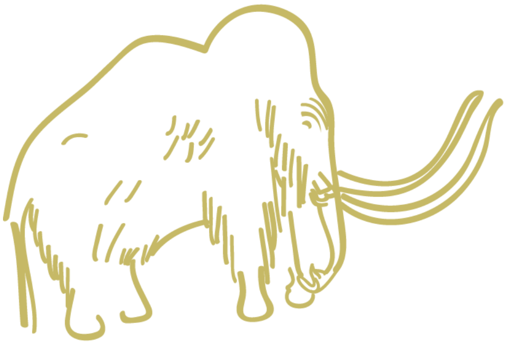

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XVIIIe Congrès

Book of abstracts

XVIII° CONGRES UISPP PARIS JUIN 2018
18th UISPP WORLD CONGRESS, PARIS, JUNE 2018

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XXXI-1. Through time, space and species: implication of new discoveries, technological developments and data diffusion improvement in Biological Anthropology.

Phylogeny and paleoanthropology. Just talking about or never mind?

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The conflation and misinterpretation of data, as well as the propagation of half-informed, sensational analyses imply that a palaeoanthropological consensus exists for what essentially amounts to the repetition of conjectural anthropological phylogeny. A reviewing of current papers leads us to conclude that nowadays the palaeoanthropological discourse mainly resembles a phylogenetical discussion where palaeoanthropologists no longer appear to use phylogenetical tools and methods. Following Bonde (2012): "*Is it really impossible to convey such simple and logical biological methodology (cladistics) to anthropologists – or don't they care?*", shall we definitely consider the palaeoanthropologists to be extraneous to the realm of Systematic?

Keywords: Palaeoanthropology, Systematics, Phylogeny

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*Speaker

CT scans of pathological cranial fragments from neolithic Switzerland: a differential diagnosis.

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A project is currently underway to establish a paleoepidemiological profile of the neolithic population of Western Switzerland (7 sites, 620 individuals), dated from the middle Neolithic to the Bell Beaker culture. The aim is to observe all bones present for pathological lesions, propose a diagnosis for these lesions whenever possible, and establish disease frequencies for this region for the chronological interval studied.
The necropolis of Barmaz is situated in the High Rhone valley, in Switzerland, and dates from the middle Neolithic (4500 – 3800 BC). It contains 59 tombs, some dug directly in the ground and some of the cistes Chamblandes type. Some of these graves contained more than one individual, bringing the total population for the necropolis to 77.

Tomb T16 (middle Neolithic I, 4300 – 4100 BC) contained a single individual, R16, represented by three cranial fragments. These present obvious pathological signs: unusual thickness, bone organisation that differ from the norm, porosities. As a result, a CT-scan investigation was conducted in order to narrow down possible diagnoses.
From the CT-scan and comparison with the literature, three possible diagnoses are submitted for consideration: Paget's disease, metastatic disease, and thalassemia/severe anaemia. The diagnosis remains open. These results are significant; indeed, no matter which of the diagnosis is the right one, it would be the first case identified in the neolithic population of Western Switzerland.

Keywords: paleopathology, CT scans, neolithic Switzerland, Paget's disease, metastatic disease, thalassemia

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*Speaker

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The question of ‘groups’ among Homo erectus population: study on external dental character

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Java biogeography was impacted by Pleistocene climatic and sea-level changes which could be affecting the dispersals and/or isolation of the hominins in the region. The aim of this study is to characterize the variability of ancient human populations in Java based on dental collections. Material of this study are maxillary and mandibular teeth collection which came from several localities in Sangiran site, Central Java, consisting 44 teeth from 15 mandibles and 35 teeth from 9 maxillae. Approach of this study will be used metric measurement and morphological assessment of the external dental character by ASUDAS parameters. We test a similarity and differentiation by metric and non-metric statistics analysis based on a set of teeth from Premolar and Molar of mandible and maxilla, to observe group clustering among the specimens. The preliminary result shows there are at least three groups of hominins during Pleistocene time. This result suggested there are groups seems to be overlapping and appear chronologically throughout the Lower to the early Middle Pleistocene. Implication of this study will shed light on the history of ancient human occupation in Java during the Pleistocene times.

Keywords: Homo erectus, Pleistocene, Taxonomic Diversity, Dental Character, Morphometric, ASUDAS

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*Speaker

The Xuchang Human crania and New advances in Chinese human fossils

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In the transition stage of Late Middle Pleistocene to early Late Pleistocene, there found there had various ancient humans living in China, including archaics, early modern humans and some undetermined humans. Some human fossils who presented both Neanderthal and east Asian archaic features. Whether or not gene flow exited between Chinese fossil humans and Neanderthals in the Late Pleistocene, need more fossil evidences to confirm. In 2007 and 2014, two human crania (≈105-125 ka) were found from Lingjing, Xuchang, north of China. They provide a morphological mosaic relative to their western contemporaries: 1) ancestral and reminiscent particularly of early Middle Pleistocene eastern Eurasian humans, 2) derived and shared by earlier Late Pleistocene humans elsewhere, whether morphologically archaic or modern, and 3) distinctive features of the Neandertals. This morphological combination reflects Pleistocene human evolutionary patterns in general biology, and both regional continuity and interregional population dynamics. It produced the morphological diversity of later Pleistocene humans.

Keywords: Human fossils, China, Xuchang, Pleistocene, Archaics

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Reassessment of the Middle Pleistocene human remains from Rabat-Kébibat (Morocco)

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The peopling of North Africa and the emergence of the first *Homo sapiens* is an ongoing debate, recently enriched by the discovery of a new human fossil remain in Jebel Irhoud (Morocco), attributed to a modern human and dated to ca 300 ka (Hublin et al, 2017).
It seems then important to reassess all the human fossil remains available in the area. In this context, through the geological and chronological recontextualization of the Rabat-Kébibat quarry, a Franco-Moroccan team has reassessed the human remains discovered in the site.

The human remains consist in cranial fragments (n=23), a mandible (including on the right I1, P3, P4, the roots of M1, M2 and M3 and of the left I1, I2, C, P3, P4, M1 and M2), and a left portion of a maxillary (including I1, I2, P3, P4, M1 and M2). Through a multidisciplinary approach, all the bones fragments were examined internally and externally. Data of the morphological and morphometrical analysis were compared to a conspicuous reference collection composed of African, Asiatic and European hominid fossils belonging to different chronological range.
The results obtain brings new data on the fossil remain from Rabat-Kebibat and allow to precise its phylogenetic affinities, particularly in terms of North-African peopling.

Keywords: Human fossils, MicroCT, internal bone structures, Genus Homo, geometric, morphometrics

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*Speaker

Two methodologies to infer the diet: The case of Cova de La Guineu (Font-Rubí, Barcelona, Spain)

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Dental microwear is a widely used technique to infer the diet of our ancestors. This method allows us to determine not only the physical properties of the food such as hardness and abrasiveness, but also to show how food was processed before being consumed (Grine, 1986).
This technique is applied, in both buccal and occlusal dental surface, by means of the Scanning Electron Microscope (ESEM). While the occlusal surface shows the diet of the last weeks of the individual's life (Grine, 1986; Jarosová, 2008), the buccal surface provides information about the long-term diet of an individual, as it has slower *turnover* than in the occlusal surface (Pérez-Pérez et al., 1994; Romero et al., 2007, 2012).

Microwear studies have employed either buccal or occlusal surface, however there are no extensive studies that have compared the information obtained by both surfaces in the same population (García-González et al., 2015).

Our aim is to study the use of both methodologies in the same population to compare the microwear pattern in the two surfaces, and test if the characteristics of the diet inferred depend on the surface observed. With that, we intend to deepen in the different dental microwear techniques, to have a comprehensive reconstruction of the diet of a population studying.
A sample consisting of 27 deciduous molars from the Late Neolithic (4500 ± 40 BP) burial place La Cova de la Guineu (Font-Rubí, Alt Penedès, Barcelona) (Morales et al., 2013) was chosen to carry out this study. We also proposed future work on the use of new technologies such as the Confocal Electron Microscope to fully understand how several dental microwear methodologies infer dietary patterns in the same population.

Keywords: Dental microwear, Diet, Buccal surface, Occlusal surface, Scanning Electron Microscope

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Non-alimentary tooth use in European Prehistory

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Non-alimentary tooth wear refers to the use of the anterior dentition as a "tool" or "third hand" and provides evidence of hominin manipulative behaviors in Prehistory. The frequency and geometry of dental wear features affecting occlusal, labial, and lingual tooth surfaces can be used to test hypotheses concerning context-dependent behavioral differentiation among hominins that relate to chronological, species-specific, or ecological factors. When coupled with bioarchaeological data on individual age or sex, non-alimentary wear features can be used to understand the patterning of socioeconomic tasks and social identities.
The antiquity of non-alimentary behaviors dates to at least the Early Pleistocene in Africa (OH-65), Western Eurasia (Atapuerca, Boxgrove and Dmanisi sites), and East Asia (Meipu 1). However, much less is known about non-alimentary behaviors of *Homo sapiens* from the Upper Paleolithic to Holocene food-producing societies during early European Prehistory.

Here, we explore variation in non-alimentary dental wear features affecting anterior teeth in the form of labial instrumental scratches, occlusal enamel chipping and polished surfaces among individuals spanning the Middle Pleistocene from Sima de los Huesos (Sierra de Atapuerca, Spain; N=28), Mid-Upper Paleolithic from Dolní Věstonice (Czech Republic; N=4), Mesolithic from El Collado (Oliva, Valencia; N=15), Neolithic from Can Gambús 1 (Sabadell, Barcelona; N=55), and Chalcolithic/Bronze Age from El Mirador Cave (Sierra de Atapuerca, Spain; N=23). Our findings imply a change in non-alimentary tooth wear related to economic and cultural differences across different time periods. Dental features of cultural origin on labial and occlusal surfaces are found in Middle Pleistocene individuals. However, in the Upper Paleolithic group, all individuals have cultural wear features on the labial and lingual surfaces. Mesolithic individuals only show evidence of non-alimentary tooth wear on occlusal surfaces. Meanwhile, the greatest difference is documented in Neolithic and Chalcolithic populations whereby only some of the individuals show non-alimentary tooth wear on occlusal surfaces. This might relate to a greater degree of social division of labour in more recent periods.

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*Speaker

Keywords: Dental wear, bioarchaeology, paleobiology, dental anthropology

Root for cementochronology – An efficient method for age at death estimation

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Age at death estimation is a fundamental component of creating a biological profile in bioarchaeological context. Even if physiological and structural biological background of the dental cementum deposit are still not perfectly elucidated, acellular cementum is considered to be formed continually throughout life and - unlike bone - to not undergo remodelling processes. Originally developed for nonhuman mammalian species, cementochronology based on the counting of incremental lines is considered to be a method with the potential for directly assessing chronological age. Even if most of the studies have assumed the method's superior performance for age at death in adults, we address the paradoxical disregard for cementochronology by debating the aspects that may contribute to the limited use of this method and by illustrating its potential. Cementochronology clearly suffers from a lack of standardization that slows down the adoption of this method and hinders the assessment of its precision that remains unclear as well as the impact of taphonomical processes. In order to define the boundaries of the cementum ageing technique, we applied a certified protocol on a sample of 200 healthy canines from individuals of known age, sex and postmortem interval from anthropological and anatomical collections. We scored readability and preservation of cementum tissue and measured the agreement between cementum estimates, i.e. the precision, and assessed the quality of the accordance between chronological age and estimates, i.e. the accuracy. To investigate the applicability of this method on ancient material, 200 additional canines extracted from archaeological assemblages were included. Accuracy and precision were analysed for each age group in considering postmortem intervals and taphonomical conditions. A strong global correlation was found between chronological age and estimated age [r=0.927; p=0.000]. Even if results revealed a notable difference in both precision and accuracy between individuals under and over 50 years, cementochronology's performance compared to classical osseous and dental methods justifies a more regular implementation in anthropology. This presentation aims, on a large standardized sample, to argue cementochronology's potential and limitations, and to propose a prediction model to reduce differences between estimated age and chronological age.

Keywords: Age at death, Cementochronology, Taphonomy, Acellular cementum, Precision, Accuracy

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3D VIRTUAL RECONSTRUCTION AND REGIONAL VARIATIONS OF THE MASTOID AIR CELLS – TAKE MODERN SKULLS IN NORTH CHINA AND EUROPE FOR EXAMPLE

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Mastoid air cell system is the most important component in temporal bone pneumatic cavities. They reduce the weight of the temporal bone, and maintain the balance of air-pressure inside human body. In addition, mastoid air cells pneumatization was thought to be associated with otitis media. However, the morphological features of mastoid air cells inside the bone wall are still unclear. With recent development of high-resolution industry computed tomography (CT) and three-dimensional (3D) visualization computer techniques, researchers were able to study the morphological variations of mastoid air cells without destroying the specimens and reveal morphological features among the ancient humans. In this study, the morphological variations of mastoid air cells of modern human were analyzed using high-resolution industry CT and 3D virtual reconstruction.

A total of 127 complete mastoids were obtained from 65 modern human skulls used in this study. 33 of these skulls were collected from north China area, while the other 31 skulls were brought mainly from Austria Belgium in the 1920s or 1930s. CT imagines were used for 3D virtual reconstruction to study the volumes and other features of mastoid air cells. Besides, the data obtained from previous research about 112 mastoids obtained from 58 Yunnan skulls, were compared with the results of north China and Europe mastoids. Chi-square test and t-test were used in this study to analyze the area difference of mastoid air cell system.

We found: (1) In 66 mastoids from north China, 65% of the mastoid air cells were classified in pneumatic type, whereas only 15% were in diploetic type, and the rest were in mixed type. Mastoid air cell system of sclerotic type was not found in all samples. (2) The mean mastoid air cell volume of skulls from north China was 5.10 cm3 (0.47_˜10.32 cm3SD=2.92 cm3). (3) In 61 mastoids from Europe, 72% of the mastoid air cells were classified in pneumatic type, 12% were in mixed type, and 16% were in diploetic type. (4) The mean mastoid air cell volume of skulls from Europe was 5.25 cm3 (1.38_˜9.34 cm3SD=2.35 cm3). (5) Mastoid air cells did not show significant difference in pneumatization, surface areas or volumes among samples from different area.

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Keywords: mastoid air cell, CT, 3D virtual reconstruction, modern skulls

Accessing early-life record of early humans: New multi-modal analytical imaging techniques of fossil teeth

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Early-life records are an essential aspect to understanding how different species of *Homo* have adapted over the past 2.8 million years (Ma) to changing environmental challenges or during their migration into new regions of the world. Yet, our current knowledge of the human evolutionary journey is largely based on the study of cultural material and the anatomy of adult hominin remains. Such studies reveal only limited aspects of the early-life record of extinct species, and struggle to decipher important factors such as nursing, dietary, stress, or mobility patterns, which represent paramount information to understanding the full spectrum of adaptive strategies by our ancestors. Dental tissues represent a unique temporal record of the paleoecology of the individual early-childhood development. The mineralization of dental tissues is extremely valuable for reconstructing early life records occurring during teeth formation. Each day the ameloblast and ondotoblast cells, responsible for the formation of enamel and dentine respectively, deposit a new layer of tissue, thus creating a sequential record. The elemental intake and mineralization pattern of the dental tissues are strongly influenced by the individual interaction with their immediate surroundings. Our advanced methodological framework that combines multi-modal analytical imaging techniques, allows us to obtain important early-childhood information of extinct *Homo* species, thereby gaining new perspectives on palaeoenvironmental conditions, health and social structure of our ancestors.

Keywords: Human evolution, geochemistry, Homo, diet, trophic level, Neanderthal, nursing, breastfeeding, fossils, teeth

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*Speaker

Technological improvement in the assessment of bone quality and osteoporosis: a new method of evaluation in ancient and modern skeletal remains using Quantitative Ultrasonometry

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Osteoporosis is a complex and heterogeneous disorder with a multi-factor aetiology. It is currently one of the major diseases in contemporary Western society, especially affecting people over 50 years old. Clinically, osteoporosis is defined as an abnormal bone loss and its most severe form is accompanied by the presence of fragility fractures occurring with the minimal trauma. A diagnosis of osteoporosis is given through the assessment of bone mineral density (BMD) which can be determined, above all the possible methodologies, by dual-energy X-ray absorptiometry (DEXA) or Quantitative Ultrasonometry (QUS). The latter is commonly used by physicians for the diagnosis of bone mineral density and bone quality, since it is relatively simple, cheap and easy to use.

In the last years paleopathologists have focused their attention on the study of osteoporosis and bone mineral density in ancient skeletons, in relation to sex, age and cultural background. The study of bone quality in past populations is particularly important because it can provide a relevant insight into the diachronic evolution of a seemingly modern pathology. However, a number of challenges remains in determine the bone loss in ancient remains, these mainly due to the methodological approaches used in the anthropological analysis. This underline the need of a new methodology and new standards specifically created and adapted for human skeletal remains.

The current study aims to develop a new methodology in order to assess bone quality in modern and ancient human skeletal remains using Quantitative Ultrasonometry, applied for the first time to skeletal samples (Frassetto collection, University of Bologna). The use of Quantitative Ultrasonometry (QUS) allowed us to evaluate bone tissue quality, analysing not only the characteristics related to bone mass and density, but also bone structure and to its elastic component.

Keywords: Bone mineral density, Bone quality, Quantitative Ultrasonometry, Paleopathology

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New automatic tools for the reproduction of internal and external structures of bony elements

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The virtual reproduction of inner details and/or external surfaces of skeletal and fossil specimens is becoming an essential new approach to the study of human anatomy and palaeontology, since these disciplines started to rely on virtual models for the morphological analysis. For what concerns the study of inner structures, in digital specimens (e.g., acquired by CT scan), the extraction of internal cavities is traditionally carried out by manually filling the regions of interest slice by slice ('segmentation'), whereas the isolation of the external surface is usually obtained by selecting the visible surface via 3D imaging software. The former procedure, in particular, is time-consuming and prone to generate topological artefacts, due to the almost unavoidable inaccuracies in the manual closure of holes and gaps, such as foramina or missing portions. In this communication, two new methods for the reproduction of virtual images of both inner and outer surfaces of fossil remains are described. The first method, Computer-Aided Laser Scanner Emulator (CA-LSE), provides the reconstruction of the external portions of a 3D mesh by simulating the action of laser scanners, and further allows the reconstruction of internal surfaces by subtraction. The second method, Automatic Segmentation Tool for 3D objects (AST-3D), performs the digital reconstruction of anatomical cavities, and further allows the reconstruction of the outer surface by subtraction. We applied the two methods on specimens of different size and shape: a modern human skull (FU-3115, Natural History Museum collections, University of Florence, Italy), a *malleus* bone (PO 2010 US 23, XI century A.D., Department of Biology, University of Florence, Italy), and a Neanderthal deciduous tooth (Kr-d1, Krapina Neanderthal Museum, Croatia). Both methods demonstrated to be faster, cheaper, and more accurate than other traditional approaches: they can be applied to single meshes instead of complete DICOM stacks from CT-scan acquisition, requires few seconds of processing and can be run by using open source software. Such implementations are available as add-ons in two existing Arothron and Morpho R packages. In addition, the automation of the process returns output reproducible and not subjected to manual errors or topological artefacts.

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Keywords: virtual anthropology, human evolution, endocast, malleus bone, maxillary sinuses

On the shoulder of the past. The scapula of the Neanderthal from Altamura, Italy

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The exceptionally well-preserved human fossil skeleton discovered in 1993 (Pesce Delfino & Vacca, 1993; Vacca & Pesce Delfino, 2004) in the Lamalunga karstic system near Altamura (Alta Murgia, Puglia, Italy) has been recently referred to *Homo neanderthalensis* and dated to a range bracketed between 187.0 and 128.2 ka (Lari et al., 20015). Its fragmentary right scapula is now suitable for direct scientific investigations, having been removed from the cave according to a protocol aimed at preventing any biological contamination; further, it has been delivered for DNA extraction and analysis to the laboratory of Molecular Anthropology and Paleogenetics at the University of Florence. The specimen is composed by three large fragments, which were collected with the aid of telemanipulators in 2009 (A1) and 2015 (B1 and B2) respectively, all from a small chamber just behind the so-called "abside dell'uomo", where the main assemblage of the human bones lies. The three fragments have been digitally acquired via micro-tomography (μ CT-scan); the 3D volumes were then used to compose the fragments anatomically. The probable original morphology of the scapula this now includes the well-preserved glenoid fossa, the roots of the coracoid and of the acromial processes, the superior third of the axillary border, the scapular spine and part of the supraspinal fossa. We used a sample of fossil and extant hominin specimens (*Australopithecus* and *Homo*) for morphometric comparisons. The results confirm that the overall morphology of the scapula from Altamura, despite some peculiar traits, is consistent with the morphology and proportions of both Early and Ẃurmian Neanderthals.

Keywords: Neanderthal, Middle Pleistocene, Southern Europe, Italy, scapula

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Age at death estimation on burnt human remains: application and validity of the auricular surface method – preliminary results

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The estimation of age at death is an important topic in the anthropological analysis, assessing a crucial part of the biological profile of an individual. One of the most classical methods using in assessing age at death is the one proposed by Meindl, Lovejoy and Mensforth (1985) in their famous and reliable work based on the analysis of the auricular surface of the ilium. This methodology, however, has so far concerned only the skeletal remains of the inmates, whereas no specific study was carried out on the cremated remains. The analysis of this kind of skeletal remains represents an important field of study in anthropology, both for archaeological and forensic purpose. In archaeology it represents a way to know cultural and anthropological aspects of a population, while forensically it is fundamental to know times and cause of death, context and characteristics of a fire and osteological features of the fire victim for the purpose of a personal identification. The purpose of this preliminary study is to assess the validity of the auricular surface method on burnt human remains, by analyzing the conservation of the area and the applicability of the method on a modern sample of 20 known age at death individuals whose remains have been subjected to cremation. The use of a modern sample of known sex and age from a homogeneous and controlled burning context provided a high grade of systematicity to our research. This methodology was chosen in particular for this study for a matter of conservation of this specific area during the cremation process; we found that in the context of a controlled and homogeneous cremation with burning temperatures kept among 650 and 1200$\circ$C the area of the ilium was preserved almost in all cases, while other diagnostic skeletal areas such as the sternal surface of the 4th rib or the pubic symphyses were very rarely preserved. Thus, we believe that a validation of the method of the analysis of the auricular surface on the specific context of the cremation would be useful for the anthropological analysis of burnt remains, which is still a not fully understood area of study. This preliminary analysis involved a sample of 20 individuals of known age and sex, aged between 16 and 70 years old, and deceased between June 2016 and September 2017 and cremated at the crematorium of Ferrara (Italy). We found that in the younger individuals some morphological features were not preserved, such as the typical billowing of the first stages (stage 1-3): the surface appears to be darker in color and

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without roughness, porosity, tuberosity or billowing, and shallow. In individuals over 40 years of age there was a better conservation and observability of the morphological characteristics of the area, which appeared deepened and presenting roughness and other typical morphological features (irregularity of the surface, lithic areas, osteophytes and other characteristics).

Keywords: Cremation, Anthropology, Burnt human remains, Age at death estimation, Methodology, Archaeoanthropology, Forensic anthropology

Digital alignment and virtual reconstruction of the cranium of the 'Altamura man' (Bari, Italy)

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The so-called "Altamura man" is a unique example of potentially complete non-modern human skeleton. After almost 25 years from the discovery (October 1993), we present and examine the virtual reconstruction of its cranium, waiting for the expected as well as extremely complex extraction from the cave. As a matter of fact, the skeleton is still inside the Lamalunga karstic system near Altamura (Bari), at a depth of some meters from the surface, embedded in calcite concretions that divide the small chamber where it is preserved – named "abside dell'uomo" or "Apse" – from a smaller one beyond it. Thus, a vertical flowstone enfolds the cranium and there is visual access to only a few points of contact between the anterior and posterior components (later referred to as component "A" and "B"), respectively visible from the Apse and from the small cavity beyond the Apse. While part of the face and the frontal region of the cranium are directly visible (A), the palate, the cranial base and large part of the vault can be recorded only with cameras or other photographic probes inserted in the small cavity beyond the Apse (B). The component A of the cranium was acquired via laser scanner at a resolution of 40 μm, whereas the component B was photogrammetrically reconstructed in 3D; eventually, the images were processed using the software Agisoft Photoscan. For both the digital alignment of the two components and the virtual reconstruction of the missing portions, which were not possible to acquire digitally, it was designed an unreleased protocol in R environment. Among a sample of mid-to-late Pleistocene fossil specimens we identified the Neanderthal cranium from Saccopastore (S1) as the most appropriate reference model for the digital alignment, using a geometric morphometric approach. Therefore, the components A and B of the cranium were aligned separately on the retrodeformed and scaled version of S1. We corrected the orientation of the two halves by the identification of the best fit on the mid-sagittal plane and eventually adjusted the angle between the lines *nasion-prosthion* and *prosthion-inion.* The reconstructed cranium allowed us to perform a preliminary morphological analysis that we performed according to a list of Neanderthal discrete features, combined with a selection of plesiomorphic traits.

We thank our colleagues of the Digitarca company (Bari) for the great work did *in situ.* We thank also the Centro Altamurano Ricerche Speleologiche, for their assistance, particularly Vincenzo Martimucci.

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Keywords: Neanderthal, virtual anthropology, human evolution, digital acquisition, middle Pleistocene, southern Italy

THE HUMAN REMAINS OF GROTTA DEL POGGIO

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Grotta del Poggio is part of a system of caves and shelters opening into the rock wall of the Poggio limestone spur located east of Marina di Camerota (Cilento, Southern Italy). This complex is considered one of the chrono-stratigraphic point of reference for the Middle Palaeolithic (250-40 thousand years ago) in the Cilento region. At the bottom of the Poggio sequence there is a marine conglomerate, probably dating back to MIS 7. This conglomerate is covered by continental deposits whose formation occurred in a period of cold climate hypothetically referred to MIS 6. The anthropic series contains 12 layers with Mousterian occupations characterized by non-predetermined lithic productions.
The human remains retrieved in the cave consist in a left talus from layer 4 and a first permanent left upper molar (LM1) from layer 6. Here we present results for the LM1.

Three-dimensional digital models of the enamel and dentine were obtained by segmenting micro-CT image data of the tooth. The digital models were then oriented in Rapidform XOR2 software (INUS Technology, Inc., Seoul, Korea) as follows: a spline curve was digitized on the cervical line of the tooth and a best-fit plane of the curve (i.e., cervical plane) was computed: the tooth was oriented with the cervical plane parallel to the xy-plane of the Cartesian Coordinate System, and with the lingual side parallel to the x-axis. The outline of the oriented tooth was imported in Rhino 4.0 Beta CAD environment (Robert McNeel & Associates, Seattle, WA) and centered superimposing the centroid of its area to a comparative sample of *Homo heidelbergensis* (HE), Neandertal (N), Early *Homo sapiens* (EHS), Upper Paleolithic *Homo sapiens* (UPHS) and recent *Homo sapiens* (MPE, MPAS, MPAF). Then, the centered outline was represented by 24 pseudolandmarks obtained by equiangularly spaced radial vectors out of the centroid. Finally, a principal components analysis (PCA) of the matrix of shape coordinates, was carried out.

Our results confirm previous suggestions based on chrone-cultural basis. In particular, the tooth from Poggio cave has a remarkable size and falls into the morphological variation of Neandertal M1s. It is characterized by an extremely large and protruding hypocone and relatively small metacone, finding large similarity with specimens from Krapina (e.g., KRP-136 and KRP-164). Overall, size and shape are more likely consistent for an attribution of the molar from Poggio

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cave to ancient than classic Neandertals.

Keywords: HUMAN REMAINS, Middle Palaeolithic, cervical line, Neandertal M1s

Elemental Analysis using pXRF to Assess Human Diet and Mobility

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Elemental analysis of human bone to study diet and mobility is an established methodology, yet the number of studies done is relative few when compared to those on carbon, nitrogen, oxygen, and strontium isotopes. Elemental analysis of calcium, iron, barium, strontium, lead, zinc, arsenic and other elements nevertheless can support and supplement isotope-based interpretations, and be of significant use in cases where bone collagen is not preserved, or when only non-destructive methods of analysis are permitted. Most previous elemental studies have been just as destructive as isotope analyses, with samples well-cleaned, ashed, and put into solution for analysis by atomic absorption or ICP spectrometry. Over the last decade, non-destructive portable X-ray fluorescence (pXRF) spectrometers have become widely available to archaeologists. While regularly used for trace element analysis of obsidian and other lithics, and major element composition of metals, it appears potentially useful for studies of skeletal remains as well. Elemental analysis, however, has potential reliability issues due to degradation and contamination of the mineral portion of bone, especially near the surface.

In the United States and other parts of the world, permission to conduct destructive isotope analyses of human skeletal remains has become increasingly limited. In part for that reason, experimental studies using the pXRF have been conducted to test the precision and heterogeneity of bone surfaces and interior, with different amounts and methods of cleaning as well as analytical settings. One of the first studies done was on individuals from inland and coastal sites in Florida, with the small variation in barium and strontium among individuals at each site suggesting little contamination, and the clear differences between the sites most likely due to varying proportions of aquatic food in the diet. This has been followed by analyses of nearly 1000 individuals from many sites in Latin America, Europe, and the United States, most of whom were also analyzed isotopically and with interpretations made about the dietary importance of maize, millet, and aquatic resources with patterns based on sex and status.

The precision of the pXRF on the elements of interest is excellent, and proper calibration is now established for bone and other calcium-based materials, so that direct comparisons may be made with other elemental studies. Also, further studies are being conducted on tooth enamel and roots, to test whether non-destructive analysis may be reliable for assessing childhood diets. Examples from Italy, Peru, and the United States will be presented.

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Keywords: diet, mobility, elemental analysis, human bone

Novel Strategies for the Interdisciplinary Study of Mummified Remains from the Egyptian Collection at the Museum of Ethnography and Anthropology of the University of Turin, Italy

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Mummified human bodies are perhaps the most fascinating source of biological and environmental information over the life and death of past individuals: their health, diet, patterns of mobility, causes of death. However, multi-disciplinary studies of mummies, integrating explicitly historical, archaeological and anthropological aspects, novel technologies for geochemical and biomolecular analyses (ancient DNA, paleoproteomics, stable isotopes) and museology are still relatively rare.

Here we present preliminary results from a new project which aims at achieving such integration of traditional physical anthropology and novel approaches of archaeological science in order to bring back into the spotlight an exceptional Egyptian collection: the "G. Marro" collection, established at the beginning of the 20th century and now hosted at the Museum of Anthropology and Ethnography of the University of Turin, Italy. This includes thirty one mummies of predynastic and dynastic age and their grave goods (including baskets woven with vegetable fibers, ropes, and bandages) and it therefore represents an ideal sample for reconstructing a variety of aspects of people's lifeways in ancient Egypt through time. These remains are in varying states of preservation, and are currently being held at the Centre for Conservation and Restoration "La Venaria Reale", of international reputation, where they will undergo conservation and restoration interventions.

The main research aim is that of establishing a non-destructive and/or micro-destructive analytical pipeline which optimises the use of precious samples, maximising the amount of information. This would improve the confidence of curators and conservators in the value of sampling for scientific analyses, and at the same time yield important clues on the state of preservation of the tissues and, in general, of the organic materials.

The preliminary results presented were obtained on "Mummy N◦ 14063", a mummified body of

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Pre-Dynastic - Proto-dynastic Epoch (Protohistory), macroscopically very well preserved. We used the novel information gathered through biomolecular and anthropological analyses in order to develop our scientific and archaeological understanding of this individual, but also to inform and reflect upon museology and audience engagement strategies, which will be used to design a museum display according to the most advanced international standards for the exhibition of human bodies.

Keywords: Mummified human bodies, multi, disciplinary studies

Revealing mobility patterns in early Medieval northeastern Italy through strontium and oxygen isotope analysis: challenges and first results

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In northeastern Italy, the area between Ferrara and Ravenna was particularly important in Late Antiquity, with Ravenna serving as capital of the Empires and Kingdoms that controlled the region between the fourth and eighth centuries AD. The study of a series of fortuitous findings of skeletal material was done in an area in which migration and mobility was probably significant, but poorly quantified. The research is targeted on one hundred individuals from the area north of Ravenna, dating mostly to the sixth and seventh centuries AD, towards the corridors that brought the Barbarian populations into the Italian peninsula. Both strontium isotope analysis by multi-collector ICP mass spectrometry and oxygen isotope analysis by stable isotope mass spectrometry are used to determine both the approximate percentage of individuals not born in the area and how many different geological areas are represented among the immigrant population.

All samples followed established procedures for cleaning and analytical preparation techniques, while also dealing with interpretations for individuals where no teeth were available and thus limiting our ability to verify movements during their life. The combination of strontium isotopes with oxygen isotopes for mobility studies strengthens our ability to provide data revealing some patterns. The statistical sampling of small cemeteries across a broader area instead of sampling individuals at one site is also valuable in providing a more robust perspective of mobility in the region during the early Medieval period. It is likely that officials and soldiers based in Ravenna itself would affect the burial composition of urban cemeteries, while smaller and sparser cemeteries, often overlooked, provide a view of the composition of the larger society and the impact of the sociopolitical situation in the area.

Our study is important in that it targets the demographic composition at a regional level. The viewpoint from strontium and oxygen isotopic data is also compared to our understanding of non-local identities as inferred from material culture to explore the relationship between mobility and material culture.

Keywords: stable isotopes, mobility, Italy, strontium, oxygen

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The Neanderthals from Grotta Breuil (Monte Circeo, Latium, Italy): a reappraisal

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Survival in geographical and climatological refugia might have been a critical aspect in the evolution and demise of the Neanderthals, in a way that makes it crucial to investigate human dispersal dynamics and paleoecology during the Late Pleistocene. South of the Alps, bound by the Appennines to the east and the Tyrrhenian coast to the west, Latium constitutes a possible refuge area during the Pleistocene, as also mirrored in the fossil record [Manzi et al. 2011]. In this perspective, we present a reappraisal of the Middle Paleolithic site of Grotta Breuil (Monte Circeo) [Bietti et al. 1991], within a multidisciplinary framework. The cave is a Mousterian site that was in use while, elsewhere in the Peninsula, Upper Paleolithic technocomplexes (e.g. the Protoaurignacian) were already present. Human fossil remains, associated with layers 5 and 6, with the former dated to about 34,600 ± 330 BP (AMS uncalibrated date) [Grimaldi & Santaniello 2014], have been attributed to *Homo neanderthalensis* [Manzi & Passarello 1995]. Zooarchaeological analyses revealed changes through time in hunted species [Stiner 1994], as well as variation in adaptive strategies along the stratigraphic sequence, with lower layers showing residential use and upper layers associated with a more ephemeral occupation of the cave throughout the year. A new project of research on both the site and the material collected at Grotta Breuil envisages a paleoantropological, archaeological, and paleoecological investigation paired with a systematic isotopic study, aimed at reconstructing the paleoecology for the Neanderthals in this area. In this context, the human specimens have been imaged by X-ray microtomography (μCT), with the aim to perform detailed morphometric analyses. The isotopic investigation includes oxygen (δ18O) and carbon (δ13C) isotope ratios measured in the carbonate fraction of animal teeth (with multiple species available for our study) sampled from the whole stratigraphy at the site.

Keywords: Neanderthal, Grotta Breuil, Italy, isotopes, carbon, oxygen

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Chronology and subsistence strategies of inhabitants of the Late Neolithic Abora settlement, Latvia

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The Late Neolithic *Abora* settlement is an inland site, located in South-eastern Latvia at the Lake *Lubāns* wetland approximately 200 km from the Baltic Sea. The wetland with its 27 Mesolithic and Neolithic sites is an important Stone Age inhabitation complex not only in Latvian, but also in a wider North European context. So far, archaeological excavations have been conducted in 18 sites.

Abora settlement, amongst others, is distinguishable by a few dozen burial finds within the inhabitation layers. Archaeological research and excavations at the site started at the last century with several excavation seasons during the 60s and 70s. As radiocarbon dating were already available for Latvian archaeologists at the time, several organic samples were dated during 70s and 80s. In 2008 research at the Abora settlement was renewed with excavations and new radiocarbon datings of organic samples.

This study, as a part of a larger researche of the Lake Lubāns Stone Age, focuses on the chronology of the buried individuals and their paleodiets that would indicate the general subsistence strategies at the time. Carbon and nitrogen stable isotope analysis of 13 individuals show no indication of farming as a general occupation. All of the human results, when put into context with the local animal stable isotope dataset, indicate fishing, hunting and gathering as the main subsistence strategy. The radiocarbon dates, however, clearly shows the settlement with the burials to be a Late Neolithic site. Besides, the six dated individuals indicate a local dietary shift from a mixed to a more freshwater diet during the occupancy of the site, therefore raising some questions about previous archaeological interpretations.

Keywords: Late Neolithic, radiocarbon, stable isotopes, paleodiets

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Ancient and recent phenotypic variation in Oceania: 3 millennia of migrations in South-Melanesia documented by linear morphometry

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Currently, the South-Melanesian region shows a wide cultural and linguistic diversity related to a complex history of interaction and peopling episodes. Two main migratory events were identified so far thanks to linguistic and archaeological data. The first episode is associated with human groups related to the Lapita culture (originating from South-East Asia and generally considered admixed with Papuan groups) who colonized the islands of Vanuatu and New-Caledonia around 3000 BP. The second episode, that occurred around 1000 BP, is associated with the dispersal of the Polynesian groups, amongst which some reached a number of South-Melanesian islands. We discuss here this pattern of island settlement through a morphometric study of human remains from Vanuatu archaeological contexts representing these two episodes. We present results obtained on the mandible of thirteen archaeological individuals (Teouma c. 3000 BP, Uripiv/Vao c. 2500-2000 BP and Futuna c. 1300 and c. 275 BP). Comparative statistical analysis (Principal Component Analysis and Linear Discriminant Analysis) were applied to twenty two mandibular measurements recorded in 239 modern individuals distributed in 9 series from South-East Asia and Oceania. Dominant Asian affinities characterize the earliest individuals from Teouma, mixed Melanesian and Asian affinities distinguish those from Uripiv and Vao, while dominant Melanesian affinities differentiate the more recent individuals from Futuna. Our results, which are consistent with paleogenomic and morphometric results obtained on the neurocranium, point to the rarity of early interbreeding between migrants and populations already existing in Near Oceania around 3000 BP and suggest a later dispersal of Near Oceanian groups in South-Melanesia, favoring opportunities of admixture. Futhermore,

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our current study failed identifying recent Polynesian biological influences in South Vanuatu possibly related to the relative antiquity of the studied specimens.

Keywords: linear morphometry, mandibular morphometric variability, phenotypes, Pacific settlements, Lapita

Mosaic evolution in hominin evolution and the case of Neandertals and Modern Humans

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Reconstructing patterns of evolution is a central issue in paleoanthropology ever since Darwin (Arsuaga, 2010). Concerning the shape of the hominin phylogenetic tree, there are two possible geometries: basically linear (called anagenetic) or primarily branching (called cladogenetic). They correspond to two of the three classic modes of evolution defined by G.G. Simpson (1944): phyletic evolution and speciation. Concerning the tempo, speciation can be slow or fast. Supporters of Punctuated Equilibrium Theory favor a rapid speciation event followed by a long period of evolutionary stasis as predominant in evolution. On the contrary, phyletic evolution is generally considered gradual (and called "phyletic gradualism" by punctuationists). Traditionally, neo-Darwinism tends to favor anagenesis as the main mode, and evolution is envisioned as a slow accumulation of changes in the alele frequencies of the populations.

If we substitute characters for genes, and character states (traits) for aleles, the neo-Darwinian definition of evolution used in population genetics ("accumulative slow changes in the alele frequencies of the populations") would translate into "accumulative slow changes in the frequencies of the character states of the populations". The "accretion model" posited for the origin of the Neandertals seems to correspond to this phyletic mode of evolution (Dean et al., 1998; Hublin, 1998).

The first 'missing link' discovered in human paleontology was the Taung Child and resulted in an unexpected mosaic of apish and human traits. To everybody's surprise, bipedalism came earlier that encephalization in hominin evolution. As it happened in Darwin's times with *Archaeopteryx*, the "missing links" seem to be "mosaic links" with combinations of primitive and derived traits that are almost impossible to predict.

Almost one century later, it seems that evolution of Neandertals (Arsuaga et al., 2014; 2015; Dennell et al., 2011; Martinón-Torres et al., 2012) and modern humans (Hublin et al., 2017) has also been mosaic-like, with changes in the face and the masticatory apparatus and teeth preceding brain expansion. Does this mean that mosaic evolution is preponderant in hominin

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evolution?

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Keywords: Speciation, mosaic evolution, anagenetic, cladogenetic, accretion, Neandertals

Can muscle architecture explain the variability in the first metacarpal morphology? Inferences on human hand evolution.

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Previous studies have proposed that our ability to produce and use stone tools has been the primary selective pressure explaining the evolution of the human hand. Derived traits in the human hand include a robust thumb metacarpal, particularly at the head and the base, and a moderate trapeziometacarpal joint curvature in both radioulnar and dorsovolar aspects. Along with other anatomical peculiarities, humans can exert forceful precision and power grips, and resist load during tool production and use. Despite that this is a biomechanical explanation for the morphology of the human hand, limited work had been done using soft tissue and therefore, the relationship between the muscles most strongly recruited during tool production/use and the derived traits in the hand bones remains to be thoroughly investigated. We have dissected 15 forearms of wet human cadavers of known sex and age at death. An estimate of the force magnitude was calculated by means of the physiological cross-sectional area (PCSA) of the muscles that arise and insert on the first metacarpal (first dorsal interosseous, opponens pollicis and abductor pollicis longus muscles). Variation in PCSA, muscle mass and fiber length was compared with metacarpal morphology. The bones were documented using photogrammetry and the 3D models were analyzed by applying geometric morphometrics. For comparison purposes, analogous information from non-human primates available at the literature and digital databases were studied. We aim to relate muscle architecture and the functionally influenced bony variables, and provide some light into the question of whether the evolution of the first metacarpal was related to its musculature.

Keywords: First metacarpal, muscle architecture, photogrammetry, geometric morphometrics

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Conservation methodology applied to the Homo neanderthalensis remains from Cova Foradà site (Oliva, Valencia, Spain)

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Cova Foradà is an archaeological site located in Oliva village (Valencia, Spain) in South-Eastern of Iberian Peninsula. The site is placed inside a karstic cave where several archaeological levels have been documented, from Upper Pleistocene to Holocene (including Mesolithic and Bronze Age levels). The excavations started at the end of the 70's in the twentieth century to the first decade of the twenty-first century. Between 2000 and 2010 field seasons different human remains were recovered associated with abundant fauna and Mousterian lithic industry. These fossils belong to different anatomical parts of the cranial and postcranial skeleton and have been attributed to *Homo neanderthalensis*. When the human remains are excavated at Cova Foradà site their state of conservation is deficient. They are fragile due to diagenetic processes and the hard sediment that cover their surfaces and difficult the excavation. Although the hard sediment concretion contributes to the preservation of the fossils, at the same time it difficulties their morphological and anatomical study and prevents the analysis of the bone and teeth surfaces. Since 2009 the fossils where transported to the Laboratory of Conservation at Institut Català de Paleoecologia Humana i Evolució Social to clean the human remains and to perform a new paleoanthropological study. In this work we explain the methodology and criteria applied to clean, to reconstruct and to store the human fossils recovered at Cova Foradà from 2000 to 2003. We describe the methodology to record the state of conservation before, during and after the conservation by 3D techniques and we propose a packing system to store and transport with the objective of guarantee their conservation in the best conditions.

Keywords: Cova Foradà, Conservation, Neanderthal, 3D conservation, Photogrammetry.

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*Speaker

Virtual Reconstruction of the Sima de los Huesos Cranium 16

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The Sima de los Huesos (SH) site is located inside the Cueva Mayor–Cueva del Silo cave system, in Sierra de Atapuerca (Burgos, Spain). To date, over 6,600 human fossils from at least 28 individuals are represented in a single stratigraphic level that has been dated to 434 +36/-24 ka. The SH human crania collection includes twenty crania, more or less complete, and up to 1200 isolated cranial fragments. Both females and males of different ages are represented. Most of the SH crania were discovered broken in many pieces and their reconstruction is an inevitable first step towards any comparative analysis. Despite virtual approaches have a great flexibility in cranial reconstructions, each specimen represents a particular case study. Here we present a detailed virtual reconstruction of Cranium 16 (Cr16), the most complete late adolescent of the SH population. Although there is no plastic deformation in Cr16, the left side of the neurocranium is badly preserved, lacking the temporal, parietal and sphenoid bones. Besides, only the right side of the facial region has been recovered. A high-resolution CT scan was used to create a 3D digital representation of the Cr16. As a first step, the original reconstruction was evaluated. The misalignment between the neurocranium and the facial region appeared evident when their respective midsagittal planes were computed. Besides, the CT images revealed that the left half of the frontal bone was more upward displaced. Therefore, the cranium was disassembled along two cracks, separating the face and the frontal bone. Finally, virtual reconstruction of the skull was accomplished using mirror-imaging and reference-based methods, employing 3D geometric morphometrics from a sample of SH crania to compute coordinatebased estimates of both, the missing and isolated parts. This reconstruction represents the first almost complete skull of a late adolescent from the SH population and provides a great opportunity for the study of the morphological development in a Middle Pleistocene human population.

Keywords: Virtual Reconstruction, Middle Pleistocene, Human evolution

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The bony labyrinth in Aroeira 3 cranium

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The Gruta da Aroeira site is part of the Almonda karst system (Torres Novas, central Portugal). Fieldwork in 2013 led to the discovery of a partial human cranium (Aroeira 3) encased in hard breccia and preserving the right temporal bone. The Aroeira 3 cranium most likely dates to 390–436 ka and it is approximately contemporaneous to Sima de los Huesos site (Sierra de Atapuerca, Spain). We have studied the bony labyrinth in the cranium Aroeira 3 using 3D virtual reconstructions generated from micro Computed Tomography (CT) scans. The Aroeira 3 specimen was compared with Sima de los Huesos hominins and with other Pleistocene and recent members of the genus *Homo.* Neandertals show some derived features in the bony labyrinth, including a low placement of the posterior canal, a relatively small posterior canal and a relatively large lateral canal. The Sima de los Huesos hominins show the derived canal proportions seen in Neandertals, but not the low placement of the posterior canal. In contrast, all of these features are absent in Aroeira 3, which shows a generally primitive morphology, more similar to *Homo erectus* or modern humans. Nevertheless, like the Sima de los Huesos sample, Aroeira 3 shows a low cochlear shape index, indicating a reduction in the height of the cochlea, and this may be a derived feature. Given the temporal and geographical proximity of the Sima de los Huesos and Gruta de Aroeira sites, the results of our study have potential implications for understanding microevolutionary processes and population dynamics in the Iberian Peninsula during the Middle Pleistocene.

Keywords: Human evolution, Middle Pleistocene, Iberia, Aroeira, Inner ear

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[*] Speaker

How many fossils do we have to study hominin evolution? The example of the Omo-Turkana basin

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Our entire knowledge on human evolution relies on the analysis of hominin fossil remains. Yet, there is no global or even a continental database listing the entire hominin fossil record. This gap precludes any integrated analysis and does not even allow to answer questions as simple as, for instance, "How many hominin fossils do we have in Africa?" or "How many specimens do we have to address the issue of the origin of the genus *Homo*?" We propose here the presentation of a database for this purpose. On a preliminary basis, we will present the example of the Omo-Turkana basin. With more than one thousand remains, this basin, with a coherent geological and paleoenvironmental history, has yielded almost a third of all the African hominin fossil remains for the time period between the upper Miocene to the boundary between lower and middle Pleistocene. Based on published data, we will present some factual elements about the fossil record unearthed in this basin: the number of remains, the distribution of these remains in regard to geological age, the date of discovery or date of first publication, the type of anatomical element studied (cranium, mandible, isolated tooth, post-cranial element), or taxonomic allocation. This type of integrated approach allows to better highlight biases inherent to the representability of the fossil record on our interpretations of hominin evolution.

Keywords: Fossil record, hominin, Omo, Turkana basin, history of paleoanthropology

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[*] Speaker

Conservation treatment of the middle Pleistocene human cranium from the site of the Gruta da Aroeira (Almonda karst system, Torres Novas, Portugal)

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A human cranium (Aroeira 3) was recovered from the middle Pleistocene site of the Gruta da Aroeira, (Almonda karst system, Torres Novas, Portugal). From the time of its discovery, the cranium required extensive conservation treatment to preserve and visualize it as well as to allow it to be handled safely for scientific study.
The cranium is heavily fossilized and well-preserved and the main portion was contained within a cemented breccia. Due to the extreme hardness of the sediments and the difficulty of excavation, several fragments of the cranium became separated from the main portion at the moment of discovery. The detached fragments and the contour and thickness of the sectioned cranial vault made it immediately apparent that it was a human fossil.

Here we present the conservation treatment of the Aroeira 3 fossil carried out over a period of nearly three years. The visible sections of the main portion of the fossil were protected with gauze coating impregnated with consolidant. Subsequently, the fossil was completely covered with a polyurethane resin to protect it further during the rock-cutting, with appropriate machinery, of a large block of the hard calcareous breccia that contained it. This was difficult and slow work, lasting a total of 10 hours.

Once in the laboratory, the restoration process consisted of extracting the cranium from the

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breccia and adhering speleothem coating and cleaning and removing sediment and limestone pebbles in between the fossil and the speleothem. This was done using two different types of drills and with ultrasound techniques. Portions of the skull were consolidated as this work progressed and the fossil was reconstructed.

The results of the conservation treatment can be considered optimal. The cranium has been reconstructed, the fossil was protected for handling and scientific study, the specimen was CT scanned and the results of the anthropological analysis were published in the international scientific journal the Proceedings of the National Academy of Sciences (PNAS).

Keywords: hominin, restoration, fossil, Europe, Neandertal, paraloid, acetone

Emergence of the genus Homo : news facts, new paradigms

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The evolutionary history of humankind has become considerably more complex over the last twenty-five years through the discoveries of new fossil remains and archaeological sites, but also with the development of new methods of analysis. The findings in both East and South Africa have highlighted a wide range of anatomical diversity, greater geographical distribution and a broader chronological framework. Who are the first humans? What are the anatomical characteristics that initially define the genus *Homo*? What is the part of cultural, behavioural and psychomotor skills in this definition?
Since the discovery of the first specimens attributed to *Homo habilis* in the Olduvai Gorge in 1959, no consensus has been achieved concerning the taxonomic allocation of the specimens of early *Homo*, and the hypodigm constitution of the species defined by Louis Leakey, John Napier and Phillip Tobias in 1964. Furthermore, this debate has been extended by the discoveries of new specimens of early *Homo* in East Africa, as well as the description of new taxa (*Kenyanthropus platyops* and *Australopithecus sediba*).

The goal of this presentation is to test whether the specimens allocating to *habilis* and *rudolfensis* belong to the genus *Homo* or to another genus. For that purpose, a comparative study and a numerical cladistic analyses on morphological cranial characters were carried out on the Plio-Pleistocene specimens commonly attributed to early *Homo*, *Homo erectus/ergaster, K. platyops, A. afarensis*, *A. africanus*, *A. sediba*, *P. aethiopicus*, *P. robustus* and *P. boisei.* The results of the cladistic analyses (based on the cranial specimens) show on the one hand that the taxonomical position of *A. sediba* could be debatable and on the other hand that the specimens of *habilis* and *rudolfensis* belong to the *Homo* genus and not to *Australopithecus* or *Kenyanthropus.*
Furthermore, we will discuss about the archaeological context and behavioural data of these hominins. The archaeological discoveries (Harmand *et al.*, 2015) made by West Turkana Archaeological Project (WTAP) at the Lomekwi 3 site (West of Lake Turkana, Kenya), dated to 3.3 millions years, i. e. 500,000 years before the oldest remains attributed to the genus *Homo*, rewrite the paradigm concerning the identity of the stone-tool makers and the emergence of material cultures.

Keywords: early Homo, cladistics, Hominin/culture

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*Speaker

Studying the joint evolution of the skull and brain in Homo species

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Cranial features have long been been favoured by palaeoanthropologists as clues to reconstruct the story of human evolution. The relative abundance of skulls in the fossil record, as well as the high number of diagnostic features which can be observed on them, makes them robust objects of enquiry. Perhaps equally important in the history of studying fossil crania is the consideration that the development of large brains and of complex cognition is among the major characteristics of human evolution. As "being human" means thinking like a human, the evolution of brains in fossil hominins and in *Homo sapiens* draws considerable attention. The study of endocasts - their volume, general morphology, convolutional patterns, and the development of cognitive areas recognised in extant humans - may have little to tell us in terms of function, but it does allow for the identication of derived characters with potential phylogenic and evolutionary value. Because of the high morphological integration between the outer vault of the skull and the endocranium, it is diffcult to list reliable independent diagnostic features for these two aspects of the head. The pressures on skull morphology may relate to environmental changes, diet, modications of the sensory organs, brain development, or the use of language, whereas the brain undergoes reorganisations which may be due to the development of cognitive areas. There is however very little literature concerning the joint evolution of the skull and endocast. We will discuss this topic through examples including morphometrical data derived from a sample of extant and archaeological *Homo sapiens*, and fossil hominins (*Homo erectus*, Neandertals, Mid-Pleistocene *Homo* specimens). Thanks to these data, we will be able to discuss the relationship between the morphologies of the skull's outer vault and the endocranium throughout the evolution of the genus *Homo*.

Keywords: Palaeoanthropology, Palaeoneurology, Homo species, Morphometrics

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*Speaker

Taphonomic insights into the Middle Pleistocene in the Iberian Peninsula. The human cranium from Gruta da Aroeira (Portugal)

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A partial human cranium has recently been recovered from the Gruta da Aroeira site in the Almonda karst system (Torres Novas, Portugal). The site forms part of the network of galleries located in the uppermost part of the 70-m high escarpment rising above the extant spring of the Almonda river, a tributary of the Tagus River. The fossil, also known as Aroeira 3, is represented by most of the right half of the calvarium.
The cranium was recovered from the Acheulean layer (Unit 2) dated to 390-436 ka. Together with the cranium, abundant faunal remains and lithics were found, including Acheulean handaxes, along with additional bifacial tools, other types of retouched tools, cores, flakes and flake fragments. Highly fragmented faunal remains are also abundant, consisting of isolated teeth, phalanges, carpal/tarsal bones, and antler fragments of large mammals. The presence of carnivores is scarce, with just a few bear and canid skeletal remains.

This specimen is, together with the Sima de los Huesos fossils, the only Middle Pleistocene human cranium to have been recovered in the Iberian Peninsula. Taphonomic and forensic analyses on human remains are essential to understand the site formation processes and to draw inferences about the mortuary behavior of hominin species. Here, we report the first taphonomic analysis of the Aroeira 3 cranium, based on its bone surface modifications and bone breakage pattern.

Aroeira 3 presents substantial bone loss of the left supraorbital arch and the outer cranial

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[*] Speaker

table of the frontal squama. Most of the fractures present features consistent with postmortem injuries of post-depositional origin. The fracture in the posterior region of the parietal bone, however, displays a different pattern, with the presence of a large cortical delamination, an oblique angle and a smooth fracture plane, features more usually present in perimortem (fresh) bone fractures. No evidence of other anthropogenic activity has been identified, which means cannibalism and secondary treatment of the corpse can be discarded, and no carnivore activity has been observed. None of the expected features of interpersonal conflict are observed in Aroeira 3, making an accident the most plausible explanation for the fracture. Finally, the bone loss in the frontal squama and the supraorbital arch could be attributed to different agencies, which means traumatic breakage cannot be totally ruled out.

Keywords: taphonomy, cranial breakage, Aroeira, Middle Pleistocene

Maxillary pneumatization in Sima de los Huesos (Atapuerca) Middle Pleistocene fossils and the origin of the Neanderthal facial morphology.

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Some traits of the facial morphology are considered essential elements of the Classic Neanderthal diagnostic anatomy. Much of the Neanderthal facial morphology is determined by the extension of the pyriform aperture away from the base of the skull. Projection of the nasal opening is also accompanied by changes in the infraorbital plate orientation and in the expansion of the maxillary sinuses. The maxillary hyper-neumatization was described by Heim (1989) as an anterior prolongation of the maxillary sinus that modifies the adjacent bone surface, flattening both maxillary and malar exocranial faces and smoothing out the canine depression. In this study, we present virtual reconstructions of the maxillary sinuses of crania from Sima de los Huesos (SH), a Middle Pleistocene population related to Neanderthals. Our main goal in this study is to describe and compare the SH maxillary sinus morphology with other human fossils, including Neanderthals and other Middle Pleistocene hominins. The mid-facial region of SH and comparative samples were digitalized using a high-resolution CT scan. The maxillary sinuses were virtually reconstructed with manual segmentation techniques. Mimics 18 (Materialise, Be) software packages were used to measure the volume and surface of the maxillary sinuses from the CT data as well as to create three-dimensional images. The bone was thresholded relative to the air in the sinus using a modified version of the half-maximum height protocol used by Fajardo (2002). The Sima de los Huesos fossils exhibit a morphology of the maxillary sinuses that resembles that of Neanderthals, which is characterized by multiple communicated maxillary sub-chambers including one more anteriorly placed.

Keywords: Sima de los Huesos, maxillary sinuses, facial morphology, virtual reconstruction

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Endostructural features of Neandertal and modern human permanent canines: 3D enamel proportion is not taxonomically powerful than nonmetric traits

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Teeth are useful to discuss taxonomic distinction, notably between Neandertals and modern humans. Investigations on 2D enamel thickness and more recently, on 3D enamel thickness revealed that Neandertal permanent canines and molars have thinnest enamel than modern Humans. As generally observed in biometric analyses, the range of variation of Neandertals overlap a part of that of modern humans, thus limiting the taxonomic assignment of certain teeth. Here we propose the investigation of permanent canines of Neandertals (n=25) and recent modern humans (n=24) by means of 3D enamel thickness. We take a particular look at the overlapping area of variation ranges of Neandertals and recent modern humans and compare our result with those obtain previously with restrict geographical origin (Buti et al., 2017). Neandertals individuals in this study are dated between MIS 7 and 3, and recent modern humans sample include large geographical origin (Pygmies, Europeans, Amerindians, Australians, Inuits). Secondarily, nonmetric traits at enamel dentine junction (EDJ) are recorded, which comes in support especially for no discriminating canines with volumetric parameters.

Results for lower canines show Neandertal have a 3D average (3DAET) and 3D relative enamel thickness (3DRET) lower than recent modern humans (p=0.02 and p=0.005). Despite a significant difference for 3DAET, 7/13 Neandertals fall in the variation range of modern humans and 2/12 modern humans are out of Neandertal variation range. For 3DRET, 5/13 Neandertals fall in the variation range of modern humans and 8/12 modern humans are out of Neandertal variation range. For non-discriminating canines, the presence of a distal accessory crest, a faint shovel-shape and a flat aspect of the lingual middle part at the EDJ characterized Neandertal canines. Concerning upper canines, Neandertal have a 3DRET lower than modern humans (p=0.02). However, 7/12 Neandertals fall in the variation range of modern humans and 1/11 recent modern humans are out of the variation range of Neandertals. For non-discriminating canines, the presence of a distal accessory crest, a moderate shovel-shape and a developed *tuberculum dentale* at the EDJ characterized Neandertal canines.

Our study confirms that statistically, Neandertal canine enamel is thinner than that of recent modern humans. However, this study shows no significant difference of the 3DAET for upper canines between Neandertals and recent modern humans, probably due to a larger geographical and genetic origin of our modern human sample compared to previous studies. For no discriminating canines with volumetric parameters, nonmetric traits at the EDJ are useful for

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distinguishing Neandertals to recent modern humans. Finally, 3D enamel proportion is not taxonomically powerful than nonmetric traits. This implicates for more efficient to investigate Neandertal and modern human teeth with multiple methods.

Keywords: 3D AET, 3D RET, enamel dentine junction

Morphological variability of the brain in Asian Homo erectus

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Based on the latest discoveries of the most ancient human fossil remains from the first "out of Africa", the limits of the morphological variability of *Homo habilis*, *Homo rudolfensis*, *Homo* ergaster and *Homo erectus* seem unstable and variable. So much so that Lordkipanidze and colleagues prefer include all the hominines from Africa, Georgia and Asia (both insular and continental) in a same large group that they call *Homo erectus s.l.*

The re-examination of an important anatomical element, which is the brain, on a large sample of *Homo erectus* coming from Asia continental from the site of Lower Cave of Zhoukoudian (Zkd II, III, V, X, XI and XII), Hexian (Hexian 1) and Nanjing cave (Nanjing 1) will be fruitful to try to elaborate a list of taxonomically informative endocranial features. The results of an exhaustive morphological description of the encephalic reliefs, the vascular imprints of the cranial sinuses and the middle meningeal system will be compared with hominines from other geographical regions such as Insular Asia and particularly with the island of Java. The comparative sample comprises the human fossil specimens from Trinil (Tr2), from the Kabuh layers of the Sangiran dome (Sangiran 2, 10, 12, 17, 38) and the more recent ones from the sites of Sambungmacan (Sb1, Sb3) and Ngandong (Ng1, 2, 4, 5, 6, 7, 8, 9, 10, 11 and 12) sites.

The morphological results will be completed by a morphometric analysis taking into account the major endocranial measurements. These first results obtained by the comparison between these two geographical areas will be very informative concerning the limits of the morphometrical variability of this large *Homo erectus* sample.

Keywords: endocast Homo erectus Asia morphological variability

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The variability of frontal and occipital features of H. erectus: a comparative analysis of unpublished Indonesian fossils

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After its initial publication by Dubois in 1894, the working diagnosis of *Homo erectus* is based on a list of morphological features established and updated after successive major discoveries made in the 20th century (e.g. Le Gros Clark, 1964, Rightmire, 1991, Wood, 1991). This growing fossil record also resulted in the recognition of several distinct hominin species within the hypodigm of *Homo erectus s.l.,* such as *H. ergaster* for the African specimens or *H. georgicus* for the Dmanisi fossils. While the existence and limits of those species are still debated, the homogeneity of the Indonesian *Homo erectus,* which covers a chronological period of ca. 1.5 million years, is also regularly questioned. But most of the studies addressing this question remain focused on the few best preserved specimens, although a significant number of fragmentary specimens are available for a better appreciation the encompassed morphological variability. In this work, several unpublished fragmentary frontal (n=6) and occipital (n=9) bones recovered from the Pucangan and Kabuh layers in the Sangiran dome (Central Java) are described and analyzed. Virtual 3D models of the original specimens were reconstructed by photogrammetry and compared to the 3D models of contemporaneous (Trinil, Sangiran) and younger (Solo series) Indonesian *H. erectus*, specimens from Zhoukoudian Lower Cave in China, Dmanisi (Georgia), as well as East African hominins (East and West Turkana, Olduvai). The results reported here focus on the size and shape variation of the features corresponding to the supra-orbital torus and occipital torus, which are frequently used as autopomorphic traits of *Homo erectus.* Potential implications for the taxonomy of *H. erectus* will be discussed.

Keywords: Homo erectus Indonesia Frontal Occipital

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From footprints to locomotor anatomy? The contribution of geometric morphometrics to the study of the hominin footprints from the Upper Pleistocene site of Rozel (Normandie, France)

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In recent years, different sites providing hominin footprints have been discovered such as the Pleistocene site of Rozel (Manche, France) dated to ca 80ky ago. Le Rozel delivered 290 footprints attributed to Neandertals that represent a potentially important source of biological information for this species. In that perspective, it is necessary to evaluate the impact of the substrate on the footprint morphology, and then the relation between this morphology and the anatomical features of the functional foot.

We report here the results of a geometric morphometric analysis of 39 complete footprints coming from a single occupation layer at Le Rozel. This Upper Pleistocene sample is compared with experimental footprints realised by 22 individuals on substrate conditions similar to that of Le Rozel. Our comparative sample also includes 52 3D models available online, of Pliocene, Holocene as well as experimental footprints made on different substrates. Each footprint is described by a set of 11 3D landmarks, indicative of the shape of the outline and the depth distribution (according to Bennett et al., 2009). We then proceeded to a Generalized Procrustes Analysis and a Principal Components Analysis.

The results show that the different anatomically modern footprint samples cannot be morphologically distinguished according to the substrate conditions where they have been realised. The Rozel footprints are clearly different from that of the Laetoli site. They slightly differ from the modern human samples: the heel and the midfoot are mediolaterally wider which could reflect a less pronounced plantar vault. These anatomical features of Le Rozel footprints are consistent with our knowledge of the anatomy of the Neandertal foot. Ongoing analyses of the impact of taphonomic agents on the footprints' morphology will help improving our interpretation of Le Rozel footprints.

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Keywords: Neandertals, footprints, Le Rozel, morphometrics, anatomy

The Bézier curve model applied to human evolution

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Most craniometric form and shape change studies in Palaeoanthropology are based on multivariate statistical analyses of distances between cranial landmarks or semi-landmarks. This predominant morphometric approach fails to take into account information of biological significance such as changes in curvature between homologous cranial points. Closed contour curve fitting techniques such as Fourrier and Eigenshape may be used to that effect. However, there exists a more suitable contour approximation method with a unique ability to extract parameters which allow to render accurately form and shape in a way that fits perfectly the original data: the Bézier curve model. I will explain the Bézier curve approximation method which is well suited to open contours and satisfies the requirements of curve-fitting accuracy and form reproduction: in particular its fundamental mathematical characteristics, its most important properties which makes this model suitable for the analysis of form and shape changes, the behavior of the curve related to its control polygon, and its limitations. The model will be illustrated with an application to the contentious issue of archaic *Homo sapiens* morpho-species recognition (also erroneously known as *Homo heidelbergensis*) with a fossil sample showing substantial cranial variability and including fossils, among others, such as Atapuerca SH and Petralona from Europe, Broken Hill 1, Saldanha, Eliye Springs, Omo Kibish 2, LH 18 and Djebel Irhoud 1 Singa from Africa, and Dali and Ngandong specimens from Asia. Finally, we will demonstrate how, thanks to its unique properties of form and shape rendering, one can implement dynamic graphic evolutionary simulations.

Keywords: Geometric morphometry, Bézier curve, human evolution

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*Speaker

Re-examination of ”old fossils”. The Mid-Twentieth discovered specimens from the Late Middle Pleistocene Montmaurin caves (South-west of France).

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In 1945, the activity of the quarries settled near the village of Montmaurin, 75km south-west from Toulouse in France, led to the discovery of several caves filled by archeological deposits. After the visit done by H. Begou´en and the Abbey H. Breuil, L. Méroc started excavations from 1946 to 1961 mainly in the Coupe-Gorge cavity which has yielded a lot of lithics and bones. Among them, there were human remains: a juvenile partial mandible (corresponding to the symphyseal part), a right maxillar bearing P3 and P4 and 4 isolated teeth (2 canines, P4 and M1). In a very closed vertical gallery called La Niche, one complete adult mandible bearing its molars, 2 vertebras and one fragmentary tibia were also discovered. All these fossils, except the 3 latter ones, where published in details. But, due to the lack of radiometric dating, such fossils were less and less included in the studies. This is the purpose of this paper to re-examine these human remains which are relevant to discuss the emergence of the Neandertal lineage in Europe. Indeed, the mandible from La Niche, dated to the OIS7 based on biochronology, is not fully Neandertal but it shows a combination of archaic and derived features, respectively on the bone itself and on teeth, which keeps open the discussion.

Keywords: Neandertal lineage, Homo heidelbergensis

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*Speaker

Les Homo erectus tautavelensis de la Caune de l'Arago et les Homo erectus européens évolués en voie de néandertalisation de la grotte du Lazaret

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Les Homo erectus tautavelensis de la Caune de l'Arago et les Homo erectus européens évolués en voie de néandertalisation de la grotte du Lazaret

Keywords: erectus, neandertal, Europe

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XXXI-2. Ancient DNA.

Analyse d'ADN ancien sur un chantier de fouilles et dans des musées de sites au moyen d'appareils mobiles

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Les recherches en instrumentation mobile ont permis le développement d'appareils de terrain pour les analyses génétiques au chevet du malade ou la recherche de traces d'agents pathogènes dans l'environnement. L'acquisition rapide d'un diagnostic génétique là où les échantillons sont collectés ou conservés est susceptible d'enrichir les pratiques archéologiques et a dont été testée dans deux configurations.
À l'occasion de fouilles réalisées dans la Grotte Maldidier (La Roque-Gageac, Dordogne), nous avons utilisé un prototype mis au point au CEA de Grenoble. Cet appareillage, basé sur la technologie microfluidique, est constitué d'un module pour l'extraction d'ADN, et d'un module pour son amplification par PCR en temps réel. Au moyen d'essais TaqMan mis au point au laboratoire pour l'ADN mitochondrial de différentes espèces de carnivores, nous avons montré durant une campagne de fouilles la présence d'ADN d'hyène des cavernes (*Crocuta crocuta*) dans des fragments de coprolithes pour lesquels aucun diagnostic n'avait été possible par analyse morphométrique. Cette étude démontre pour la première fois la fréquentation de la Grotte Maldidier par l'hyène des cavernes.
Nous avons par ailleurs testé au moyen d'instruments commercialisés (mini-centrifugeuse, appareil de PCR en temps réel MIC de la société Bio Molecular Systems) les échantillons de deux grottes ariégeoises conservés dans des musées. Au musée de Tautavel, nous avons analysé des coprolithes d'hyène de la Grotte du Portel, ce qui nous a permis d'identifier ceux où l'ADN est préservé. Dans le musée de l'Association Louis Bégou´en dédié aux cavernes du Volp, nous avons analysé les ossements de grands herbivores chassés par les magdaléniens de la Grotte d'Enlène, et montré au moyen d'essais TaqMan pour l'ADN mitochondrial de bovinés la présence récurrente de bison des steppes (*Bison priscus*). Nous concluons que l'analyse d'ADN ancien au moyen d'un appareillage mobile permet le diagnostic rapide (3h) d'échantillons archéologiques. Applicable à des coprolithes et des ossements pléistocènes, cette approche pourrait être utilisée à l'avenir en complément des méthodes de fouilles traditionnelles, et servir à la sélection des échantillons ensuite analysés en laboratoire pour le séquençage de génomes complets.

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*Speaker

Keywords: ADN ancien, analyse de terrain, Enlène, Le Portel, hyène des cavernes, bison des steppes, Magdalénien

The population genetic origins of domestic dogs

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Despite numerous investigations leveraging both genetic and archaeological evidence, the geographic origins of dogs remain unknown. On the basis of an ancient Irish dog genome and an assessment of the spatiotemporal appearance of dogs in the archaeological record, a recent paper suggested that dogs may have been domesticated independently in Eastern and Western Eurasia from distinct wolf populations. 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 _˜10 Mesolithic 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.

Keywords: dogs, domestication, ancient DNA

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Genome-wide investigation of the West European Mesolithic-Neolithic transition

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In recent years the expansion of early farmers from the Near East across Europe has been investigated in greater detail using genomic data. Incoming farmer groups have been shown to have a clear Near Eastern/Anatolian cultural and genetic background with only limited biological contact with autochthonous hunter-gatherers for at least two millennia, despite considerable evidence of mutual material exchange. The contribution of hunter-gatherer ancestry is very low in Central and Southeastern Europe, whereas early farmers from the Iberian Peninsula showed generally higher genetic contribution, albeit with regional variations.

Other parts of western Europe, in particular modern-day France, are less well-studied despite the fact that this region archaeologically displays a complex mosaic pattern of interaction with late Mesolithic hunter-gatherer societies. Here, archaeological research also attests the convergence/overlap of two main routes (Danubian and Mediterranean) of the Neolithic expansion of early farmers. Despite this crucial geographic position in the process of Europe's Neolithisation,

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thus far only mitochondrial DNA studies have explored the underlying biology of these interactions. Analyses of maternal lineages of 7000-year-old farmers from northern France suggest equivalent contributions of maternal lineages from farmer groups associated with both expansion routes to local gene pools, as well as a higher proportion of hunter-gatherer lineages than described for regions in Central or Southern Europe.

As part of a joint collaboration between French and German teams, we will generate the first detailed genomic data from Western European individuals. We will analyse a wide variety of geographical and cultural contexts, from the 7th to the 4th millennium BCE, and will investigate whether the archaeologically derived entities also represent genetically homogenous clusters. Through a solid contextualisation with archaeological data, this will allow us to shed light on cultural/biological contacts, modes of exchange, and to carry out demographic modelling. Here, we will present our project outline and preliminary data investigating the complexity and variability in cultural and biological interactions between human groups during the Neolithic period in Western Europe.

Keywords: Ancient DNA, Neolithic, Mesolithic, Neolithic transition, population genetics

The evolutionary history and population dynamics of bison in Europe was influenced by climatic fluctuations

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The largest European mammal that survived into the present is the bison or wisent, *B. bonasus.* It appears in the fossil record with the onset of the Holocene, but its origin was not known. The fossil finds in Upper Pleistocene Eurasia have been mainly attributed to the steppe bison, *B. priscus.* Other species precededing the steppe bison have been described on morphological grounds, such as *B. schoetensacki.*

We performed a paleogenomic study of bison in Europe and Asia covering roughly 150,000 years that uncovered the succession of different bison species in an environment-dependent manner influenced by climatic fluctuations. We identified an ancient form of the European bison that lived in the territory of France around 150,000 ago, corresponding to MIS5, and (again?) between more than 50,000 to 34,000 years ago, during the first half of MIS3, but also in the northern Caucasus. With decreasing temperatures in the second half of MIS3, we see the steppe bison arriving in France. The two species overlapped for some thousands of years during about 38 – 34,000 years ago as testified in a painting on a pillar in the Chauvet cave. While the population of the ancient wisent declined and then disappeared during the second half of MIS3, the population of the steppe bison thrived and populated the area until the end of the last glacial period, MIS2, around 14,000 years ago. With the dramatic warming at the beginning of MIS1, the ancestors of the present-day wisent that had survived the LGM in the southern Caucasus, arrived in and spread over Western Europe. In France they survived up to the Middle Ages and in Poland up to now.

We will discuss our results in the light of our newly compiled osteological data, new paleogenomic data and analyses as well as recently published data from other groups and in particular of genomic data from the present-day and 100-year-old wisent.

Keywords: ancient DNA, paleogenomics, population dynamics, climate change, bison

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Paleogenetics uncovers the cat's fast conquest of the world and long voyage to domestication

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Where does the domestic cat come from? Archeological finds hinted to southwest Asia and Egypt, but could not settle the question. Genetics of modern cats established that all domestic cats are descendants of the north African/southwest Asian wildcat *Felis silvestris lybica*, but the complete lack of a population structure hampered the characterization of the domestication process.

We analyzed the DNA preserved in a large amount of cat remains covering roughly the last 9,000 years. Cats in pre-Neolithic Europe all belonged to the European subspecies *Felis silvestris silvestris* while the cats in Anatolia at the beginning of the Neolithic belonged to the *F.s.lybica* subspecies. These latter ones showed up in early Neolithic sites in southeast Europe suggesting that they had been translocated by migrating early farmers. We identified another lineage in cat remains from Ptolemaic Egypt and found them in large numbers in Roman sites in the eastern Mediterranean area, and then in Viking sites at the Baltic Sea. The distribution pattern retraces human migrations as well as trading and raiding routes confirming historical sources indicating that cats were travelling with humans, mainly on ships.

Genomic data from modern cats showed that domestic cats and wildcats are not very different, and that the genomic differences mainly concern the behavior. Through the analysis of a gene that is responsible for the coat pattern of cats, we showed that the blotched tabby marking, typical of present-day domestic cats, was a late phenotypic change, while wildcats and all human-associated cats up to the 14th century were carriers of the genetic variant coding for the mackerel tabby marking and thus had a striped coat.

We conclude that the domestication process of cats was commensal, long and light and allowed the cat to stay wild for a long time.

Keywords: ancient DNA, paleogenetics, animal domestication, commensalism, Felis silvestris lybica

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*Speaker

Metagenomic analysis of a 35,000-year-old Canis lupus coprolite of the Chauvet-Pont d'Arc Palaeolithic cave

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To get insights into the genome and diet of ancient wolf in Europe, we performed high-throughput sequencing of DNA from coprolites collected in the Palaeolithic painted cave of Chauvet-Pont d'Arc (Ardèche, France). Shotgun sequencing of DNA from a well-preserved coprolite, radiocarbon dated to 35,600-33,600 year calBP, enabled reconstruction of the complete mitochondrial (mt) genome sequence of a Pleistocene wolf specimen. The genome sequence lies outside the diversity of the sequences that have been reported for extant dogs and Holarctic wolves. Phylogenetic analysis demonstrates that the mtDNA sequence corresponds to a hitherto unknown *Canis lupus* maternal lineage that diverged from the extant dog/Holarctic wolf lineage approximately 340,000 years ago. We found that this mitochondrial sequence is closely related to the mtDNA of other *Canis lupus* Pleistocene wolf specimens originating from Belgium that were recently described. However only the mitochondrial sequences of the belgian wolf specimens were characterized whereas we will also discuss the conclusions that can be drawn from the study of the nuclear genomic data of the *Canis lupus* Chauvet-Pont d'Arc specimen (we obtained a 10x coverage for the nuclear genome). Analysing the coprolite for other species to indicate the diet of our specimen, we detected cave bear (*Ursus spelaeus*) DNA sequences. This finding points to the cave as a reservoir of food for carnivores when bear carcasses were abundant, some 35,000 years ago, and helps to explain wolf intrusion into the deep cave sectors. Thus, with the characterization of a vanished maternal lineage and wolf-cave bear interaction, this study provides new insights into the evolution of *Canidae* and the paleoecology of a reference archaeological site.

Keywords: ancient DNA, Canis lupus, mitochondrial genome, phylogeny, Pleistocene, Ursus spelaeus.

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*Speaker

ABSENCE OF Equus hydruntinus IN THE IBERIAN BRONZE AGE FAUNAL ASSEMBLANGE: THE MITOCHONDRIAL DNA EVIDENCE FROM THE MIRADOR CAVE (ATAPUERCA, SPAIN)

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Equus hydruntinus had a broad distribution in Europe during the Pleistocene, with a decline starting after the Last Glacial Maximum. During the Holocene, the European *Equus hydruntinus* populations were highly fragmented, becoming extinct at different times. Based on scarce Iberian faunal remains from Neolithic to Bronze Age, it has been suggested that the Iberian Peninsula kept a residual *Equus hydruntinus* population. Nevertheless, different reanalyses of the faunal remains and stratigraphical conditions, have cast doubts about their chronological timeframes and even their taxonomic association. Furthermore it has been proposed that *Equus hydruntinus* was not present in Iberian Peninsula during the Holocene.
On the other hand, two new iberian Holocene faunal remains have been described as *Equus hydruntinus*. This taxon has been identified in a recent study on the faunal assemblage from the Mirador cave (Atapuerca, Spain), from Neolithic and Bronze Age cultural contexts. Two teeth were recovered from stratigraphic layers associated to each cultural period, and morphological and metric dental criteria were applied on them.

In order to corroborate the *Equus hydruntinus* presence in Mirador cave site, we have carried out genetic analysis from the two faunal remains. Mitochondrial DNA control region extractions and phylogenetical analyses were performed. Comparative sequences included extant members of the genus *Equus* (including sequences from modern and ancient individuals) and extinct *Equus*

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species, paying special attention to the *Equus hydruntinus* relationships.

We obtained DNA only from the Bronze Age tooth, and the phylogenetic analyses clustered its sequence among ancient and modern *Equus caballus* populations. The Mirador Bronze Age sequence clustered to the Lusitano group C, an haplogroup defined after Lusitano horse mitochondrial DNA analyses, and documented in the past exclusively in the Iberian Neolithic - Bronze Age horse populations.

This new study highlights the complexity in the taxonomic identification of *Equus hydruntinus* based on biometrical analysis, a question previously detected in other publications. Moreover our results reinforce the proposal that this equid was not present in Iberia during the Bronze Age times.

Keywords: Iberian Peninsula, Equus hydruntinus, Neolithic, Bronze Age, Mitochondrial DNA, ancient DNA

Reconstructing the first plant and animal colonizers within North America's ice-free corridor using ancient environmental DNA

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During the Last Glacial Maximum, continental ice sheets isolated Beringia (northeast Siberia and northwest North America) from unglaciated North America. By around 15 to 14 thousand calibrated radiocarbon years before present (cal. kyr bp), glacial retreat opened up an approximately 1,500-km long corridor between the ice sheets. However, it remained unclear when plants and animals colonized this corridor and when it became biologically viable for human migration. We used a combination of radiocarbon dates, pollen, macro fossils and shotgun sequencing of ancient environmental DNA from lake sediment cores to reconstruct the timing and succession of plants and animals within the interior of the corridor. We found evidence of steppe vegetation, bison and mammoth by approximately 12.6 cal. kyr bp, followed by open forest, with evidence of moose and elk at about 11.5 cal. kyr bp, and boreal forest approximately 10 cal. kyr bp. Our findings reveal that the first humans in America, whether Clovis or earlier groups in unglaciated North America prior to 12.6 cal. kyr bp, are unlikely to have been able to travel this route into America. However, later groups may have used this north-south passageway.

Keywords: ancient DNA, human migration, environmental reconstruction

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Tracking Six Millenia of Horse Selection, Admixture and Management with Complete Genome Time-Series

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

Keywords: Horse domestication, animal husbandry, human, animal relationship

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*Speaker

Paleogenomics of a French population, from the Neolithic to the Bronze Age.

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Methodological and technical advances in ancient DNA studies make it possible to have an ever deeper look into the genomes of individuals who lived several thousands of years ago. Benefits from this are two-fold: on one hand, we can directly address questions about the genomic diversity of ancient populations, and on the other hand relate this information to modern patterns of variation. Despite a rich archaeological record, little is known about how the multiple migrations that punctuate the history of present-day France have shaped its modern population. To tackle this question, our current project uses targeted enrichment to study informative SNPs and alleles in a wide panel of individuals from periods ranging from the Neolithic to the Middle-Ages, sampled from various sites across France. In this talk, we will report both mitochondrial and nuclear data obtained from 215 individuals from Neolithic and Bronze Age France. Besides a comparison with contemporary populations from across Europe, these complete mitochondrial genomes revealed contrasting population dynamics between northern and southern France, as culture once again proved to be a major determinant of the genetic differentiation between populations. The study of 120 nuclear SNPs, covering both physical and physiological traits, allowed us to follow the evolution of the allelic frequency of several phenotypes that characterize modern Europeans. This project significantly increases the amount of genetic data available for Neolithic France, which contributes to clear up the complex picture of Europe before the onset of Bronze Age.

Keywords: Ancient DNA, paleogenomics, Neolithic, Bronze Age, France

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7000 Years of the Human Oral Microbiome in France

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The study of ancient microbial DNA recovered from the dental calculus of human remains permits an unprecedented view into the prehistoric origins of the modern human oral microbiome. Several studies have attempted to describe the impact changing dietary and hygiene practices have had on our oral microbiota over time, as well as begun to retrace the evolution of oral pathogens. In order to better understand to what extent our oral microbiomes can enlighten us to the behavior of past populations, as well as to follow the regional appearance and coevolution of commensual and pathogenic oral microbes, we have mapped out the oral microbial landscapes of several distinct geographical regions of France over a period spanning 7000 years, from the Neolithic to the Middle Ages and beyond. We have performed high throughput shotgun sequencing of dental calculus from over 300 individuals, and use these data to see what can be learned about past human communities through their oral microbiome and human oral microbial evolution, and to comparatively explore the complexity of our changing oral microbiome across individuals, populations, geography and time.

Keywords: ancient DNA, dental calculus, France, oral microbiome

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*Speaker

Unveiling the importance of mule breeding in antiquity using minimal DNA data

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The members of the *Equus* genus, which includes horses, asses and zebras, can develop first generation (F1-) hybrids, despite their striking karyotypic and phenotypic differences. These hybrids are viable but mostly infertile, and often present characters of considerable interests for breeders with mules – the offspring of a mare and a jack – showing stronger working capacities, longer life spans, and better resistance to diseases than horses. They were extremely valued in antiquity, especially for trade, transport and warfare, and are relatively commonly represented in art. However, taxonomic identification of such hybrids in archaeological assemblages based solely on morphological data remains problematic. This is mostly due to the often fragmentary nature of the material available as well as the relative scarcity of the comparative morphological panel. Using high-throughput DNA sequencing technologies, we developed a full, accurate and automated methodological procedure capable of identifying F1-equine hybrids from minute amounts of sequence data. Our procedure thus limits experimental costs while remains compatible with samples showing extremely limited DNA preservation levels. We apply our procedure to the most extensive equine sample panel hitherto characterized and provide insights into the extent to which mules were essential to management strategies of different past empires and societies, including the Romans and the Byzantines.

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*Speaker

Keywords: horse, mule, species identification, ancient DNA

Ancient DNA from waterlogged wood as a new proxy for evolutionary studies on trees

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Long-lived tree species build up global forest ecosystems and have been exploited by humans for thousands of years. They are presently of particular concern as their long generation times may limit their adaptability to fast-changing environments. Temporal-series from ancient tree populations can provide a unique perspective on tree evolutionary and forest use history, that may not be detected by studies relying exclusively on extant populations. This information, and a better knowledge of the interplay between forest tree species, humans and climate will likely be paramount for anticipating the potential consequences of ongoing environmental changes. In this study, we took European white oaks (*Quercus robur* and *Q. petraea*) as a tree model species group with the aim to use ancient DNA to track past population dynamics and selective trajectories in the face of major environmental changes. Since ancient DNA studies on trees, in particular in temperate regions, are still in their infancy, we first investigated subfossil and archeological wooden remains from different taphonomical and temporal contexts to define conditions that optimize access to authentic ancient DNA. Following optimized aDNA extraction methods and shotgun sequencing, we succeeded in authenticating genetic data retrieved from 167 ancient oak DNA samples aged between 550 and 9,500 years. We will present the first analyses on this extensive dataset, focusing on key drivers of endogenous DNA preservation, temporal insights on degradation, and postglacial patterns of haplotype distribution.

Keywords: Quercus petraea/robur, oak, ancient DNA, degradation, temperate trees, chloroplast DNA

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*Speaker