eva-Maria Geigl

Little is known about the domestication of the cat, and it is even unclear to what degree it is domesticated. Archeological evidence is scarce as cats never were a subsistence species although they were eaten and their fur was appreciated. Their utility for humans, however, became obvious during the Neolithic when the early farmers started to accumulate cereals which attracted rodents that devastated the harvests. Wild cats started to feast on them thus entering the human niche and initiating a commensal relationship with humans that lasts until now. This can be deduced from the archeological record showing that cats were translocated to remote places where no cats had been prior to the arrival of humans, as first seen in Cyprus. In this particular situation, the archeozoological analysis alone could yield such a result. In other contexts, however, it is difficult to conclude on the location and processes of cat domestication and the spread of the tamed or domestic cat based on archeozoological data alone as the differences between the wild and the tamed and later domestic cat are subtle. Based on the paleogenetic analysis of around 250 cat specimens all around the Mediterranean, we retraced the spread of the cat in the Old World starting with the early Neolithic farmers migrating out of the northern Fertile Crescent, to the inhabitants of the Eastern Mediterranean during Classical Antiquity, the Vikings during the Middle Ages as well as traders of the later centuries. The present study extends the scope of the former one in that more archeological remains have been analyzed. Moreover, in addition to the mitogenomes, we also analyzed nuclear markers, such as the coat color, an analysis that had been restricted in the former study to a specific coat pattern, the mackerel tabby or blotched.

#### **P6 The Mexican Wild Turkey. Modelling the phylogeography of an elusive subspecies**

Eduardo Corona M., Jose Alberto Cruz, Aurélie Manin, Camilla Speller



The domestication of animals in the Americas is the subject of renewed analyses showing a close relationship between human societies and a great diversity of animals, where many management strategies are applied. In America, lives the endemic phasianid of the genus *Meleagris*, with two species: the wild or northern turkey (*M. gallopavo*), culturally the most well known species with a natural distribution from North America to Central Mexico; and the ocellated turkey (*M. ocellata*), restricted to the Yucatan Peninsula. However, the cultural movements of both species began with the first sedentary societies, obscuring the natural distributions of both species in central and southern Mexico. The population of wild turkey is classically divided in six subspecies: Rio Grande (*M. g. intermedia*); Merriami (*M. g. merriami*), Gould (*M. g. mexicana*), Florida (*M. g. osceola*), Eastern (*M. g. silvestris*) and South Mexican (*M. g. gallopavo*). For many authors, this last one is at the origin of the domestic lineage, and its distribution is hypothesized in Central Mexico. However, no specimen was collected or has a thorough description. This work uses phylogeographic approach, where the combination of recent aDNA analysis and the biogeographic methods produces models to discuss an historical panorama for the contemporary geographic distributions of populations. The elusive situation of the Mexican wild turkey subspecies as a possible domestic lineage origin is discussed.

### **P7 Mandibular Morphology Reveals Dietary Signatures in Primates**

Kimberly Plomp, Joseph Owen, Mark Collard, Keith Dobney

Diet and feeding adaptations account for a major proportion of primate behavioural and morphological variation. Thus, the ability to accurately reconstruct the diets of fossil primates would allow us to infer a great deal of information about extinct taxa. Along with dentition, mandibular fragments are among the most commonly recovered skeletal elements in the primate fossil record. However, based on previous studies that relied on 2D morphometric analyses, the relationship between primate mandibular morphology and diet is surprisingly weak. Considering this, we initiated a study that used 3D geometric morphometric (GM) techniques to investigate mandibular shape in extant primates. Our goal was to test if dietary categories can be accurately classified based on mandibular shape regardless of phylogenetic classifications. The sample consisted of 214 mandibles from five primate families divided into 6 dietary categories. Our results found that mandibles were correctly classified to dietary category with an accuracy rate of 85%. In addition, the results of pairwise MANOVAs were all statistically significant ( $p < 0.0001$ ), except in four comparisons that involved different levels of frugivory. Thus, our findings indicate that 3D shape analyses can accurately identify dietary categories in extant primates based on mandible shape and, by extension, could enable more accurate determination of dietary behaviour in fossil primates.

### **P8 Domestication of South American Camelids: a new multi proxy approach**

Manon Le Neün, Elise Dufour, Nicolas Goepfert, Jane Wheeler, Thomas Cucchi

Llamas (*Lama glama* Linnaeus, 1758) and alpacas (*Vicugna pacos* Linnaeus, 1758) were domesticated in the pre-ceramic period from two wild species: guanacos (*Lama guanicoe* Müller, 1776) and vicuñas (*Vicugna vicugna* Molina, 1782). Both domestic species have played a major economic and symbolic role in the development of pre-Hispanic societies. However, documenting the timing and place of their domestication process has proven very challenging for zooarchaeologists. To approach the domestication process of South American Camelids (SAC), our project focus on the central Andean zone which is documented from the Telarmachay site (Peru) covering a long sequence between 9000 BP to 2000 BP. This unique site has suggested that this region was a primary focus of camelid domestication 2000 years before the rest of Andean area. Over the 7000 years long sequence of the Telarmachay, we will use a multi proxy approach combining kill off patterns, 3D geometrics morphometrics on post-cranial bones and isotopics geochemistry to explore demographic, phenotypic and life traits changes induced by the domestication process of SAC.

### **P9 A genetic research on the ancient Chinese Domestic Cats**

Yu Han, Xin Zhao, Chong Yu, Xinlin Dong, Canping Chen, Zhuang Wu, Zhipeng Li, Jing Yuan, Greger Larson

Domestic cats (*Felis catus*) were originated from *Felis lybica* in the Near East around 10,000 years ago through a commensal pathway. China today harbors a large population of cats. Due to the affinity between cats and human, the occurrence of this population in history could, in no small extent, be associated with various aspects of the development of ancient Chinese society. Given the importance of Chinese domestic cats, the discussion of its evolutionary history is merited. Regarding the origin of the Chinese domestic cats, through the Zooarchaeological research and literature records, we hypothesized that this species might firstly be imported to China in the West Han Dynasty (202BC-8AD), but this population went extinction shortly after this period. The reintroduction of domestic cats could occur in the Chinese Medieval Ages influenced by the geographic expansion of Egyptian cats.

In the meantime, given the broad geographic distribution of the interfertile subspecies of wild cats in Asia, the admixtures between the wild and domestic cats might potentially happen in history. However, currently, minimal studies have been conducted on the Chinese domestic cat, especially ancient DNA research, which is a paucity. Thus, its dating, demographic trajectory and geographic spread, remains ambiguous and controversial. This ongoing research is aiming to use the ancient DNA analysis on a series of historical cats samples ranging from Neolithic age to the iron age (800-5,500BP) unearthed in China to test the hypothesis shown above in order to permit a better interpretation of the history of the Chinese domestic cats and their interactions with ancient Chinese society.

### **P10 Late Bronze Age animal mobility and veterinary practices: A geometric morphometric study of sheep and goat remains from Hittite period Şapinuwa, Turkey**

Gonca Özger, İrfan Kandemir, Evangelia Pişkin

Animal husbandry was the basis of agrarian production in Hittite Anatolia. The faunal analysis of different Hittite sites indicate well-developed animal husbandry and a good knowledge of breeding practices which is also mentioned in Hittite cuneiform archives. At the same time animal mobility is high since animals are sent to the capital from all over the empire as taxes, booty and offers for sacrifices. In this paper we explore the animal mobility and selective breeding in Hittite Late Bronze Age period taking as the case study the materials recovered from the excavation of Şapinuwa (Ortaköy, Turkey). Şapinuwa, which was thought as the second capital of Hittite Empire in 14th century, is located in North Central Anatolian Steppe. It has been both an administrative and a ritual center. In this research two-dimensional geometric morphometric analysis of sheep (*Ovis aries*) and goat (*Capra hircus*) mandibles and astragali is employed to investigate animal mobility as well as whether a specialized veterinary activity was practiced by the Hittite Empire. Materials from different contexts were selected such as administrative buildings, palatial workshops and ritual area. The results showed different clusters of sheep and goat plus sub-cluster within these clusters probably indicating animals of different origin. Most interesting was the separate grouping of the animals that originated from ordinary people's meals remains (workshop) and the animals originated from the sacrificial area of the site. This suggests that there is a selection of animals intended for different uses and levels of consumption, a possible sign of developed veterinary practices. This work was supported by the Turkish National Agency, TÜBİTAK 117K382 project.

### **P11 Skins for Shoes – Species Identification of Archaeological Leather using Peptide Fingerprinting**

Tuuli Kasso

Organic finds are rare in Finland by standard due to the poor preservation caused by acid soil. Therefore, the recent excavations of the market place in Turku have produced a phenomenal interest and group of finds, as the clay-rich soil has preserved organic material extremely well. After presenting the background of this study at the ICOM-CC 11th Interim Meeting for Leather in Related Materials in Paris, June 2019, this paper presents the results from the zooarchaeological approach applied to the leather finds from Turku. ZooMS (Zooarchaeology by Mass Spectrometry) allows us to identify animal species from archaeological leather from micro-destructive samples. As each animal species has their own characteristic peptide fingerprint, analysing the proteins of the sample allows us to differentiate the animals used despite the poor preservation of hair follicles in archaeological leather. As conservation treatments act as a contaminant for eZooMS, the sampling has been conducted prior to conservation. Current hypothesis of Louise Ørsted Brandt (Aarhus University) of historical shoe making has found that cattle skin was chosen for the soles, goat for the upper and lamb for the strings of the shoes. This was likely not implemented as an economical reason, but as a choice based on the crafter. Complete and fragmental shoes found in Turku were sampled with a focus on this differentiation between the animal species, targeting on the dunghill that falls close to historical documentations of a shoemaker's shop in Early Modern Age Turku. The results of the analysis of the Turku shoes are compared to the hypothesis by Ørsted Brandt and evaluated critically to cast light on life in late medieval and early modern age Finland – in the shoemaker's shop.

### **P12 Preservation Pre-ZooMS Results? Collagen Peptide Preservation and Recovery from Problematic Bone**

Ruairidh Macleod, Meaghan Mackie, Alberto Taurozzi, Ryan Rabett, Matthew Collins

Zooarchaeology by Mass Spectrometry (ZooMS) is currently a prominent tool for species identification of visually unidentifiable bone fragments through species-specific collagen peptide sequences. In archaeological contexts

however, sufficient collagen preservation is often a limiting factor. This poster presents findings testing ancient collagen recovery and ZooMS through: 1) recovering and analysing ancient material from degradation-prone hot and tropical climates, and 2) attempting to match similar peptide mass fingerprints (PMFs) for modern and ancient species. Implications are also discussed for collagen preservation patterns and proteomic techniques. Ancient samples studied here include 32 samples corresponding to six contexts at Thung Binh 1 cave, Vietnam, dated at ~12ka cal BP, and a comparison of ancient and modern samples from *Testudo graeca cyrenaica* carapace at the same locality of the Gebel Akhdar region of Libya. Isotope Ratio Monitoring Mass Spectrometry (IRM-MS) and Fourier Transform Infrared Attenuated Total Internal Reflection (FTIR-ATR) spectrometry are applied as exploratory analyses to gauge collagen preservation. An adapted ZooMS protocol was then applied to produce PMFs (generated through Matrix Assisted Laser Desorption/Ionization Time of Flight Mass Spectrometry - MALDI-ToF-MS), from which collagen preservation quality indices were determined to gauge evidence for differential preservation quality between contexts. A protocol for 'gentle' slow cold-temperature demineralization of samples was found to be less effective than rapid demineralisation. Frequentist analysis (two-sample T-tests) indicated differences between contexts are not statistically significant, though other evidence of differential collagen preservation quality is also discussed, including mechanisms such as glutamine deamidation. Results further indicate counterintuitive preservation patterns, and particularly remarkable also is the recovery of PMFs from MIS5 chelonid remains from Libya recognisably comparable with modern results, including a high quality Liquid Chromatography with tandem Mass Spectrometry (LC-MS/MS) sequence for modern *T. graeca cyrenaica*. Further conclusions focus on the implications of findings for future perspectives in modelling biomolecule preservation.

### **P13 Exploring Merino sheep origins and wool production in Medieval Spain through the study of parchment**

Laura Viñas Caron, Eva Andersson Strand, Matthew J. Collins

Libraries and archives preserve millions of books and manuscripts written on parchment, which is made from animal skins, and are thus an outstanding reservoir of biological information from these animals. This research, that has recently been funded by an ERC project Beasts to Craft (ercb2c.org), hopes to use a range of imaging and biomolecular methods such as genomics and proteomics to extract information which may help reveal clues about the domestication and improvement of animals; and the development of past economies such as wool textile production. In this paper, we aim to investigate the origins of the Merino sheep, which is characterized by very fine wool and constitutes one of the most important breeds today. It originated in Spain during the Middle Ages and its development could have been facilitated by the introduction of new herds during the Islamic period, possibly from North Africa. However, its origins and genetic history remain poorly understood. Here, we present preliminary image data and discuss the potential of follicle pattern analysis for species identification and characterization of type of wool in the context of our understanding of animal management in such texts as the Vidal Mayor.

### **P14 From pannage to sty keeping: a two Dimensional Geometric Morphometrics study of tooth size and shape differences between Medieval and Post-Medieval English pig populations**

Lenny Salvagno

The transition between the Late (1400-1500 AD) and Post Medieval periods (1500-1750 AD) in England is very important for the history of pig management, as this is the period in which some of the mechanisms of breed selection and livestock improvement, which have so deeply influenced modern husbandry, have their roots. One of the main changes sees the progressive replacement of pannage with sty-keeping, which meant a greater control over the animal life cycle and also generated the opportunity to test selective breeding and pursue breed improvements. Zooarchaeological records for the end of the Middle Ages provide some indication of the impact of such change on the size and shape of pigs. An increase in size has been detected in both postcranial bones and teeth, even though bones were far more affected. A further, greater, increase in pig size has been recorded in the Post-Medieval levels and, interestingly, the Late and Post Medieval pig bones increased in size relatively more than teeth. Since changes also affected the more conservative teeth, rather than just bones, were the Late Medieval pigs genetically different from the Medieval animals? Moreover, since bones increased in size far more than teeth, does this confirm that the increase in body size was accompanied by a shortening of the snout? This paper will present the preliminary results from a two-dimensional Geometric Morphometrics study of pig teeth from the Late and Post Medieval levels at Shapwick, Launceston Castle, Hereford and Winchester to address

these questions and gain a better understanding of the profound changes that took place in England during this period.

**P15 Archaeobiogeography of extinct rice rats (*Oryzomyini*) in the Lesser Antilles during the Ceramic Age (500 BC to 1500 AD)**

Marine Durocher, Jose Utge, Violaine Nicolas, Allowen Evin, Sandrine Grouard

In the Lesser Antilles, rice rats (*Oryzomyini* tribe) – now extinct in the region – were one of the few non-flying terrestrial mammals to be present and eaten by the pre-Columbian ceramic societies inhabitants (between 500 BC to 1500 AD). Rice rats have a dual interest, both biological and cultural. Here, we aim to characterize their spatiotemporal distribution, complete their systematics and taxonomy, and assess their relationship with humans. We used an integrative approach combining geometric morphometrics, genetics and archaeozoology. Using a two-dimensional sliding semi-landmark based geometric morphometric approach, we quantified and visualized tooth size and shape differences between chronological cultural periods and between islands. To test whether the phenotypic groups reflect environmental adaptations or phylogenetic history we conducted ancient DNA analysis on the mitochondrial genome (Cytochrome b gene) of 70 archaeological specimens originating from all studied islands. From the 659 archaeological specimens representing seven different islands of the Lesser Antillean archipelago, three morphological groups emerged. They were geographically consistent and present from the beginning of the Ceramic Age: one in Saint-Martin in the northern part of the archipelago characterized by very small molars, one in Martinique in the south, and one in the central region (*i.e.* Antigua, Barbuda and the Guadeloupe archipelago: Basse-Terre, Grande-Terre and Marie-Galante). Within the central region each island has its own morphotype. This strong archaeobiogeographic signal, stable over time, suggests limited human influence on the spatiotemporal distribution of rice rats, despite their importance to past human diet. The wet and hot environmental condition typical of the tropical regions do not favor DNA preservation and likely preclude DNA analysis of the ancient remains we have studied so far. Yet, the phenotypic geographic distribution appeared consistent with DNA clusters from previous studies.

**P16 The population diversity of equids from Shahr-i-Qumis, north-eastern Iran, through 3D geometric morphometrics of metapodials**

Azadeh Mohaseb, Marjan Mashkour, Thomas Cucchi, Raphaël Cornette, Ludovic Orlando, Antoine Fages

A very large assemblage of equid bones corresponding to more than 150 individuals was recovered in Shahr-i-Qumis, a city in north-eastern Iran, dating to the Antiquity Iran. There are debates on the origin of these deposits that may be ritual. The equids belong to three species horse, donkey, hemione and one hybrid (Donkey x Horse) that were identified using classical 2D metrics. However some identifications, namely those of the middle-sized specimens (hemiones and hybrids) remain problematic when using this approach. We initiated a new research using 3D geometric morphometrics approach only on the metapodial bones. We first tested the method on modern equid specimens from various European and Iranian collections. The most important part of this project was the identification of mules, not only because of the insufficient number of modern mules in museum collections, but also because of the high similarity between mules to either donkeys or horses. We compare our results with the genetic identifications done on several of the specimens.

**P17 AgroCanis. A project on dog's mobility and adaptation in the first farming societies in Western and Central Europe, and Central and South America**

Stéphanie Bréhard, Aurélie Manin, Régis Debuyne, Christine Lefèvre, Nicolas Goepfert, Céline Bon, Christophe Hitte, Pauline Joncour, José Utge-Buil, Morgane Ollivier

This presentation introduces AgroCanis, a multidisciplinary project involving archaeologists, archaeozoologists and paleogeneticists, and financed by the Muséum national d'Histoire naturelle and the Brittany region. Previous analyses from Eurasian Neolithic contexts have highlighted how dogs, originally domesticated by hunter-gatherer groups, adapted to agricultural societies. In particular, the increase of the number of copies of the *Amy2B* gene, allowing a better ability to digest starch, may have permitted a variation in their diet, shifting from an exclusive carnivorous regime to a wider range of food, including cereals and leguminous plants. The neolithisation of Western Europe would have also been associated with the introduction of a new lineage of dogs. AgroCanis seeks to expand this research by initiating a comparative study between the Neolithic in Europe and proto-historical contexts in Central and South America. DNA was extracted from 100 bone remains from France, Romania, Mexico and Peru. The mitochondrial DNA and regions of interest on the nuclear DNA were amplified

using an in-solution hybridization-capture approach. The results will allow us to complete the European panorama and provide new data for Central and South America.

### **P18 Iberian Chalcolithic Canis: a genomic approach to know them better**

Ludmilla Blaschikoff, Octávio Serra, JI Cardoso, Carlos Fernández-Rodríguez, Ana Catarina Sousa, Marta Moreno-Garcia, Silvia Guimarães, Fernanda Simões, Cleia Detry, Eduardo Ferreira, Anders Götherström, Catarina Ginja, Ana Elisabete Pires

Domestic dogs exist in the Iberian Peninsula at least since the Upper Late Paleolithic. However, their origins are still poorly understood. Are they a product of a local domestication event from the Iberian wolves, or were they brought from anywhere else? It is crucial to unravel the genetic composition of past European peripheral populations to better understand the global evolutionary trajectories of early dogs. In this work, shotgun resequencing was carried out to recover the mitogenomes and nuclear genomic data of *Canis* from some Iberian prehistoric archaeological sites dated to the Chalcolithic [ca. 5000-4000 years BP], in particular: two dogs from Leceia, Portugal; two dogs from Caset\_on de La Era, Spain; and one wolf from Penedo de Lexim, Portugal. Using the best practices to analyze ancient DNA and the most up-to-date bioinformatics tools, mitogenomes and nuclear genomic data were obtained for these *Canis* specimens (mitochondrial genome coverages ranged between 1x and 17x, and endogenous nuclear DNA contents were between 0.09% and 3.75%). Genetic variants identified through read alignments against the dog reference mitochondrial genome allowed the assignment of these sequences to the established domestic dog mitochondrial DNA haplogroups. Furthermore, the nuclear genome, although more challenging to recover and analyze, allowed to determine the sex of these 5 *Canis* specimens. For these Iberian ancient *Canis*, we were successful in applying NGS methods to investigate their genomic composition. This is, to the best of our knowledge, the first genomic data available from a Eurasian wolf specimen from this chronology.

### **P19 Genomic variability of Western Mediterranean Roman cattle**

Sílvia Guimarães, Irene Ureña, Cleia Detry, Simon Davis, Ana Arruda, Catarina Viegas, Alexandre Gonçalves, Joaquina Soares, Carlos Tavares Da Silva, João Pimenta, Anders Götherström, Silvia Valenzuela-Lamas, Ana Elisabete Pires, Catarina Ginja

Cattle mitochondrial DNA (mtDNA) is geographically structured. It is therefore possible to associate maternal lineages to specific regions. Thus, the T1 and T3 haplogroups predominate in Africa and Europe, respectively. Genetic studies of both past and extant domestic cattle indicate chronological continuity over time between cattle populations from the same location, with strong maternal founder effects resulting from initial colonization. However, there is considerable mtDNA diversity in Western and Southern Europe: the phylogenetic analysis of complete mitochondrial sequences in extant Iberian breeds showed a high occurrence of ~17% of T1-matrilines. Ancient DNA of cattle bones from well-characterized archaeological sites enables tracking changes in genomic diversity associated with mobility and animal production traits. In Roman times an increase in cattle size is more apparent in the Roman Empire and less so in the periphery. Our aim is to understand whether the Roman state enhanced cattle genetic diversity in the Western periphery? A PCR-based analysis of a few short mtDNA sequences indicates presence of various lineages in Roman Spain. We used whole-genome shotgun resequencing (Illumina HiSeqX) to analyse ancient DNA from 9 Roman Portuguese cattle specimens. They include a metacarpal and a humerus from S. Miguel de Odrinhas (Sintra), a metacarpal and two molars from Chibanes (Setúbal), an astragalus from Monte dos Castelinhos (Vila Franca de Xira), an astragalus from Conimbriga (Coimbra), and two metacarpals from Alcáçova de Santarém. Mitochondrial genome coverages were between 2x and 60x. These cattle from Roman Iberia carried mostly the T3-matriline, but the T1-African lineage was also observed in two specimens from Chibanes. We interpret these findings from a population genomics perspective to model genomic variation over time and investigate genetic relationships between past and extant cattle from this region.

### **P20 Differentiation of American camelid fibres by proteomics, a preliminary approach**

Clara Azémard, Antoine Zazzo, Elise Dufour, Nicolas Goepfert, Séverine Zirah

New World camelids are composed of four species: *Vicugna vicugna* (vicuña) and its domesticated form *Vicugna pacos* (alpaca), *Lama guanicoe* (guanaco) and its domestic form *Lama glama* (llama). The two domestic species are currently used by humans for different purposes, alpaca for their fibres and llama to carry charges, and have therefore different fur. Yet, the morphology of camelids hair may have change since the precolombian times. As the microscopy studies do not permit us to differentiate the species, the identification of archaeological camelid

fibres found in South America is a challenge. Proteomics is a method based on the analysis by mass spectrometry of proteins. Fibres are mainly composed of keratins. The peptide composition differs from one to various amino acids between species and the specific peptides can be used as markers to identify the origin of the fibres. This technique generally relies on a bioinformatic treatment of the results and the comparison to international databases. Although proteomic of animal fibre has already proven to be an effective method to identify fibre origin, no work has been done on the New World camelids yet. This might be explained by the absence in the databases of three species on four. The knowledge of Ancient World camelid and alpaca's keratin sequences is not enough to establish useful peptide markers. Therefore we decided to create our own database thanks to modern samples coming from Peru and various French zoo. 42 samples were collected and analysed. A statistical treatment with R software enabled us to separate the species and propose markers for the differentiation of the modern species. If applicable to ancient species these results could have strong impact on the study of archaeological camelid remains in South America and the comprehension of the exploitation of camelids and their fur by the precolombian populations.



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***8th ICAZ AGPM Working Group meeting***

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