Podium Presentation, Session 11, Saturday 13:50 – 15:30

New cranial and postcranial remains from the Neandertal specimens from Neander Valley

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In August 1856, quarry workers discovered the Neandertal type specimen in the 'Kleine Feldhofer Grotte' cave in Germany. They collected only the skull calotte and 15 of the larger bones of a male individual (Neandertal 1). In 1997, the sediments of the destroyed cave were rediscovered by R.W.S. and Jürgen Thissen. The field campaigns brought to light 73 bones and bone fragments of the type specimen and a previously unknown Neandertal female (Neandertal 2) [1-2], alongside faunal remains and lithic artifacts. A screening of questionable fragments using "ZooMS" revealed 18 additional hominin fragments in 2016 [3]. During the taphonomic analysis of human remains conducted since 2022, a comprehensive review was undertaken of all the faunal remains and finds from wet sieving from the excavations dating back to the late 1990s. The primary aim of this review was to provide contextual insights into the bone surface modifications observed on the human remains in comparison with the rest of the bone assemblage. This fauna review has yielded significant findings, disclosing the presence of fourteen previously unidentified human remains, intermingled among the animal skeletal collection.

The discovered remains include: a complete distal hallucal phalanx of the left foot; a complete hamate bone of the right side; three fragments of the ischiopubic ramus from both sides, likely belonging to the pelvis of Neandertal 1, although these fragments do not directly refit with the original coxae; two fragments of the radial head that fit together; a small cranial (parietal) fragment; two rib and three vertebra fragments; and a small portion of the proximal articular surface (head) of the left humerus. Furthermore, 50 smaller bone fragments, presumably human, have been selected for scrutiny through ZooMS. Among the findings, the complete bone remains of the hand and foot and the fragments of the pelvis stand out. Those specimens exhibit Neandertal traits, evident in their robustness and morphology and are compatible with the type specimen.

Despite the total destruction of the site due to quarrying activities, these newly found remains provide highly pertinent insights into skeletal part representation of the two Neandertal individuals. Elements such as distal phalanges of the feet or carpal bones are exceedingly rare in contexts lacking complete skeletons (e.g., accumulations by carnivores, cannibalism, or other agents). Conversely, in sites where Neandertals have been recovered, these small elements are mainly found in funerary contexts [4]. While the accumulation origin of these two skeletons remains unknown, these new findings suggest that the original Kleine Feldhofer Grotte cave likely contained complete skeletons. These new remains help expand the sample of one of the most iconic human fossils in the field of the paleoanthropology, broadening the scant representation of some anatomical elements within the Middle Paleolithic fossil record.

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References: [1] Schmitz, R.W., Serre, D., Bonani, G., Feine, S., Hillgruber, F., Krainitzki, H., Pääbo, S., Smith, F.H., 2002. The Neandertal type site revisited: Interdisciplinary investigations of skeletal remains from the Neander Valley, Germany. Proceedings of the National Academy of Sciences of the United States of America. 99, 13342–13347. [2] Smith, F.H., Ostendorf Smith, M., Schmitz, R.W., 2006. Human skeletal remains from the 1997 and 2000 excavations of cave deposits derived from Kleine Feldhofer Grotte in the Neander Valley, Germany. In: Schmitz, R.W. (Ed.), Neandertal 1856 – 2006. Rheinische Ausgrabungen 58, Philipp von Zabern, Mainz, pp. 187-246. [3] Lanigan, L.T., Mackie, M., Feine, S., Hublin, J.-J., Schmitz, R.W., Wilcke, A., Collins, M.J., Cappellini, E., Olsen, J.V., Taurozzi, A.J., Welker, F., 2020. Multi-protease analysis of Pleistocene bone proteomes. Journal of Proteomics 228, 103889. [4] Pablos, A., Gómez-Olivencia, A., Arsuaga, J.L.. 2019. A Neandertal foot phalanx from the Galería de las Estatuas site (Sierra de Atapuerca, Spain). American Journal of Physical Anthropology. 168, 222-228.

Poster Presentation Number 101, Session 2, Friday 17:00 – 18:30

Middle Palaeolithic asymmetric stone tool design and use: functional analysis to assess Neanderthal technology

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Variability within the Palaeolithic archaeological record, including temporal and spatial diversification, is exemplified by its lithic technologies. Consequently, research questions on how to link this variability with human behaviour centre upon the design, the production, the function, and the use of lithic artefacts. Especially tool design seems to play a key role in the case of Central and Eastern European Late Middle Palaeolithic bifacial backed knives (late OIS 5 until mid OIS 3; hereafter Keilmesser) [1]. The asymmetric Keilmesser is produced in a highly standardised mode, displaying a single active edge located opposite to a blunt back, resulting in the tool's wedge-shaped section. The active edge itself is often composed of sections of significantly varying edge angles. Keilmesser function and use, however, remain speculative but have been inferred from tool morphology and their well-documented production sequences, assuming repeated phases of re-sharpening and re-use, leading commonly to extended tool-life-histories.

The study presented here attempts to comprehend how the special edge design of Keilmesser is related to their function and use. In support of this, we present the results of functional analysis conducted on asymmetric lithics from three archaeological sites – Balver Höhle [2], Buhlen [3], both in Germany, and La Grotte de Ramioul [4], in Belgium. The use-wear analysis was performed qualitatively as well as quantitatively. The combined results show a technology applied in a standardised manner aiming at the production and use of a handheld backed tool with a single active edge. Designed with an edge angle increasing from the distal tip to the proximal base of the tool, the tool's active edge may have served different functions.

The study highlights the complementary character of both types of analysis, qualitative and quantitative. As demonstrated, Laser Scanning Confocal Microscopy can be applied to archaeological samples to successfully discriminate varying use-wear traces and thus increases the extent of knowledge possible to gain with this type of analysis.

References: [1] Jöris, O., 2006. Bifacially Backed Knifes (Keilmesser) in the Central European Middle Palaeolithic. In: Goren-Inbar, N., Sharon, G. (Eds.), Axe Age - Acheulian Toolmaking, from Quarry to Discard. Approaches to Anthropological Archaeology. Equinox, London, pp. 287–310. [2] Günther, K., 1964. Die altsteinzeitlichen Funde der Balver Höhle. Bodenaltertümer Westfalens VIII, Münster. [3] Jöris, O., 2001. Der spätmittelpaläolithische Fundplatz Buhlen (Grabungen 1966-69) : Stratigraphie, Steinartefakte und Fauna des oberen Fundplatzes. Universitätsforschungen zur prähistorischen Archäologie 73, Bonn. [4] Ulrix-Closset, M., 1975. Le paleolithique moyen dans le bassin mosan en Belgique. Éditions Universa, Liege.

Poster Presentation Number 102, Session 2, Friday 17:00 – 18:30

The Laschamps event (~41 ka BP) straddles the Mousterian-Châtelperronian transition in Western Europe

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The Laschamps event (named after the type site in the Massif Central in France) was one of the first geomagnetic excursions to be identified, and has since been found in both sedimentary and volcanic contexts across the planet [1]. The event is currently dated to around 41 thousand years ago (ka BP) and had a duration of less than one thousand years ([1] and ref therein). Given its proximity to the estimated disappearance date of Neandertals from the fossil record, the Laschamps event may serve as an important geochronological marker to refine our spatiotemporal understanding of the transition from Neandertals to *Homo sapiens* across Eurasia. The event caused a large increase in atmospheric ^{14}C and is considered by some as a driver of global environmental and evolutionary changes [2-3]. Furthermore, the Laschamps event could help refine the chronologies of sites without organic preservation, allowing these to be linked to sites with well-defined radiocarbon chronologies, potentially on a global level. Historically, the use of the Laschamps event as a geochronological marker in archaeology has been confined to Russia and central Asia, including at Kostenki 14 [4]. In this poster, we present a paleomagnetic study of the archaeological sequence of Quinçay, France, where the Laschamps event is found to straddle the Mousterian and Châtelperronian layers. The cave site of Quinçay, near Poitiers, West-Central France, was discovered in the 1950s and contains a succession of Mousterian and Châtelperronian industries [5]. The site was reopened in 2019. These new campaigns included a detailed paleomagnetic study of the whole stratigraphic sequence. This study found evidence of reversed paleomagnetic signals, indicating a temporary geomagnetic excursion that straddles the Mousterian and Châtelperronian levels that we interpret as the Laschamps event. This identification enhances the geochronological constraints of the chrono-cultural sequence and represents the first identification of the Laschamps excursion in a western European archaeological context. Our results suggest that the final Mousterian and Châtelperronian occupations at Quinçay may have occurred very close to, or possibly during, a one thousand year period around 41 thousand years ago (ka BP). Finally, we discuss the potential implications of these results for the dating of the Châtelperronian and sub-contemporaneous archaeological industries.

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References: [1] Channell, J.E.T., Singer, B.S., Jicha, B.R., 2020. Timing of Quaternary geomagnetic reversals and excursions in volcanic and sedimentary archives. Quaternary Science Reviews. 228, 106114. [2] Cooper, A., Turney, C.S.M., Palmer, J., Hogg, A., McGlone, M., Wilmshurst, J., Lorrey, A.M., Heaton, T.J., Russell, J.M., McCracken, K., Anet, J.G., Rozanov, E., Friedel, M., Suter, I., Peter, T., Muscheler, R., Adolphi, F., Dosseto, A., Faith, J.T., Fenwick, P., Fogwill, C.J., Hughen, K., Lipson, M., Liu, J., Nowaczyk, N., Rainsley, E., Bronk Ramsey, C., Sebastianelli, P., Souilmi, Y., Stevenson, J., Thomas, Z., Tobler, R., Zech, R., 2021. A global environmental crisis 42,000 years ago. Science. 371, 811–818. [3] Picin, A., Benazzi, S., Blasco, R., Hajdinjak, M., Helgen, K.M., Hublin, J.-J., Rosell, J., Skoglund, P., Stringer, C., Talamo, S., 2021. Comment on "A global environmental crisis 42,000 years ago." Science. 374. [4] Gernik, V.V., Guskova, E.G., 2002. Палеомагнитные характеристики отложений разреза ст. Костенки 14 (Маркина гора) [Palaeomagnetic evidence for sediment sequences of Kostenki 14 (Markina gora)]. In Sintsyn, A.A., Sergin, V.Ya., Hoffecker, J.F. (Eds.), Особенности развития верхнего палеолита Восточной Европы [Trends in the evolution of the East European Palaeolithic]. Kostenki in the context of the Palaeolithic of Eurasia. – Proceedings of Kostenki expedition IHMC RAS, ser. Research. 1, 247–249. [5] Roussel, M., Soressi, M., Hublin, J.-J., 2016. The Châtelperronian conundrum: Blade and bladelet lithic technologies from Quinçay, France. Journal of Human Evolution. 95, 13–32.

Poster Presentation Number 103, Session 2, Friday 17:00 – 18:30

Between teeth: morphological covariation in the human postcanine dentition

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Morphological covariation within the modern human postcanine dentition is still an open field of study. Understanding covariation patterns of the three-dimensional (3D) shapes between different tooth types is relevant for the advancement of human biology and evolution, as well as dental anthropology, phylogeny and medicine. Previous 3D morphological studies of various tooth types suggest that the geographical origin of the sampled individuals does not play a decisive role in determining the shape of the individual dental crowns, whose genesis is dominated by genetic factors [1-2]. Here, we analysed 3D shape covariation of the postcanine dentition (third molars excluded), both within and between dental arches using geometric morphometrics.

Eight geographically variable samples of upper and lower third and fourth premolars (P3 and P4, respectively) and first and second molars (M1 and M2, respectively) from Sub-Saharan, Egyptian, European, South American, Southeast Asian, Oceanian, and Near Eastern modern human skeletal remains were considered in this study (N=526 teeth). The analysed samples consisted of 70 lower P3s, 74 lower P4s, 76 upper P3s, 74 upper P4s, 49 lower M1s, 48 lower M2s, 59 upper M1s and 76 upper M2s. High-resolution scans of the maxillae and mandibles were acquired at the Vienna Micro-CT lab and were further reconstructed and processed to generate 3D models of the dentinal crowns [3], which were represented by landmark configurations combining the occlusal edge of the enamel-dentine junction with the cervical outline. The landmark configurations were designed for each of the dental types specifically. Two-Block Partial Least Squares analysis was used to investigate the covariation between various dental type pairs.

We found very high pairwise correlation in tooth pairs within the dental arches (lower P3 and P4, r=0.89; upper P3 and P4, r=0.81; upper M1 and M2, r=0.83). The correlation values between antagonists of the same tooth varied notably from the highest value detected in M1s (r=0.9), to the lowest between the upper P4s and lower M1s (r=0.58). This could be explained by the need for morphological compatibility of the dental arches in order to guarantee stable occlusion and efficient function during mastication. Given that the tooth articulation does not exclusively occur between antagonists, the covariation between some of them might not be as high as expected. The morphological compatibility of the entire dental arches in occlusion is superior to the compatibility of antagonists only. Noticeably high correlation values were detected in some of the tooth type pairs that do not articulate in a normal dentition. A relatively high pairwise correlation was found in the pairs of lower (r=0.79) and upper (r=0.77) P4s and M1s, which are the only tooth type pairs of the postcanine dentition, belonging to different tooth classes and still serve the same function [4].

With this study, we provided an overview of pairwise correlations and percentages of covariation between different tooth types within the human postcanine dentition, possibly laying the groundwork for future genetic research.

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References: [1] Krenn, V.A., Fornai, C., Wurm, L., Bookstein, F.L., Haeusler, M., Weber, G.W., 2019. Variation of 3D outer and inner crown morphology in modern human mandibular premolars. American Journal of Physical Anthropology. 169, 646–663. [2] Šimková, P.G., Wurm, L., Fornai, C., Krenn, V.A., Weber, G.W., 2024. Shape variation in modern human upper premolars. PLOS ONE. 19, e0301482. [3] Weber, G.W., and Bookstein, F.L., 2011. Virtual anthropology: A guide to a new interdisciplinary field. Springer, New York. [4] Kraus, B.S., Jordan, R.E., Abrams, L., 1969. Dental anatomy and occlusion; A study of the masticatory system. Williams and Wilkins, Baltimore.

Pecha Kucha Presentation, Session 2, Thursday 11:20 – 12:50

Cracking the code of the marked mammoth rib from the Gravettian of Hohle Fels Cave, Germany

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Marked objects from the Upper Palaeolithic are among the most intriguing and puzzling artifacts of human antiquity. Geometric engravings in particular can pose challenges in how we interpret meaning and extract information they store about past hunter-gatherer groups. One such example comes from Hohle Fels Cave in the Swabian Jura of southwestern Germany. During the 2017 season, excavators recovered a 44 cm-long mammoth rib, which we subsequently dated with radiocarbon to 31.3 kcal BP, establishing a Gravettian age for this remarkable artifact [1]. Finding such a large, well-preserved mammoth bone is a rare occurrence in the Swabian Gravettian, but even more noteworthy are the anthropogenic modifications that the rib bears. The makers of the artifact removed the head of the rib and rounded the remaining surface. They also truncated the distal end but did not round or polish it to the same extent. The rib preserves a series of pronounced markings, including two rows of 83 and 90 engraved parallel marks on the cranial edge of the rib and 13 longer, shallower incisions on one of the broad surfaces of the rib. The structure and regularity of the markings suggest potential use of the bone for artistic, symbolic or functional purposes. The markings are clearly the result of intentional cuts using stone tools, and we argue that the Gravettian inhabitants of Hohle Fels used this mammoth rib to store information about some aspect of their lives. This study aims to develop and test a series of hypotheses about the function of these markings and to explore what they might signify. We hypothesize that the rib could represent a calendrical device, a numerical counter or a decorative object. We use the dimensions and morphological characteristics of the individual marks to compare the mode and manner of their production. We consider if sequences of marks were made using the same tool in close temporal proximity and consider arguments for reconstructing the order in which the marks were made. Additionally, we examine whether or not the different groups of marks exist in relation to one another as part of a cohesive design. Detailed microscopic observations combined with spatial and contextual information help us evaluate the plausibility of competing hypotheses to explain the markings and decode their meaning.

References: [1] Conard, N.J., Janas, A., 2018. Fortsetzung der Ausgrabung am Hohle Fels und die Entdeckung einer markierten Mammutrippe aus dem Gravettien. Archäologische Ausgrabungen in Baden-Württemberg 2017.

Podium Presentation, Session 11, Saturday 13:50 – 15:30

Hominin palaeoproteomics: potential and limitations for understanding human evolution

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Many outstanding questions in human evolution could be more clearly understood with genetic information from hominin remains whose age or contexts are substantially beyond the DNA preservation envelope. Some structural proteins degrade slower than DNA and thus appear to be preserved on million-year time-scales, but retrieved proteins have so far only covered a handful of evolutionarily informative polymorphisms [1-3]. It thus remains largely unexplored to which extent proteomic data from different tissues and degrees of preservation could distinguish between the ancestries of early hominins. More specifically, different levels of preservation might be able to distinguish hominin ancestries of different degrees of divergence and genetic differentiation. We present computational experiments of the expected evolutionary genetic resolution from ancient proteomes. We use translated genomic data from archaic humans [4], in concert with newly generated and published ancient proteomic data from humans to extract subsets of the proteome that have been successfully observed in skeletal tissue. We then apply f-statistics approaches [5] and phylogenetic methods to test statistical power to distinguish *Homo sapiens*, Neanderthals, and Denisovans at those amino acid positions, assessing statistical uncertainty with weighted block jackknife and bootstrap resampling, respectively. We compare the genetic differentiation needed as suggested by our experiments (Wright's FST) to morphological differentiation observed in the human fossil record. Using these results, we review some of the outstanding questions in human evolution that could be addressed with current resolution, and which questions seem to remain out of reach without substantial technological progress for proteome retrieval. Our results provide insights into the statistical power expected for different tissues and preservation metrics. Understanding which evolutionary questions might be possible to address with proteomic data is key to assess prior to sampling, to ensure responsible study of the fossil record.

References: [1] Welker, F., Ramos-Madrigal, J., Gutenbrunner, P., Mackie, M., Tiwary, S., Jersie-Christensen, R.R., Chiva, C., Dickinson, M.R., Kuhlwilm, M., De Manuel, M., Gelabert, P., Martinón-Torres, M., Margvelashvili, A., Arsuaga, J.L., Carbonell, E., Marques-Bonet, T., Penkman, K., Sabidó, E., Cox, J., Olsen, J.V., Lordkipanidze, D., Racimo, F., Lalueza-Fox, C., De Castro, J.M.B., Willerslev, E., Cappellini, E., 2020b. The dental proteome of *Homo antecessor*. Nature. 580, 235–238. [2] Chen, F., Welker, F., Shen, C.-C., Bailey, S.E., Bergmann, I., Davis, S., Xia, H., Wang, H., Fischer, R., Freidline, S.E., Yu, T.-L., Skinner, M.M., Stelzer, S., Dong, Guangrong, Fu, Q., Dong, Guanghui, Wang, J., Zhang, D., Hublin, J.-J., 2019. A late Middle Pleistocene Denisovan mandible from the Tibetan Plateau. Nature. 569, 409–412. [3] Welker, F., Hajdinjak, M., Talamo, S., Jaouen, K., Dannemann, M., David, F., Julien, M., Meyer, M., Kelso, J., Barnes, I., Brace, S., Kamminga, P., Fischer, R., Kessler, B.M., Stewart, J.R., Pääbo, S., Collins, M.J., Hublin, J.-J., 2016. Palaeoproteomic evidence identifies archaic hominins associated with the Châtelperronian at the Grotte du Renne. Proceedings of the National Academy of Sciences of the United States of America. 113, 11162–11167. [4] Patramanis, I., Ramos-Madrigal, J., Cappellini, E., Racimo, F., 2023. PaleoProPhyler: a reproducible pipeline for phylogenetic inference using ancient proteins. Peer Community Journal. 3, e112. [5] Reich, D., Thangaraj, K., Patterson, N., Price, A.L., Singh, L., 2009. Reconstructing Indian population history. Nature 461, 489–494.

Podium Presentation, Session 11, Saturday 13:50 – 15:30

Exploring the potential of histotaphonomy to assess the depositional context of animal and human Palaeolithic bone fragments

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Fragmented animal bones form the backbone of zooarchaeological and taphonomic studies, providing a wealth of macro-scale data on palaeoenvironment, site formation and subsistence. Additional data on depositional histories, including macroscopically invisible alterations such as bacterial bioerosion, can be obtained through the microscopic study of taphonomic alterations to the inner structure of bone, known as histotaphonomy [1]. Histotaphonomic characterisations have direct behavioural implications and can be used to assess whether bones entered the archaeological record butchered or fully fleshed (complete carcass burial or natural death) [1-3]. The integrated study of macro- and microscopic taphonomic features has the potential to provide new insights into site formation, subsistence practices, human burial and even cannibalism at Palaeolithic sites.

In a first step, we will present data from micro-CT scanning, hard tissue histology and aDNA analysis of bone fragments from the Medieval site at Northgate cemetery, Canterbury [4]. This site provided a unique dataset allowing us to develop a workflow for the identification of bacterial bioerosion in human (burial, n=20) and animal (butchered, n=20) remains. We identified more intense bioerosion in the human bones, compared to animal remains. We confirmed these results through identification and categorisation of hard tissue histological thin sections. Next, we extracted aDNA from the human bones that displayed a bioerosion signal, both from bioeroded and normal bone regions. Some potential differences between these regions were observed, including the identification of DNA from Clostridium and Fictibacillus.

The second part of the talk presents a series of ongoing case studies in which we apply histotaphonomy to Palaeolithic bone assemblages. In general, the identification of bioerosion in micro-CT scans of animal and human remains from Palaeolithic contexts was site-dependent. At Ranis (Germany, n=50), evidence for bacterial bioerosion was limited. However, micro-CT scanning of both bone and micromorphological blocks from Bacho Kiro Cave (Bulgaria, n=20) and human and animal bones from Abri Moula (France, n=50) identified signatures consistent with bioerosion. At Moula these were identified on both human and animal material and provided novel data to further investigate Neanderthal cannibalism at the site [5].

Overall, our combined approach, using micro-CT, hard tissue histology and aDNA to study different taxa (human, carnivore, or herbivore) has the potential to add novel information about site formation and human behaviour during the Palaeolithic. Further work is required to more fully understand the specific factors affecting bacterial bioerosion within and across sites, and especially in Palaeolithic contexts. Further development and application of this method are therefore ongoing.

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References: [1] Brönnimann, D., Portmann, C., Pichler, S.L., Booth, T.J., Röder, B., Vach, W., Schibler, J., Rentzel, P., 2018. Contextualising the dead – Combining geoarchaeology and osteo-anthropology in a new multi-focus approach in bone histotaphonomy. Journal of Archaeological Science. 98, 45–58. [2] Fernández-Jalvo, Y., Andrews, P., Pesquero, D., Smith, C., Marín-Monfort, D., Sánchez, B., Geigl, E.-M., Alonso, A., 2010. Early bone diagenesis in temperate environments. Palaeogeography, Palaeoclimatology, Palaeoecology. 288, 62–81. [3] White, L., Booth, T.J., 2014. The origin of bacteria responsible for bioerosion to the internal bone microstructure: Results from experimentally-deposited pig carcasses. Forensic Science International. 239, 92–102. [4] Hicks, M. and Hicks, A., 2001. St Gregory's Priory, Northgate, Canterbury: Excavations 1988-1991 (Vol. 2). Canterbury Archaeological Trust Limited. [5] Defleur, A., White, T., Valensi, P., Slimak, L. and Cregut-Bonnoure, E., 1999. Neanderthal cannibalism at moula-guercy, ardèche, France. Science, 286, 128-131.

Podium Presentation, Session 8, Friday 15:20 – 17:00

The use and misuse of trace element patterns in hominin and nonhuman primate teeth

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Assessments of elemental chemistry in teeth often employ laser ablation-inductively coupled plasma-mass spectrometry (LA-ICP-MS) sampling of discontinuous spots or linear tracks, which may fail to distinguish between precise changes in body chemistry during tooth mineralization and diagenesis after burial. By contrast, mapping the entirety of sectioned tooth crowns and roots with LA-ICP-MS provides comprehensive longitudinal developmental records of dietary behavior, health, and neurotoxicant exposure [1]. These maps permit the comparison of spatial element patterns with developmental geometry in multiple tissues and across successive teeth, and reveal differential element-specific preservation and diagenesis [1-2]. This is possible because biogenic elemental geometry is consistent with secretory patterns evident under light microscopy [1], and can be distinguished from diagenetic alteration as the later often shows more localized diffuse patterns, particularly when multiple elements are considered in tandem [2-3].

Comprehensive dental analyses of captive and wild nonhuman primates, as well as human children with prospective nursing and health records, reveal nutritional and physiological experiences of individuals in unprecedented detail. The nonessential metals barium (Ba) and strontium (Sr) are now commonly assessed with LA-ICP-MS for insights into nursing and weaning behaviours, including in fossil hominins and living humans. While much remains to be understood about their natural bioavailability and gastrointestinal absorption, Ba is generally a more reliable indicator of the initiation of milk intake than Sr, rising and falling in parallel with nursing intensity and milk concentrations in captive macaque first molars as well as in first molars of baboons and humans. Calcium-normalized barium (Ba/Ca) shows more distinct zonation in tooth enamel than Sr/Ca, enabling the timing of behavioural changes from microscopic growth lines. This pattern of Ba/Ca distribution is not substantially altered by mineral incorporation after secretion, yielding the first precise ages for the cessation of nursing (weaning) in Neanderthals [2-3].

We have also detailed how developmentally-informed trace element mapping reveals concurrent physiological disruptions in captive macaques [1,4], which differ from broader circa-annual dietary banding patterns seen in wild orangutans [5]. Recent studies have inferred substantial nutritional stress in australopithecines based on the presence of prominent elemental bands formed repetitively over months, yet also inferred greatly reduced dietary diversity due to the absence of these bands in *Gigantopithecus blacki*, supposedly contributing to their extinction. Such studies fail to consider the more likely scenario of the variable consumption of foods containing bioavailable metals, as evident in wild baboon and chimpanzee dentitions. While trace element distributions offer a potent mechanism for understanding ancient behavior and health in the past, we encourage additional research on the concentrations of these metals in dietary items, as well as the pairing of complementary isotopic systems for confidence in inferences of seasonal behaviors and illnesses [2].

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References: [1] Smith, T.M., Cook, L., Dirks, W., Green, D.R., Austin, C., 2021. Teeth reveal juvenile diet, health and neurotoxicant exposure retrospectively: What biological rhythms and chemical records tell us. BioEssays: news and reviews in molecular, cellular and developmental biology. 43. e2000298 [2] Smith, T.M., Austin, C., Green, D.R., Joannes-Boyau, R., Bailey, S., Dumitriu, D., Fallon, S., Grün, R., James, H.F., Moncel, M.H., Williams, I.S., Wood, R., Arora, M., 2018. Wintertime stress, nursing, and lead exposure in Neanderthal children. Science Advances. 4, eaau9483. [3] Austin, C., Smith, T.M., Bradman, A., Hinde, K., Joannes-Boyau, R., Bishop, D., Hare, D.J., Doble, P., Eskenazi, B., Arora, M., 2013. Barium distributions in teeth reveal early-life dietary transitions in primates. Nature. 498, 216–219. [4] Austin, C., Smith, T.M., Farahani, R.M.Z., Hinde, K., Carter, E.A., Lee, J., Lay, P.A., Kennedy, B.J., Sarrafpour, B., Wright, R.J., Wright, R.O., Arora, M., 2016. Uncovering system-specific stress signatures in primate teeth with multimodal imaging. Scientific Reports. 6, 18802. [5] Smith, T.M., Austin, C., Hinde, K., Vogel, E.R., Arora, M., 2017. Cyclical nursing patterns in wild orangutans. Science Advances. 3, e1601517.

Poster Presentation Number 104, Session 2, Friday 17:00 – 18:30

A revisit of site formation and chronology at the Middle Pleistocene hominin site Bilzingsleben

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Bilzingsleben is a well-known Middle Pleistocene site situated in the Thuringian Basin in Central Germany that was shown to preserve several hominin remains in association with cultural and a large number of faunal remains. The hominin fossils were discovered in the 1970s and followed by extensive excavations by D. Mania from 1971-2002. Exacavations were then continued by the University of Jena from 2004 to 2007. Based mainly on field observations, Mania and Mania [1] interpretated the site as an in situ preserved hunting camp with huts and fireplaces formed during marine isotope stage (MIS) 11. This early interpretation of the site formation was critiqued based on a lack of empirical data. The new excavations by the University of Jena revealed that the finds were distributed through two distinct layers, a silty and a sandy find layer. Furthermore, reinvestigation of the faunal and lithic material from the site revealed limited human modification on the recovered faunal and non-flint material [2-3]. Fabric analysis of bone and rocks from the find layer (as they were defined by Mania but based on material from the 2004 to 2007 excavation) indicate natural site formation processes of the assemblage [4,5]. Such detailed fabric data is not available for the 1971-2002 excavations. Another critical aspect is the dating of the site, with a variety of ages presented thus far. Here, we present microcontextual analysis of the find-bearing sediments as well as numerical (luminescence and IR-RF) and relative (amino acid) dating of the sediments and embedded gastropods opercula respectively. Our chronological analyses suggest a deposition of the find-bearing sediments prior to MIS 9 and thus we provide further support for an association of the fossil and the few archaeological materials with MIS 11. Microcontextual analysis in concert with a detailed re-assessments of site formation using separate fabric analysis for the two find-bearing layers situate the site within a lacustrine setting with laterally variable relocated, clastic input in a setting influenced by nearby tufa formation. These observations agree with a model of only ephemeral hominin activities and the locally restricted relocation of their physical remains by natural processes.

This research project was supported by several institutions: the Max-Planck-Society for micromorphological analysis, luminescence and IR-RF measurements; a scholarship by the Federal State of Thuringia to TD for micropalaeontological investigations; renewed excavations from 2003 to 2007, their analysis and of rock material from the previous excavations were supported by the University of Jena and two DFG grants awarded to CP (project number 35388362 and 264889190); and the European Research Council ERC under the European Union's Horizon 2020 research and innovation programme (grant agreement No. 865222 - EQuaTe) awarded to KP for amino acid analyses.

References: [1] Mania, D., Mania, U., 2005. The natural and socio-cultural environment of *Homo erectus* at Bilzingsleben, Germany. In: Gamble, C., Porr, M. (Eds.), The Hominid Individual in Context. Archaeological Investigations of Lower and Middle Palaeolithic Landscapes, Locales and Artefacts. Routledge, London, pp. 98–114. [2] Bock, C., Neubeck, V., Pasda, C., 2017. Non-flint from the Middle Pleistocene site of Bilzingsleben (excavation from 1971 to 2002): Die Gesteine aus der mittelpleistozänen Fundstelle Bilzingsleben (Ausgrabungen 1971-2002). Quartär – Internationales Jahrbuch zur Erforschung des Eiszeitalters und der Steinzeit. 64, 7–25. [3] Brasser, M., 2017. Die Megafauna von Bilzingsleben, Veröffentlichungen des Landesamtes für Denkmalpflege und Archäologie Sachsen-Anhalt 73. Landesamtes für Denkmalpflege und Archäologie Sachsen-Anhalt, Halle (Saale). [4] Müller, W., Pasda, C., 2011. Site formation and faunal remains of the Middle Pleistocene site Bilzingsleben: Fundplatzgenese und Faunareste der mittelpleistozänen Fundstelle Bilzingsleben. Quartär – Internationales Jahrbuch zur Erforschung des Eiszeitalters und der Steinzeit. 58, 25–49. [5] Pasda, C., 2012. A study of rocks and flints from Bilzingsleben. Quartär - Internationales Jahrbuch zur Erforschung des Eiszeitalters und der Steinzeit 59, 7-40.

Podium Presentation, Session 9, Saturday 9:00–10:40

Cortical bone reflects signals of intrinsic hand muscles in *Homo sapiens* and *Pan troglodytes* across the metacarpus

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To improve our reconstructions of the manual behavioural capabilities of fossil hominins we need to fully grasp the functional disparities between the hands of humans and our closest living relatives, chimpanzees. Often soft tissues are overlooked, however, reconstructing the entire musculoskeletal system can provide novel insights into bone and joint functional morphology. However, both visualising and quantifying the many relevant soft and hard tissues simultaneously has proven challenging. Understanding muscle attachments and the biomechanical capacity of the hand musculature requires consideration of all muscles simultaneously, which is not possible when using traditional dissection [1-2] that is inherently destructive. This study employs a novel workflow to visualise muscles, and other relevant soft tissues, in 3D and *in silico*, alongside documenting muscle attachment anatomy, calculating muscle biomechanical potential, and then comparing these results to variation in whole bone cortical thickness and midshaft cross-sectional properties of the metacarpals.

Individual specimens of *Homo sapiens* (N=1) and *Pan troglodytes* (N=1) were fixed in standard anatomical position, stained with Lugol's iodine and μCT scanned at 50-62 μm. Muscles, tendons and bones were segmented in Avizo, and these data were used to describe and quantify muscle volumes, attachments and orientation vectors. Avizo Xfiber software was used to visualise individual muscle fascicles, and to calculate the force generating capacity of each muscle [3]. Moments of each muscle as well as muscles in aggregate act to effect movements about the trapeziometacarpal joint. Muscle attachment anatomy and biomechanical potentials were compared to cortical bone thickness distribution and cross-sectional properties of the metacarpals at 50% of bone length. Midshaft cross-sectional properties (I, J and Zpol) and cortical bone thickness of each metacarpal were calculated, mapped and visualised using Stradview software, and cortical thickness maps were generated from Morphomap [4]. Cross-sectional properties were scaled by bone length and cortical thickness maps by the average cortical thickness of each specimen.

Results show that human thenar and hypothenar muscles tend to be stronger and more mediolaterally oriented than those of the chimpanzee, and are capable of generating higher moments about the pollical bones. There are thicker cortices on the MC1 where muscles with larger PCSAs attach directly, especially those with more transverse fibers, for example the *Homo opponens pollicis*. The *Pan flexor pollicis brevis* and *adductor pollicis* also have large PCSAs, and attach directly to bone, with some degree of cortical thickening at these attachment sites. However, the *Homo adductor pollicis* also has a large PCSA compared to the *Pan* and other *Homo* muscles, but because it does not attach directly to bone, and as such, no causal association with cortical thickness can be inferred. Chimpanzees had thicker metacarpal cortical bone overall than the human, but with relatively smaller cross-sectional properties.

This research aims to visualise and directly test the relationship between muscle morphology, muscle attachment sites and cortical bone structure within the same individual. These results indicate that cortical bone may reflect muscle size and orientation, which suggests a potential new window into reconstruction of the manual behaviours of fossil hominins, however, to gain a better understanding future research will also focus on the incorporation of the extrinsic musculature.

We thank Callum Ross for providing the *Pan* specimen, the University of Missouri Gift of Body Program for the human donor, the staff of UTCT for scanning, and Taylor Mitchell for assistance. Research supported by the University of Missouri Research Council. This research was supported by the National Science Foundation [EAR 1631684 to Casey M. Holliday, BCS 0716244 & BCS 1551992 to Carol V. Ward].

References: [1] Diogo, R., Wood, B., 2012. Comparative anatomy and phylogeny of primate muscles and human evolution. Science Publishers, U.S. [2] Marzke, M.W., Marzke, R.F., Linscheid, R.L., Smutz, P., Steinberg, B., Reece, S., An, K.N., 1999. Chimpanzee thumb muscle cross sections, moment arms and potential torques, and comparisons with humans. American Journal of Physical Anthropology. 110, 163–178. [3] Sullivan, S.P., McGechie, F.R., Middleton, K.M., Holliday, C.M., 2019. 3D muscle architecture of the pectoral muscles of European starling (*Sturnus vulgaris*). Integrative Organismal Biology. 1, oby010. [4] Profico, A., Bondioli, L., Raia, P., O'Higgins, P., Marchi, D., 2021. Morphomap: An R package for long bone landmarking, cortical thickness, and cross-sectional geometry mapping. American Journal of Physical Anthropology. 174, 129–139.

Poster Presentation Number 105, Session 2, Friday 17:00 – 18:30

Digitising and reconstructing the Upper Palaeolithic infant twin burial from Krems-Wachtberg

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After its discovery and recovery as a block in 2005, the 31,000-year-old Upper Palaeolithic twin burial from Krems-Wachtberg had been carefully excavated under laboratory conditions in 2015. Structured light 3D surface scans were produced to document this exposure. In a preceding pilot study, these surface scans were combined with the μCT images of individual skeletal elements to verify the practicability of this approach for a virtual reconstruction of the burial. So far, the left hand and parts of the skull of individual 2 were successfully reconstructed in three dimensions.

In the current project (project title: Digitising and reconstructing an Upper Palaeolithic infant twin burial from Krems-Wachtberg), μCT scans of all skeletal remains recovered from the double burial (grave 1) will be prepared. Although more than 500 skeletal elements and fragments as well as numerous tooth germs were listed during the excavation, many of these are poorly preserved and unsuitable for the reconstruction process due to structural alterations, taphonomic changes and their porosity; hence, only well-preserved and anatomically well-identifiable skeletal elements will be considered for the virtual reconstruction of the two newborns by means of surface registration. The μCT data will be provided in a database to make the data available to the scientific community and the general public. The current contribution aims to present and discuss the structure of this μCT data repository. Through the virtual reconstruction of the burial, we seek to understand taphonomic processes and deduce the chronology of activities in the context of the burial. In this way we attempt to shed light on ritual behaviours of early modern humans in Central Europe. Since the Krems-Wachtberg double infant burial provides the rare opportunity to study different aspects of neonate anatomy in ontogenetic and phylogenetic settings, the digital data produced in this study will lay the groundwork for further research.

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Podium Presentation, Session 9, Saturday 9:00–10:40

Spirals through time: evolutionary history of the modern human bony labyrinth

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The bony labyrinth inside the temporal bone houses the sensory organs of hearing and balance. It is fully formed before birth (in humans and most mammals) and remains unchanged through life. It can be studied even in ancient skeletal remains, making it an important source of evolutionary information, particularly when ancient DNA (aDNA) is not preserved. The shape of the bony labyrinth and the encasing temporal bone differ even between closely related groups: comparative analyses of linear dimensions [1] and geometric morphometrics have revealed, e.g., that the shape of the bony labyrinth can be used to distinguish between present-day humans, Upper Palaeolithic (UP) *Homo sapiens*, and Neanderthals. Moreover, within present-day humans the shape of the bony labyrinth carries a signal reflecting modern human dispersal out of Africa, likely because both the labyrinth and the temporal bone show a neutral pattern of global variation, e.g. [2-3].

Previous studies of the bony labyrinth have often been limited by insufficient representation of global human diversity, particularly from sub-Saharan Africa. Here, we studied 417 individuals from 17 Holocene modern human groups and divers global regions, including all major parts of sub-Saharan Africa, as well as 12 Upper Palaeolithic *H. sapiens*, 21 Neandertals, and 9 early *H. sapiens*, some of them not analysed before. We first extracted the 3D surface of the bony labyrinth from μCT scans of isolated temporal bones or whole skulls (resolution 0.02-0.07 mm). We then quantified the shape of the bony labyrinth using geometric morphometrics based on landmarks and sliding curve semilandmarks in Avizo™ and Mathematica™ [4].

Principal component analysis of bony labyrinth shape confirms that Neanderthals are distinct from both recent and fossil *Homo sapiens*, whereas Holocene human groups show substantial overlap. Notably, variations along PC1 suggest a geographic gradient from sub-Saharan Africa to Indigenous American groups, predominantly linked to variations in cochlear coiling. Early *H. sapiens* fall within the variation of sub-Saharan African Holocene humans suggesting that Holocene shape variation of the labyrinth in individuals from sub-Saharan Africa may include the morphology of early *H. sapiens*. UP modern humans form a cluster in shape space that shows some characteristic differences from all other *H. sapiens* groups. Our shape data analyses are in line with genetic evidence showing that the bony labyrinth of sub-Saharan African groups (in particular of Later Stone Age Southern African hunter gatherers-herders) show the highest shape variance, while variance decreases as one moves geographically away from Africa (e.g. Polynesia and the Americas.)

Our findings demonstrate the importance of morphological evidence from the bony labyrinth to obtain a deeper understanding of the evolutionary trajectories of *Homo sapiens*, complementing genetic studies and as a primary source where aDNA is not available.

We thank all the curators of extant and fossil individuals. This research was supported by the Max Planck Society.

References: [1] Spoor, F., Hublin, J.-J., Braun, M., Zonneveld, F., 2003. The bony labyrinth of Neanderthals. Journal of Human Evolution. 44, 141–165. [2] Harvati, K., Weaver, T.D., 2006. Human cranial anatomy and the differential preservation of population history and climate signatures. The Anatomical Record Part A: Discoveries in Molecular, Cellular, and Evolutionary Biology. 288A, 1225–1233. [3] Ponce de León, M.S., Koesbardiati, T., Weissmann, J.D., Milella, M., Reyna-Blanco, C.S., Suwa, G., Kondo, O., Malaspinas, A.-S., White, T.D., Zollikofer, C.P.E., 2018. Human bony labyrinth is an indicator of population history and dispersal from Africa. Proceedings of the National Academy of Sciences. 115, 4128–4133. [4] Gunz, P., Ramsier, M., Kuhrig, M., Hublin, J., Spoor, F., 2012. The mammalian bony labyrinth reconsidered, introducing a comprehensive geometric morphometric approach. Journal of Anatomy. 220, 529–543.

Pecha Kucha Presentation, Session 7, Friday 13:30 – 15:00

The genetic history of the Vindija Neandertals

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Little is known about the fine-scale genetic history of Neandertals, or the population relationships within and between different Neandertal groups. Here, we screened 19 skeletal remains from Vindija Cave in Croatia for ancient DNA preservation, and detected Neandertal DNA in 15 of them. We present new genome-wide data from these specimens, directly dated to between 49,500 and 42,000 years cal. BP. Based on the carbon and nitrogen stable isotopic values, these individuals had similar diets with their protein intake derived primarily from terrestrial herbivores, consistent with other Late Neandertals across Europe. We used in-solution hybridisation captures of single-stranded DNA libraries [1] to obtain nuclear, mitochondrial and Y chromosome data, and found that these 15 specimens represented in total at least 11 individuals, nine of which were females. Based on their nuclear data, all of these Vindija Neandertals are more closely related to the Vindija33.19 Neandertal than they are to other Neandertals. We found a mother-daughter pair, with one of them having second degree relatedness to two other individuals [2], showing that at least some of these individuals lived around the same time. Compared to a group of Neandertals who lived ~60,000 years ago in the region of Chagyrskaya Cave in Siberia [3], the Vindija Neandertals show a high mitochondrial diversity that dates back to ~100,000 years ago and captures much of the diversity seen in other Late Neandertals from Europe. Using coalescent simulations, we show that the mitochondrial diversity of Vindija Neandertals is compatible with the population size estimates obtained from the high-coverage genome of Vindija33.19 [4], suggesting that these individuals stem from a single population. Consistent with the high mitochondrial diversity, one of the specimens, Vindija33.29, carries a Y chromosomal sequence which is more similar to the ~43,500-year-old Mezmaiskaya2 Neandertal from Southern Russia than to the ~45,330-year-old Spy94a Neandertal from Belgium [5]. The higher mitochondrial diversity found in Vindija and other western Neandertals is in stark contrast to the low diversity observed in Siberian Neandertals, suggesting that the level of genetic diversity of Neandertal populations was heterogeneous across Eurasia.

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References: [1] Gansauge, M.-T., Aximu-Petri, A., Nagel, S., Meyer, M., 2020. Manual and automated preparation of single-stranded DNA libraries for the sequencing of DNA from ancient biological remains and other sources of highly degraded DNA. Nature Protocols. 15, 2279–2300. [2] Popli, D., Peyrégne, S., Peter, B.M., 2023. KIN: a method to infer relatedness from low-coverage ancient DNA. Genome Biology. 24, 10. [3] Skov, L., Peyrégne, S., Popli, D., Iasi, L.N.M., Devièse, T., Slon, V., Zavala, E.I., Hajdinjak, M., Sümer, A.P., Grote, S., Bossoms Mesa, A., López Herráez, D., Nickel, B., Nagel, S., Richter, J., Essel, E., Gansauge, M., Schmidt, A., Korlević, P., Comeskey, D., Derevianko, A.P., Kharevich, A., Markin, S.V., Talamo, S., Douka, K., Krajcarz, M.T., Roberts, R.G., Higham, T., Viola, B., Krivoshapkin, A.I., Kolobova, K.A., Kelso, J., Meyer, M., Pääbo, S., Peter, B.M., 2022. Genetic insights into the social organization of Neanderthals. Nature. 610, 519–525. [4] Prüfer, K., de Filippo, C., Grote, S., Mafessoni, F., Korlević, P., Hajdinjak, M., Vernot, B., Skov, L., Hsieh, P., Peyrégne, S., Reher, D., Hopfe, C., Nagel, S., Maricic, T., Fu, Q., Theunert, C., Rogers, R., Skoglund, P., Chintalapati, M., Dannemann, M., Nelson, B.J., Key, F.M., Rudan, P., Kućan, Ž., Gušić, I., Golovanova, L.V., Doronichev, V.B., Patterson, N., Reich, D., Eichler, E.E., Slatkin, M., Schierup, M.H., Andrés, A.M., Kelso, J., Meyer, M., Pääbo, S., 2017. A high-coverage Neandertal genome from Vindija Cave in Croatia. Science. 358, 655–658. [5] Petr, M., Hajdinjak, M., Fu, Q., Essel, E., Rougier, H., Crevecoeur, I., Semal, P., Golovanova, L.V., Doronichev, V.B., Lalueza-Fox, C., de la Rasilla, M., Rosas, A., Shunkov, M.V., Kozlikin, M.B., Derevianko, A.P., Vernot, B., Meyer, M., Kelso, J., 2020. The evolutionary history of Neanderthal and Denisovan Y chromosomes. Science. 369, 1653–1656.

Poster Presentation Number 106, Session 2, Friday 17:00 – 18:30

Postnatal cortical bone restructuring in chimpanzees and modern humans during locomotor development

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As our closest living relative, chimpanzees, provides an important comparative role when considering the reconstruction and interpretation of life history traits in extinct hominins. The amount and distribution of cortical bone of long bones changes throughout life and is highly influenced by multiple factors including genetics, hormonal status, and a changing mechanical environment [1]. As both humans and chimpanzees are behaviourally altricial, the first few years following birth are characterised by distinct shifts in locomotor behaviours and loading regimes prior to the adoption of adultlike locomotion. From a non-mobile state at birth, humans transition from a range of postural and locomotor behaviours such as crawling and standing to eventually walking bipedally [2], while chimpanzees engage mostly in suspensory and arboreal behaviours prior to becoming increasingly terrestrial knuckle-walkers [3]. Yet, with notable differences in locomotor specialism and anatomy, it is not clear whether chimpanzees undergo a similar pattern of development of cortical bone structure to humans or how these may differ in terms of timing. Here, we aim to compare developmental trajectories of femoral cortical bone structure in chimpanzees and humans during growth and locomotor development.

Cortical bone structure was examined in an archaeological sample of humans aged between birth and 14 years (N=98) and a sample of wild western chimpanzees (*P. t. verus*) aged from 2 weeks to 13 years (N=20), with most of the sample being of known age and sex. Unfused femora were micro-CT scanned and diaphyseal cross-sections were extracted at 50% of total intermetaphseal length. Outlines approximating the sub-periosteal and endocortical borders were automatically generated and cross-sectional area (cortical area, medullary area and total area), shape (Ix/Iy) and intracortical porosity metrics were recorded.

The results reveal both similarities and differences in the structural properties of cortical bone between the two groups. The relative amount of cortical porosity in chimpanzees was shown to closely follow the human trend, which is defined by a sharp increase during the first year, followed by a rapid decline and stabilization with increasing age suggesting a transient period of porosity during infancy in both species. Both humans and chimpanzees present an expansion of relative medullary cavity area during early growth followed by a stabilization. Chimpanzee values are initially higher than humans and exhibit a smaller increase in relative medullary area and a later age of stabilisation likely reflecting differences in the age of commencement of knuckle-walking in chimpanzees at 2 years and independent walking in humans at 1 year. Diaphyseal shape presented two very different ontogenetic trends, which likely reflect differences in locomotor mode and behavioural development. Humans demonstrate an increase in mediolateral reinforcement during the first 2 years which becomes progressively more anteroposterior shaped with increasing age and bipedal proficiency. In contrast, chimpanzees are born with a slightly anteroposterior shaped diaphysis which becomes consistently more mediolaterally reinforced with age. The amount of variation in Ix/Iy values, particularly in older subadults with mature locomotion, is notably higher in humans than chimpanzees and may result from a greater variability in both the amount and type of physical activity between individuals due to social influences.

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References: [1] Seeman, E., 2008. Bone quality: the material and structural basis of bone strength. Journal of Bone and Mineral Metabolism. 26, 1-8. [2] Swan, K. R., Ives, R., Wilson, L. A. B., Humphrey, L. T., 2020. Ontogenetic changes in femoral cross-sectional geometry during childhood locomotor development. American Journal of Physical Anthropology. 173, 80-95. [3] Doran, D. M., 1992. The ontogeny of chimpanzee and pygmy chimpanzee locomotor behavior: a case study of paedomorphism and its behavioral correlates. Journal of Human Evolution. 23, 139-157.

Podium Presentation, Session 5, Friday 8:30 – 10:10

Early evidence for prepared core technology ~760 Kyr at Nadung'a 13, West Turkana (Kenya)

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The emergence in the African archaeological record of prepared core technology (PCT) has historically been linked to the abandonment of the large, handheld (Mode 2) bifaces that are characteristic of the Early Stone Age (ESA) Acheulean industry, in favour of smaller flake-based Middle Stone Age (MSA) tools that are suitable for hafting (Mode 3). Dates for the ESA-MSA transition across the continent coalesce in the range ~400-200 ka, and map chronologically on to the anatomical appearance of *Homo sapiens* in the fossil record ~300 ka, implying that the roots of our species' cognition may be linked to this technological shift. However, an increasing corpus of evidence suggests some characteristic MSA behaviours including stone tool manufacture based on PCT may have accumulated gradually through the later Acheulean (~900-400 ka). This temporal span is therefore of significant interest as a potential source of the cognitive and behavioural changes underlying the evolution of *H. heidelbergensis*/archaic *H. sapiens* in the Middle Pleistocene.

The cognitive and behavioural importance of PCT lies in the fact that it involves the creation and maintenance of hierarchically organised core surfaces, and extended *chaînes opératoires* that necessitate significantly increased planning depth. The removal of products of a predictable size and shape is often contingent upon one or more skilful final strikes that are themselves a delayed return on effort. On a global scale, the earliest widely accepted evidence for PCT now comes from Canteen Kopje (1.1-0.8 Ma) in South Africa, Gesher Benot Ya'aqov in Israel (700 ka) and the Kapthurin Formation (~400 ka) in Kenya. In each of these cases, hominin knappers used prepared methods to make very large cores and flake blanks as part of a technological trajectory directly related to Acheulean biface manufacture (Mode 2).

Here we report new evidence from the ~760 ka site of Nadung'a 13 (West Turkana, Kenya) which reveals the early adoption of well-elaborated PCT reduction that was directed toward the production of small flakes that are reminiscent of the MSA (Mode 3). Refitting sets attest to their manufacture on-site and alongside - but unrelated to - the production of larger bifaces. We present a refined geological and chronostratigraphic assessment of the Nadung'a site complex, followed by the analysis of the 1101 *in situ* artefact assemblage. We foreground evidence for the co-existence of biface and PCT reduction as distinctive technological strategies and discuss the implications for the evolution of Middle Pleistocene hominin cognition and definitions of the ESA-MSA transition.

Podium Presentation, Session 6, Friday 10:30 – 12:10

All grown up: the adult Turkana boy pelvis and its implications for the taxonomic assignation of East African Early Pleistocene hominins

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Since its discovery in 1984, the skeleton of the juvenile *H. erectus* specimen KNM-WT 15000 (also known as 'Turkana boy') has provided valuable insights into the body shape of this species. However, its pelvic morphology is enigmatic due to its fragmentary nature and the fact that it represents a subadult individual with pelvic bones still not fully fused. Multiple reconstructions of its pelvis using different methodologies have been attempted, often yielding different interpretations. For instance, the initial reconstruction suggested a narrow pelvis similar to that of modern humans [1], while the most recent one indicated a wide bi-iliac breadth and marked iliac flaring also present in other early *Homo* pelves [2]. In this regard, the adult pelvic morphology of this specimen could shed light on the uncertain taxonomic attribution of other East African Early Pleistocene specimens without associated craniodental remains (e.g., KNM-ER 3228, OH 28). However, its adult pelvic morphology remains unknown because this individual died at an estimated age of 8-15 years. For this reason, the aims of this work are 1) to predict the hypothetical male and female adult pelvic morphology of the Turkana boy specimen by performing simulations of sexual dimorphism and growth using the most recent pelvic reconstruction based on modern human samples, and 2) to compare the projected adult Turkana boy pelvis with the potential *H. erectus* hipbones KNM-ER 3228 and OH 28 [3-4] to contribute to the discussion of the taxonomic attribution of these specimens based on phenetic affinities.

We segmented >300 modern human CT scans aged from 8 to 47 years. Given the uncertainty surrounding the age-at-death estimates of KNM-WT 15000, we computed ontogenetic trajectories for growth simulations between the mean pelvic morphology of adult modern humans and the mean morphologies of our sample across hypothetical ages from 8 to 15 years, encompassing the possible age-at-death of the Turkana boy. For the female pelvic morphology simulation, we applied a sexual dimorphism vector based on modern humans of the same age to our Turkana boy reconstruction to generate a hypothetical "Turkana girl". Then, we grew this pelvis along a modern human female ontogenetic trajectory to simulate the adult female morphology of *Homo erectus*. This was compared then to three differently fragmentary fossils using different landmark configurations: 64 landmarks for the entire pelvic morphology, 23 landmarks for KNM-ER 3228 and 18 landmarks for OH 18.

Our analyses revealed that the size of our Turkana boy pelvis reconstruction corresponds best to a 13-year-old individual based on modern human standards. Assuming a similar growth rate in *H. erectus* as in modern humans, our results suggest that almost 90% of adult pelvic size had been reached when this individual died. Both the adult male and female pelvic morphologies are relatively wide and show marked iliac flaring. The projected adult female pelvic morphology also reveals an expanded birth canal, a relatively wider bi-acetabular breadth and a relatively wider sub-pubic angle compared to the male version. The adult male and female projections of the Turkana boy show phenetic affinities with KNM-ER 3228 and OH 28, respectively, especially in the exaggerated iliac flaring. However, the robust iliac pillar characterizing those specimens is not present in our projections, likely because our landmark configuration does not capture this feature. Interestingly, the differences between our Turkana boy projections and the morphologies of these fossils are not larger than the intra-specific variation shown by modern humans, although it would be interesting to include other potential *H. erectus* specimens such as the pelvis from Gona BSN49/P27 [5]. Our results warrant a broader appreciation for the degree of potential morphological variation within and across hominin species and has major implications for accurate taxonomic assignation.

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References: [1] Walker, A., Ruff, C., 1993. The reconstruction of the pelvis. In: Walker, A., Leakey, R. (Eds.), The Nariokotome *Homo erectus* Skeleton. Harvard University Press, Cambridge, MA, pp. 221e233. [2] Haeusler, M., Bonneau, N., Fornai, C., 2017. The morphology of the *Homo erectus* pelvis. Proceedings of the European Society for the Study of Human Evolution. 6:82. [3] Rose, M. D. (1984). A hominine hip bone, KNM-ER 3228, from East Lake Turkana, Kenya. American Journal of Physical Anthropology, 63, 371-378. [4] Ruff, C., 2010. Body size and body shape in early hominins–implications of the Gona pelvis. Journal of Human Evolution, 58, 166-178. [5] Simpson, S. W., Quade, J., Levin, N. E., Butler, R., Dupont-Nivet, G., Everett, M., Semaw, S., 2008. A female *Homo erectus* pelvis from Gona, Ethiopia. Science, 322, 1089-1092.

Poster Presentation Number 107, Session 2, Friday 17:00 – 18:30

Re-assessing toothpick grooves in fossil hominins: insights from a wild orangutan

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This study reassesses the interpretation of ´toothpick grooves´, non-carious cervical lesions (NCCLs) found commonly on the interproximal regions of posterior teeth in fossil hominins [1-2]. Today, almost universally, these grooves are considered indicative of tool use behaviour, for dental hygiene purposes or for alleviating discomfort associated with oral pathologies, supported by experimental studies [3]. In this study, we describe a wild orangutan (*Pongo pygmaeus*), curated at the Field Museum (Chicago, US), that exhibits a typical 'toothpick' groove on the mesial surface of a lower left second molar. This case provides a novel opportunity to reconsider these dental features not just as products of unique human cultural behaviour, but possibly also as outcomes of natural masticatory behaviours and dietary/environmental influences. Analyses of microscopic features of the orangutan root groove were undertaken, and dental tissue loss was estimated with an intraoral scanner. Comparisons with fossil *Homo* and archaeological human samples were then carried out. This includes NCCLs found in a variety of *Homo* species (*H. sapiens*, *H. neanderthalensis*, *H. heidelbergensis*, *H. erectus*, *H. antecessor* and *H. habilis*), and archaeological human samples from around the world (Americas, Australia, Africa and Eurasia). The orangutan case shows hallmark features of ´toothpick´ grooves, including buccal-lingual fine striations and a tapered profile from the buccal towards the lingual root surface, accompanied by a carious lesion beneath it. However, rather than toothpick-type behaviour to alleviate the discomfort associated with the carious lesion, this NCCL is likely caused by normal masticatory processes, supported by the presence of steep and severe wear on the adjacent first molar and associated periodontal disease. Such observations challenge the automatic attribution of similar grooves in fossil hominins to tool use, since if this tooth was found isolated in the fossil record a ´toothpick´ aetiology would likely have been proposed. Our findings invite a re-evaluation of the conventional understanding of toothpick grooves in fossil hominins, and support some earlier studies that suggested at least some of these interproximal root grooves may have a multifactorial aetiology, that does not always involve tool-use [4].

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References: [1] Estalrrich, A., Alarcón, J.A., Rosas, A., 2016. Evidence of toothpick groove formation in Neandertal anterior and posterior teeth. American Journal of Physical Anthropology. 162, 747–756. [2] Frayer, D.W., Russell, M.D., 1987. Artificial grooves on the Krapina Neanderthal teeth. American Journal of Physical Anthropology. 74, 393–405. [3] Hlusko, L.J., 2003. The oldest hominid habit? Experimental evidence for toothpicking with grass stalks. Current Anthropology. 44, 738–741. [4] Wallace, J.A., 1974. Approximal grooving of teeth. American Journal of Physical Anthropology. 40, 385–390.

Poster Presentation Number 108, Session 2, Friday 17:00 – 18:30

Microtomographic analysis of fossil dental tissue of Neanderthal in situ maxillary and mandibular teeth from Krapina (Croatia, 130 ka)

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Comparative morphometric analysis of the Neanderthal dentition has contributed significantly to our understanding of the biology and phylogenetic relationships of this extinct hominin taxon which displays a species-specific pattern of dental traits, in terms of both morphology and ontogeny. Specifically, enamel thickness and dental tissue proportions have been widely used traits in making taxonomic decisions and subsequent phylogenetic inferences among hominins and within the genus *Homo* [1-2]. This preliminary work presents results of volumetric analysis on a sample of 43 in situ permanent teeth from 5 mandibles and 3 maxillae, belonging to 8 different individuals from the site of Krapina (Croatia, 130 ka) [3]. The remains were discovered in 1899 AD and yielded, to date, the largest collection of fossils attributed to *H. neanderthalensis* from a single locality [4].

The fossil specimens were measured by X-ray computed microtomography (XμCT) at Elettra Synchrotron facility in Basovizza (Trieste, Italy) using the FAITH instrument equipped with a microfocus source. Volumes were reconstructed with pixel sizes of 35 μm and 55 μm, and subsequently partitioned by semi-automatic segmentation. A subsample (N=23) of unworn teeth were selected for dental tissue proportions (DTP) analysis. Following protocols previously reported in the literature, bucco-lingual diameters, coronal tissue volumes and topographic changes in enamel thickness were calculated [5]. The indices obtained were then compared with a large comparative set for Neanderthals obtained from the literature.

Preliminary results suggest considerable intra-population variability among the Krapina individuals and, in general, the average tooth dimensions exceed the average of the Neanderthal comparative set. In particular, the analysis of the maxillary and mandibular dentition reveals that almost all teeth analysed exhibit greater volume in the tissues' coronal portion and enamel, as well as a greater diameter. The relative enamel thickness also follows a similar pattern, although there are differences between the anterior and posterior maxillary dentition. This is due to the Krapina specimens having larger molars and premolars, but smaller incisors when compared to the Neanderthal average. This places the Croatian sample at the upper end of Neanderthal phenotypic variation, as well as substantially enriching the high-resolution digital documentation of Neanderthal fossil dental specimens. Furthermore, our preliminary results highlight the importance of integrated morphological analyses for the purpose of taxonomic inferences, as it is the "whole package" of anterior and posterior dental proportions that most strongly distinguishes the Krapina group from the rest of the Neanderthals. Finally, our findings seem to underscore a significant between-group variability in *H. neanderthalensis*, possibly the result of strong genetic isolation between groups, as extensively highlighted by recent aDNA research.

References: [1] Olejniczak, A.J., Smith, T.M., Feeney, R.N.M., Macchiarelli, R., Mazurier, A., Bondioli, L., Rosas, A., Fortea, J., de la Rasilla, M., Garcia-Tabernero, A., Radovčić, J., Skinner, M.M., Toussaint, M., Hublin, J.-J., 2008. Dental tissue proportions and enamel thickness in Neandertal and modern human molars. Journal of Human Evolution. 55, 12–23. [2] Macchiarelli, R., Bondioli, L., Debénath, A., Mazurier, A., Tournepiche, J.-F., Birch, W., Dean, M.C., 2006. How Neanderthal molar teeth grew. Nature. 444, 748–751. [3] Rink, W.J., Schwarcz, H.P., Smith, F.H., Radovĉiĉ, J., 1995. ESR ages for Krapina hominids. Nature. 378, 24–24. [4] Wolpoff, M.H., 1979. The Krapina dental remains. American Journal of Physical Anthropology. 50, 67–113. [5] Macchiarelli, R., Bayle, P., Bondioli, L., Mazurier, A., Zanolli, C., 2013. From outer to inner structural morphology in dental anthropology: integration of the third dimension in the visualization and quantitative analysis of fossil remains. In: Scott, G.R., Irish, J.D., (Eds.), Anthropological Perspectives on Tooth Morphology: Genetics, Evolution, Variation. Cambridge Studies in Biological and Evolutionary Anthropology. Cambridge University Press, Cambridge, pp. 250–277.

Podium Presentation, Session 9, Saturday 9:00–10:40

More than a deme: semicircular canal shape reveals local evolution in Neanderthal paleodemes

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Two main hypotheses have been proposed to explain the evolution of the derived Neanderthal cranial morphology, with some scholars arguing for a gradual emergence [1] and others proposing distinct phases [2]. However, several Middle Pleistocene specimens show an incipient Neanderthal morphology characterized by a mosaic of derived and primitive characters. Two Middle Pleistocene European fossils, Reilingen (Re) and Ehringsdorf H3 (EH3), retain several archaic characters shared with individuals from the Sima de los Huesos and Steinheim [3]. Nevertheless, Re and EH3 are considered more Neanderthal-derived than the Sima de los Huesos (SH) fossils, but still lack some derived features characteristic of Late Pleistocene Neanderthal [3-4].

We assessed the potential phylogenetic affinities of Re and EH3 by analyzing their semicircular canal and vestibule morphology using a deformation-based geometric morphometric method (diffeomorphometrics). This approach is a more powerful alternative than landmark-based geometric methods due to its ability to discriminate subtle changes in continuous morphological shapes [5]. The semicircular canal and vestibule of Re and EH3 individuals were compared to a fossil sample including SH humans (n=13), Krapina Neanderthals (Kr; n=10), and Eurasian Late Pleistocene Neanderthals (LN; n=9), as well as Upper Paleolithic (Cro-Magnon 1) and recent modern humans (RMH; n=18). The aligned, raw shape data was investigated using principal component analysis (PCA) to assess patterns of shape variation in the sample. Group classification accuracy and the group memberships for Re and EH3 were tested using a cluster analysis approach through a K-means unsupervised machine learning classification algorithm. For classification comparisons and verification, we also performed Neighbor-Joining (NJ) analyses on Mahalanobis (D^2) and Euclidean distance matrices between Re, EH3, and the comparative sample. D^2 was computed on PCA scores, whereas Euclidean distances were calculated from the raw shape data.

Our results highlight close morphological affinities between Re, EH3, and LN, particularly in the presence of an inferiorly positioned posterior canal, and a large, superiorly positioned lateral canal. Their semicircular canals are also more slender than in both SH and Kr. The SH sample shows an oval, latero-superiorly projecting posterior canal, and entirely overlaps with Kr in the morphospace. Our cluster analyses (D^2 and Euclidean distances) largely separated SH, Kr, LN, and RMH and grouped Re and EH3 with LN. SH individuals clustered separately from LN and Kr in both approaches, whereas Kr were either identified as a separated cluster or nested within LN as a single cluster. The K-means cluster analysis also accurately partitioned the known group clusters (94% classification accuracy) and classified both Re and EH3 as LN, reflecting small phenetic distances between these specimens and LN.

This study suggests that the bony labyrinth morphology in Re and EH3 is most similar to LN, indicating a stronger phenetic affinity with LN than previously considered, and implies that they might represent better candidates than Kr for the ancestral morphology to LN. The Kr sample instead appears rather primitive and may show features that evolved locally, suggesting that this sample represents a distinct deme within the Neanderthal lineage. The results of the present study support a mosaic pattern of evolution in Neanderthals and implies that a LN-like bony labyrinth emerged as early as 250 kya.

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References: [1] Hublin, J.J., 2009. The origin of Neandertals. Proceedings of the National Academy of Sciences. 106, 16022–16027. [2] Rosas, A., Bastir, M., Alarcón, J.A., 2019. Tempo and mode in the Neandertal evolutionary lineage: A structuralist approach to mandible variation. Quaternary Science Reviews. 217, 62–75. [3] Dean, D., Hublin, J.-J., Holloway, R., Ziegler, R., 1998. On the phylogenetic position of the pre-Neandertal specimen from Reilingen, Germany. Journal of Human Evolution. 34, 485–508. [4] Tattersall, I., Schwartz, J.H., 2006. The distinctiveness and systematic context of *Homo neanderthalensis*. Vertebrate Paleobiology and Paleoanthropology. 9–22. [5] Urciuoli, A., Zanolli, C., Almécija, S., Beaudet, A., Dumoncel, J., Morimoto, N., Nakatsukasa, M., Moyà-Solà, S., Begun, D.R., Alba, D.M., 2021. Reassessment of the phylogenetic relationships of the late Miocene apes *Hispanopithecus* and *Rudapithecus* based on vestibular morphology. Proceedings of the National Academy of Sciences. 118, e2015215118.

Poster Presentation Number 109, Session 2, Friday 17:00 – 18:30

Can scapular origin area predict rotator cuff muscle volume in hominoids?

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Humans are the only extant hominoid species in which the upper limb has no weight-bearing or propulsive function. While obligated bipedalism defines our species today, it is only a couple of million years old. Hominin forerunners are thought to have relied heavily on the shoulder and upper limb for vertical climbing and arm-swinging when navigating arboreal environments [1]. These locomotor modes are still employed to different degrees in extant hominoids. As climbing is functionally demanding, especially for the largest-bodied apes, there is a common understanding that all non-human hominoids possess adaptations to arboreal locomotion in their musculoskeletal morphology. However, the precise nature of these adaptations in the hominoid shoulder is still shrouded in mystery.

Previous research investigating climbing adaptations in non-human hominoids has focused on the identification of advantageous traits in skeletal and muscle morphology. Great emphasis was put on certain skeletal traits in the scapula, which distinguish extant humans from non-human apes. These include the relative sizes of the scapular fossa areas, with the supraspinous fossa being generally greater in apes compared to humans [2]. These fossae constitute the origin sites of the rotator cuff muscles, which are important to counteract the forces applied on the shoulder during arm-swinging. However, past studies were unsuccessful in establishing direct correlations between fossa size and muscle volume [3].

This study aims to bridge these knowledge gaps by investigating the link between shoulder musculoskeletal morphology and locomotor behaviour in the Hominoidea. Using virtual 3D reconstructions of bones (from CT) and muscles (from surface scans), we estimate functionally and biomechanically relevant parameters of the rotator cuff muscles, including length, volume and attachment area [4]. The focus hereby lies on the conclusions that can be drawn from single bones, such as predicting muscle volume from attachment area, to enhance functional interpretations of the fossil record. By comparing these parameters across hominoid genera, our study aims to encompass a wide range of shape and locomotor variations.

Through this interspecific comparison we aim to provide valuable insights into hominoid evolution and contribute to our understanding of the functional morphology of the primate shoulder complex. The findings also have broader implications for biomechanics and biological anthropology, and will contribute to an evidence-based interpretation of the hominin fossil record.

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References: [1] Larson, S.G., 2013. Shoulder morphology in early Hominin evolution. In: Reed, K., Fleagle, J., Leakey, R. (Eds) The Paleobiology of *Australopithecus*. Vertebrate Paleobiology and Paleoanthropology. Springer, Dordrecht, pp. 247–261. [2] Bello-Hellegouarch, G., Potau, J.M., Arias-Martorell, J., Pastor, J.F., Pérez-Pérez, A., 2013. A comparison of qualitative and quantitative methodological approaches to characterizing the dorsal side of the scapula in Hominoidea and its relationship to locomotion. International Journal of Primatology. 34, 315–336. [3] Larson, S.G., Stern, J.T., 2013. Rotator cuff muscle function and its relation to scapular morphology in apes. Journal of Human Evolution. 65, 391–403. [4] Eigen, L., Nyakatura, J.A., 2021. Architectural properties of the musculoskeletal system in the shoulder of two callitrichid primate species derived from virtual dissection. Primates. 62, 827–843.

Poster Presentation Number 110, Session 2, Friday 17:00 – 18:30

Advanced radiocarbon dating methods for palaeolithic samples in new pre-treatment laboratory at the University of Vienna

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Bone collagen is one of the most used materials for radiocarbon dating of archaeological contexts, but also one of the most challenging ones. Rigorous pretreatment protocols are required to remove all possible contamination and obtain an accurate age, which is especially acute when dating complicated (i.e. contaminated) samples that are in age close to the limit of the method. In our new laboratory at the University of Vienna, we have been chemically pretreating samples since the start of 2023. Our standard protocol for bone collagen focuses on using the ultrafiltration method after Higham et al. [1] and Brock et al. [2]. In addition, we have also developed further a method of purifying bone collagen amino acids using an XAD-2 resin approach. We quantified the background limit for these methods using repeat dates of a mammoth bone standard (the "Hollis" bone) which comes from a >50,000 year old specimen. The collagen blanks from this standard are consistently in the range of ~50,000 BP (with an error of <1%), for both ultrafiltered and non-ultrafiltered bone collagen samples. For the XAD method our Hollis bone collagen blank yields ages of 45-46,000 BP. We are currently working to get even lower blank values.

The XAD method enables us to process, in a reliable manner without compromising on sample size, challenging old and contaminated samples, whether this contamination originates from the burial environment (e.g. humic acids) or conservation treatments (e.g. glues and consolidants). Crosslinked contaminants are known to affect ^{14}C ages, because these are often not effectively removed through the traditional ABA chemistry with ultrafiltration, and a hydrolysis step is required to release this contamination from the collagen. We combust and graphitise our samples at the VERA (Vienna Environmental Research Accelerator) AMS facility in Vienna, and measure AMS samples there and at the Keck AMS facility, University of California at Irvine. We will outline the XAD setup implemented in the laboratory and present the ^{14}C results of standards and blanks, as well as contaminated bone samples analysed using both ultrafiltration and the XAD treatment.

References: [1] Higham, T.F.G., Jacobi, R.M., Ramsey, C.B., 2006. AMS Radiocarbon Dating of Ancient Bone Using Ultrafiltration. Radiocarbon. 48, 179-195. [2] Brock, F., Higham, T., Ditchfield, P., Ramsey, C.B., 2010. Current pretreatment methods for AMS radiocarbon dating at the Oxford Radiocarbon Accelerator Unit (Orau). Radiocarbon. 52, 103-112.

Poster Presentation Number 111, Session 2, Friday 17:00 – 18:30

Piercing wounds or blunt force trauma: testing the efficacy of different hafting configurations

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A variety of lithic technocomplexes across Europe and Africa contains semi-circular backed artefacts variously termed crescents, lunates or segments and often interpreted as functioning as part of projectile weapons. Here, we focus on the backed segments characteristic of the southern African Howiesons Poort technocomplex (~65–60 ka; [1]). Based on use-trace evidence, they have been interpreted as arrowheads, yet various hafting configurations have been proposed (e.g. [2]). We decided to experimentally compare the efficacy of penetration and the amount of damage caused by two of the proposed hafting configurations. For our experimental lithic tools, we base ourselves on the segments from the Howiesons Poort phase of Umhlatuzana rockshelter (KwaZulu-Natal, South Africa). This site has yielded quartz segments interpreted as arrowheads [3] and is the focus of ongoing research of one of us (see e.g. [4]). We use the dimensions of the quartz segments recorded by Lombard [2] from the site.

We commissioned arrows, tipped with segments in flint replicating the dimensions of the quartz backed segments from Umhlatuzana. We compared two different hafting configurations, transversal and oblique (with the segment angle ~45°). We used an installation to ensure uniformly drawing the bow for the different shots and shot the arrows into a gelatine block. We measured if there is a difference between these hafting configurations in penetration depth and size of entry and exit wounds. Our results show that transversally hafted arrows penetrate much better than obliquely hafted arrows. The size of entry and exit wounds shows more variation, but on balance, transversally hafted arrows appear to create larger wounds. Our results confirm observations in earlier experiments not specifically aimed to record penetration effectivity (e.g. [5]), but more realistic conditions with arrows needing to penetrate animal hide are needed to confirm the results.

We thank Dr. Morgan Roussel for producing the arrows for the experiment and Dr. Paul Kozowyk for the use of and assistance with his arrow shooting equipment. The experimental materials were funded by NWO Vidi grant 276-60-004 to Dusseldorp.

References: [1] Lombard, M., Bradfield, J., Caruana, M.V., Makhubela, T., Dusseldorp, G.L., Kramers, J.D., Wurz, S., 2022. The South African Stone Age updated (II). South African Archaeological Bulletin 77, 172-177. [2] Lombard, M., 2020. Testing for poisoned arrows in the Middle Stone Age: A tip cross-sectional analysis of backed microliths from southern Africa. Journal of Archaeological Science: Reports. 34, 102630.[3] Lombard, M., Phillipson, L., 2010. Indications of bow and stone-tipped arrow use 64 000 years ago in KwaZulu-Natal, South Africa. Antiquity. 84, 635–648. [4] Sifogeorgaki, I., Klinkenberg, V., Esteban, I., Murungi, M., Carr, A.S., van den Brink, V.B., Dusseldorp, G.L., 2020. New Excavations at Umhlatuzana Rockshelter, KwaZulu-Natal, South Africa: a Stratigraphic and Taphonomic Evaluation. African Archaeological Review. 37, 551–578. [5] Goldstein, S.T., Shaffer, C.M., 2016. Experimental and archaeological investigations of backed microlith function among Mid-to-Late Holocene herders in southwestern Kenya. Archaeological and Anthropological Sciences. 9, 1767–1788.

Poster Presentation Number 112, Session 2, Friday 17:00 – 18:30

Perspectives on possible and probable *Paranthropus* pelves

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Until now, there has never been a full reconstruction of a *Paranthropus* os coxae, owing to the crushed and incomplete pelvic fossils of this genus. While this genus is found in both eastern and southern Africa, the hipbone fossils most clearly associated with it are attributed to the South African hominin, *P. robustus*. These pelvic remains are represented by fossils from multiple sites, with most preserving some aspects of the ilium and ischium. However, most are also crushed or deformed with almost no preservation of the ischiopubic region, making reconstruction of this species' pelvic anatomy a challenge that has thus far been unsurmountable.

This state of preservation is particularly unfortunate given the debate over the taxonomy of the eastern African fossil, BSN49/P27. This nearly complete pelvis was found in isolation in the Busidima formation at Gona, Ethiopia. Initial analysis attributed it to *Homo erectus* [1]; however, Ruff [2] suggested that based on its seemingly small body size, it might instead be the contemporaneous and smaller bodied *P. boisei*. It is difficult to test the hypothesis that the Busidima pelvis is *Paranthropus* without knowing what a *Paranthropus* pelvis looks like.

To address the issue of what a *Paranthropus* pelvis looks like, we sought to reconstruct the *P. robustus* os coxae, SK 3155b. This right partial hipbone preserves most of the iliac blade, a nearly complete acetabulum, and part of the ischial body. Brain et al. [3] refit the three recovered pieces that make up this fossil with minor displacement due to their close proximity in the breccia and lack of distortion. The anterior superior iliac spine was lost during excavation. We chose this fossil because it has the best preserved and undistorted iliac blade of the *P. robustus* pelvic fossils, which is required in our method. However, the SK 3155b iliac crest is not complete, so we used the measurements of the reconstruction presented in McHenry [4] to estimate the missing regions of the ilium, including the anterior superior iliac spine. We then reconstructed the ischiopubic region of SK 3155b using statistical shape modeling. This machine learning approach is used to predict absent morphology during surgeries reconstructing skeletal anatomy; here, we adapted it to predict hominin pelvic anatomy. Our version was based on samples of fully preserved human (*Homo sapiens*), chimpanzee (*Pan troglodytes*), and gorilla (*Gorilla gorilla*) ossa coxae. We previously validated that the method accurately predicts the most probable ischiopubic anatomy from preserved iliac landmarks in *Australopithecus africanus* (Sts 14; mean error = 2.1 mm) and *A. afarensis* (A.L. 288-1; mean error=1.7 mm).

Using the iliac landmarks and semilandmarks developed from the measurements in McHenry [4] and a 3D scan of the original fossil, we applied different versions of the statistical shape modeling to SK 3155b, which each predicted different ischiopubic anatomy. Since reconstructing incomplete fossils always includes some subjectivity, we decided it would be best to discuss multiple possible predicted reconstructions of the *Paranthropus* hipbone rather than focus on a single version. Here, we compare the anatomy of the different predicted ischiopubic regions for SK 3155b. Overall, all models predicted a relatively long pubis that is straight and oriented anteriorly, which may indicate a heart-shaped pelvic inlet. The different reconstructions varied in the length and robusticity of the superior pubic ramus, as well as the robusticity and curvature of the ischiopubic ramus. It is noteworthy that at least some of the reconstructions resembled the Busidima pelvis, with its fairly robust ischiopubic ramus, which means our results cannot reject the hypothesis that this pelvis is indeed *Paranthropus*.

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References: [1] Simpson, S.W., Quade, J., Levin, N.E., Butler, R., Dupont-Nivet, G., Everett, M., Semaw, S., 2008. A Female *Homo erectus* pelvis from Gona, Ethiopia. Science. 322, 1089–1092. [2] Ruff, C., 2010. Body size and body shape in early hominins – implications of the Gona pelvis. Journal of Human Evolution. 58, 166–178. [3] Brain, C.K., Vrba, E.S., Robinson, J.T., 1974. A New hominid innominate bone from Swartkrans. Annals of the Transvaaal Museum. 29, 55–63. [4] McHenry, H.M., 1975. A new pelvic fragment from Swartkrans and the relationship between the robust and gracile australopithecines. American Journal of Physical Anthropology. 43, 245–261.

Pecha Kucha Presentation, Session 7, Friday 13:30 – 15:00

Femoral cortical bone and cross-sectional properties in gorilla subspecies: implications for inferences regarding hominin locomotor behaviors

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Gorilla populations inhabit a range of high and low elevation environments and exhibit habitat-specific variation in locomotor behavior, likely reflecting differences in access to trees and climbing opportunities in different locations. The behavioral differences in closely related populations make gorillas a good model for studying how early hominin femoral morphology may track ecogeographic differences in locomotor behavior in closely related taxa. Here, we examine femoral diaphyseal cortical bone thickness distribution and cross-sectional properties (CA, MA, %CA, J, IxIy) across gorilla subspecies known to inhabit a range of environments.

Medical CT or micro-CT scans were obtained for 36 adult femora from three gorilla groups [lowland gorillas, *Gorilla gorilla gorilla* n=12; mountain gorillas, *Gorilla beringei beringei* n=10; grauer gorillas, *Gorilla beringei graueri* n=14, high elevation (majority) and low elevation]. A landmark-based automatic orientation was applied to align all femora in the same way and all diaphyses were automatically segmented to extract the cortical bone. In the R package *morphomap* [1], 180 cortical thicknesses were measured on 61 cross-sections extracted from distal (20%) to proximal (80%) of the femoral biomechanical length, and cortical thickness maps were produced for each individual and for the mean of each subspecies. Cross-sectional properties were calculated for each of the 61 slices. A body mass proxy was estimated from distal femoral articular M-L breadth, and data were size-standardized following standard methods [2]. Cortical bone thickness distribution among gorilla groups was analyzed by a principal component analysis and Bonferroni-adjusted MANOVA pairwise comparison tests were performed on PC1, PC2 and PC3 scores. Differences in selected cross-sectional properties among gorilla groups was evaluated through bivariate plots and BH-adjusted pairwise Wilcoxon comparison tests.

PCA results for PC1 and PC2 found overlap between all groups, with lowland gorillas being the most distinct from other groups. Mean maps of diaphyseal cortical bone for each gorilla group showed posterior thickening of the femoral diaphysis in both *G. beringei* subspecies, with posterior thickening not present in *G. gorilla.* Additionally, we found that the lateral portion became increasingly thickened proximally going from *G. gorilla* (lowland) to *G. b. graueri* (grauer) to *G. b. beringei* (mountain), potentially tracking changes in behavior across these groups. In cross-sectional geometry, *G. b. beringei* was found to exhibit higher femoral rigidity relative to body size than the other two groups, which is consistent with its greater terrestriality (increased loading of the hindlimb in quadrupedal locomotion than in arboreality). Ix/Iy (A-P/M-L bending rigidity) showed statistically significant differences between *G. gorilla* and *G. b. beringei.* Overall, differences in the cortical bone distribution and cross-sectional geometry of the femoral diaphysis appear to be aligning with behavioral differences between the gorilla groups, providing evidence for behavioral effects on internal morphology of the femur. Furthermore, these differences are found predominantly from about midshaft towards the proximal end of the diaphysis and less so in the distal end. This location is important for future research on the internal structure of hominin femora as several fossil hominin specimens preserve only the proximal end of the diaphysis [3].

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References: [1] Profico, A., Bondioli, L., Raia, P., O'Higgins, P., Marchi, D., 2020. morphomap: An R package for long bone landmarking, cortical thickness, and cross-sectional geometry mapping. American Journal of Physical Anthropology. 174, 129–139. [2] Ruff, C.B., 2019. Biomechanical analyses of archaeological human skeletons. In: Katzenberg, M.A. Grauer, A.L. (Eds.) Biological Anthropology of the Human Skeleton. John Wiley & Sons, Inc., pp. 189–224. [3] Grine, F.E., Mongle, C.S., Fleagle, J.G., Hammond, A.S., 2022. The taxonomic attribution of African hominin postcrania from the Miocene through the Pleistocene: Associations and assumptions. Journal of Human Evolution. 173, 103255.

Podium Presentation, Session 6, Friday 10:30 – 12:10

Homo habilis as prey: a taphonomic study of OH 7 using Artificial Intelligence tools

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Understanding carnivore-hominin interactions during Plio-Pleistocene has been one of the main questions addressed in taphonomic and archaeological research for years. Following the archaeological record, at least during the first half of the span of hominin evolution, hominins played a subordinate position with respect to large mammal carnivorans. However, at some point during the human evolution process this changed with a hominin shift in the balance of power. This change has been linked with the genus *Homo* and the irruption of this group in the predatory guild. On the other hand, the primary and regular hominin access to carcasses has been documented from ~2-million-year-old (Ma) anthropogenic sites at Olduvai Gorge (Tanzania) [1-2]. For years, *Homo habilis*, who is at the base of the genus *Homo*, has been proposed as the hominin responsible for the changes which lead to that shift in the balance of power between carnivores and hominins. Here, we analyze from a taphonomic perspective the holotype of *Homo habilis* to test if around 2 Ma ago a hominin shift in the balance of power occurred. In that case, it would be expected that the modifying agent of OH 7 was a scavenger instead of a felid carnivore. Determining the taphonomic agent responsible for the modification of OH 7 hominin remains is of utmost relevance for understanding this issue. In the taphonomic analysis of OH 7 tooth marks Artificial Intelligence (AI) tools through Deep Learning (DL) and Computer Vision (CV) methods have been used. In the recent few years, these tools have yielded high accuracy in the classification of Bone Surface Modifications (BSM) through the analysis of bidimensional images of these BSM [3-4]. The results obtained after the analyses of the two tooth pits documented on the OH 7 mandible show with high accuracy that OH 7 was modified and consumed by a felid, and specifically, by a leopard, shedding light on the role played by *Homo habilis* 2 Ma ago, if we understand OH 7 as representative of the species to which it belongs [5]. Taking these results into consideration, it can be proposed that *Homo habilis* would have been a prey instead of a predator as it has been assumed during years of research.

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References: [1] Domínguez-Rodrigo, M., Barba, R., Egeland, C. P., 2007. Deconstructing Olduvai: A Taphonomic Study of the Bed I Sites. Springer Netherlands. [2] Domínguez-Rodrigo, M., Baquedano, E., Organista, E., Cobo-Sánchez, L., Mabulla, A., Maskara, V., Gidna, A., Pizarro-Monzo, M., Aramendi, J., Galán, A.B., Cifuentes-Alcobendas, G., Vegara-Riquelme, M., Jiménez-García, B., Abellán, N., Barba, R., Uribelarrea, D., Martín-Perea, D., Diez-Martin, F., Maíllo-Fernández, J.M., Rodríguez-Hidalgo, A., Courtenay, L., Mora, R., Maté-González, M.A., González-Aguilera, D., 2021. Early Pleistocene faunivorous hominins were not kleptoparasitic, and this impacted the evolution of human anatomy and socio-ecology. Scientific Reports. 11, 16135. [3] Domínguez-Rodrigo, M., Cifuentes-Alcobendas, G., Jiménez-García, B., Abellán, N., Pizarro Monzo, M., Organista, E., Baquedano, E., 2020. Artificial intelligence provides greater accuracy in the classification of modern and ancient bone surface modifications. Scientific Reports. 10(1), 18862. [4] Domínguez-Rodrigo, M., Pizarro-Monzo, M., Cifuentes-Alcobendas, G., Vegara-Riquelme, M., Jiménez-García, B., Baquedano, E., 2024. Computer vision enables taxon-specific identification of African carnivore tooth marks on bone. Scientific Reports. 14, 6881. [5] Vegara-Riquelme, M., Baquedano, E., Domínguez-Rodrigo, M., under review, Early humans and the balance of power: *Homo habilis* as prey.

Poster Presentation Number 113, Session 2, Friday 17:00 – 18:30

Morphological patterns of middle meningeal vessels and dural venous sinuses in the individual from Zlatý Kůň (Czech Republic) and other Upper Paleolithic humans

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The middle meningeal artery, toghether with its parallel middle meningeal veins (here Middle Meningeal Vessels, MMV) and the dural venous sinuses (DVS), are located within the dura mater between the skull and the brain. They leave imprints on the endocranial surface of cranial vault bones due to intracranial pressure and constant process of bone modelling and remodelling. Thus, the traces of MMV and DVS can be studied in osteological samples in the context of biological, forensic, and evolutionary anthropology, providing information about physiological processes in individuals of past populations, evolutionary adaptations, and individual life history [1-2]. In this study, the vascular traces of MMV and DVS were evaluated in the 45,000 years old skull from Zlatý Kůň (Koněprusy caves, Czech Republic) [3-4], and then compared to MMV and DVS morphological patterns in Upper Palaeolithic and recent cranial samples. Additionally, differences in vascular patterns between the Upper Paleolithic and present-day populations were tested. The sample included Early Upper Paleolithic (EUP) (N=8) and Epipalaeolithic (N=105) crania, and a control sample of recent population from the Czech Republic (N=160). Vascular morphology was visualized through CT scans in 3DSlicer, following a previously established methodology [5]. Zlatý Kůň crania displayed traces of the MMV that were distributed in more posterior parts of the endocranial cavity and showed very high degree of reticulation of the vascular network. The DVS in Zlatý kůň had quite atypical pattern, in which the superior sagittal sinus runs into the right transverse sinus, quite far from the internal occipital protuberance, and also presented imprints of paired large occipital sinuses. Regarding the comparison of the Upper Paleolithic and recent samples, there were significant differences between the EUP, Epipalaeolithic and present-day samples in MMV pattern, but not in DVS pattern. However, all groups most frequently showed more developed MMV in the anterior region of the endocranial cavity and a complex branching pattern of the vascular network. The DVS pattern in all samples most often included the superior sagittal sinus running into the right transverse sinus, which was also most often larger than the left one. Traces of occipito-marginal sinuses were detected in few well-preserved crania of EUP, Epipalaeolithic, and recent crania, but the frequency was very similar in each group (50%, 42%, and 30% respectively). Globally, the vascular morphology of Zlatý kůň seems to be most similar to the EUP sample, which is in accordance with its estimated age, falling into EUP period. This study also provides further evidence that craniovascular features differed across the time and region.

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References: [1] Píšová, H., Rangel de Lazaro, G., Velemínský, P., Bruner, E. (2017). Craniovascular traits in anthropology and evolution: from bones to vessels. Journal of Anthropological Sciences, 95, 35–65. [2] Eisová, S., Píšová, H., Velemínský, P., Bruner, E., 2019. Normal craniovascular variation in two modern European adult populations. Journal of Anatomy. 235, 765–782. [3] Prüfer, K., Posth, C., Yu, H., Stoessel, A., Spyrou, M.A., Deviese, T., Mattonai, M., Ribechini, E., Higham, T., Velemínský, P., Brůžek, J., Krause, J., 2021. A genome sequence from a modern human skull over 45,000 years old from Zlatý kůň in Czechia. Nature Ecology & Evolution. 5, 820-825. [4] Rmoutilová, R., Guyomarc'h, P., Velemínský, P., Šefčáková, A., Samsel, M., Santos, F., Maureille, B., Brůžek, J., 2018. Virtual reconstruction of the Upper Palaeolithic skull from Zlatý Kůň, Czech Republic: Sex assessment and morphological affinity. PLOS ONE. 13, e0201431.
[5] Rangel de Lázaro, G., Eisová, S., Píšová, H., Bruner, E., 2018. The endocranial vascular system: tracing vessels. In Bruner, E., Ogihara, N., Tanabe, H. (Eds.), Digital endocasts, Springer, pp. 71–91.

Podium Presentation, Session 8, Friday 15:20 – 17:00

Reconstructing the tongue in the oral cavity. The first step towards application to fossils

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The emergence of the capacity for spoken language in humans during the course of evolution is a widely debated question. It has been renewed recently by the paradigm shift undermining Lieberman's 1960s theory of laryngeal descent, as studies have shown that non-human primates are capable of producing vocal tract shapes compatible with the articulation of speech sounds [1] and of pronouncing differentiated sounds covering a vowel spectrum similar to that of humans [2].

For fossil hominines, the complexity of this question lies in the difficulty of studying their phonatory apparatus due to the poor preservation. Soft tissues and cartilage do not fossilize, while bones can be damaged, deformed, or eroded. For this reason, the capacity for language in fossil hominins is often estimated indirectly, by considering that a faculty for abstraction is necessary, and by identifying tangible evidences of the latter in various productions (carved tools, burials, cave paintings...).

For the first time, we have attempted a direct approach, aiming to reconstruct the soft tissues making up the vocal apparatus, starting with the tongue. This work benefits from long-term research carried out at the TIMC & Gipsa-lab laboratories (University Grenoble Alpes, France), which has generated a fine model of the organs of the vocal apparatus in a present-day *Homo sapiens* used as a reference. This model accurately reflects the morphology and the constitutive behaviors of tongue soft tissue (including its muscular structures) and simulates tongue deformations due to muscles activations and/or to the mechanical interactions with the mandible, palate and hyoid bone.

Here, we present the results of the first stage of this project predicting the morphology of the missing tongue and surrounding soft tissues in the oropharyngeal cavity from the geometries of the skull, mandible, and vertebrae (i.e. based only on the bone structure). To test the effectiveness of our protocol, data from a Baboon head were used because of its significant morphological differences from humans. 3D CT images enabled us to consider only the bone structure to predict the tongue of this individual from one side and to control this prediction thanks the actual soft tissues from the other side. The method generates a geometric deformation field from the reference model to build up a 3D Finite Element mesh of the baboon tongue using mathematical tools combining rigid transformations (translations, homotheties, rotations) and non-rigid transformations (i.e. non-uniform over the entire volume, with localized refinements).

The results are very encouraging [3] and will allow us to consider an application to fossil hominins with two objectives: (1) constructing a biomechanical model of the predicted fossil tongue and its surrounding structures in the oral cavity, incorporating the muscles responsible for its movements and shaping; (2) using this model to evaluate the maximal movement magnitudes of the tongue in the antero-posterior and vertical dimensions, the range of variation of achievable vocal tract shapes, and the capacity of fossil hominins to maintain stable, differentiated tongue postures, providing a basis for the production of distinctive articulated sounds.

References: [1] Fitch, W.T., de Boer, B., Mathur, N., Ghazanfar, A.A., 2016. Monkey vocal tracts are speech-ready. Science Advances. 2, e1600723. [2] Boë, L.-J., Berthommier, F., Legou, T., Captier, G., Kemp, C., Sawallis, T.R., Becker, Y., Rey, A., Fagot, J., 2017. Evidence of a Vocalic Proto-System in the Baboon (Papio papio) Suggests Pre-Hominin Speech Precursors. PLOS ONE. 12, e0169321. [3] Fitch, W.T., de Boer, B., Mathur, N., Ghazanfar, A.A., 2016. Monkey vocal tracts are speech-ready. Science Advances. 2, e1600723

Podium Presentation, Session 3, Thursday 14:20 – 16:00

Were they eating meat? First nitrogen isotope data of *Paranthropus* and early *Homo* from Sterkfontein (South Africa)

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The dietary niches of extinct animals can be reconstructed using stable isotope ratios in diagenetically robust fossil tooth enamel. Herbivore stable carbon isotope ($\delta^{13}C_{enamel}$) values reflect dietary intake of plants and are used to differentiate grazers (C4-feeders) and browsers (C3-feeders) in African ecosystems. Carnivore δ^{13}Cenamel data indicate which type of prey (i.e., grazers, browsers, or mixed-feeders) were predominantly consumed. Nitrogen isotope ($\delta^{15}N_{enamel}$) values reveal information about the trophic position of an organism within its local food-web. Due to isotopic fractionation during metabolism, which results in an increase in $\delta^{15}N$ of the organism with respect to their diet, carnivore tissues are ca. 3 to 6‰ higher in $\delta^{15}N$ than the herbivore tissues they consume. The combination of $\delta^{13}C_{enamel}$ and $\delta^{15}N_{enamel}$ can therefore be used to reconstruct modern and past dietary patterns, food web structures, and the trophic position of an individual [1-2].

Previous analyses of mammalian tooth enamel from Pliocene Sterkfontein Member 4 fauna, including seven *Australopithecus* sp. individuals, show that *Australopithecus* $\delta^{15}N_{enamel}$ values vary greatly between individuals, but are consistently lower than sympatric carnivores. This suggests a variable, but largely plant-based diet for this group of Pliocene hominins. $\delta^{13}C_{enamel}$ from the same enamel indicates that C3 plants represented the greater part of this diet.

The Pleistocene hominin-bearing fossil Member 5 (~2.2 to 1.4 Ma) of Sterkfontein Cave, South Africa, have yielded a rich and diverse faunal assemblage, including *Paranthropus robustus* associated with Oldowan tools, and early *Homo* associated with Acheulean tools. We measured carbon and nitrogen stable isotope ratios in a single aliquot (~5 mg) of fossil tooth enamel of fauna (grazers, mixed-feeders, browsers, and carnivores), including hominins and other primates, from these deposits to expand our understanding of the trophic structure at Sterkfontein.

In herbivore taxa, $\delta^{13}C_{enamel}$ shows the expected separation between browsers, grazers, and mixed-feeders. Carnivore $\delta^{15}N_{enamel}$ values are significantly higher than the values of coexisting herbivores and show a trophic enrichment within the expected range of 3-6‰. The analysed fauna coexisted with our early ancestors and represent potential competitors and/or food sources, thus serving as an isotopic baseline for the interpretation of stable carbon and nitrogen isotope values of non-hominin and hominin primate tooth enamel from Sterkfontein Member 5.

We present the first nitrogen stable isotope measurements of fossil tooth enamel from *Paranthropus* and early *Homo* specimens and thus provide insights on the onset and intensification of animal resource consumption (or lack thereof) by our early ancestors at this locality. The presence of all three hominin genera (*Australopithecus*, *Paranthropus* and early *Homo*) at Sterkfontein makes this site exceptionally valuable for assessing potential changes in ancient food webs within Plio-Pleistocene faunal communities and permits examination of the dietary behaviour of our early ancestors over time within a single locality.

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References: [1] Leichliter, J., Lüdecke, T., Foreman, A., Bourgon, N., Duprey, N., Vonhof, H., Souksavatdy, V., Bacon, A.-M., Sigman, D., Tütken, T., Martinez-Garcia, A., 2023. Tooth enamel nitrogen isotope composition records trophic position: a tool for reconstructing food webs. Communications biology 6, 373. [2] Lüdecke, T., Leichliter, J.N., Aldeias, V., Bamford, M.K., Biro, D., Braun, D.R., Capelli, C., Cybulski, J.D., Duprey, N.N., Ferreira da Silva, M.J., Foreman, A.D., Habermann, J.M., Haug, G.H., Martínez, F.I., Mathe, J., Mulch, A., Sigman, D.M., Vonhof, H., Bobe, R., Carvalho, S., Martínez-García, A., 2022. Carbon, nitrogen, and oxygen stable isotopes in modern tooth enamel: A case study from Gorongosa National Park, central Mozambique. Frontiers in Ecology and Evolution. 10.

Poster Presentation Number 115, Session 2, Friday 17:00 – 18:30

The adaptive differentiation of paleontological material as a method for reconstructing phylogeny (Darwin's genealogical classification) in paleoanthropology

Sergey Vyrskiy[1]

1 - Independent

There is no common understanding of the phylogeny (or genealogy, according to Ch. Darwin) [1] of early bipedal primates in paleoanthropology. Despite a large number of cladograms, phylograms, and dendrograms published, they are mainly based on the similarity of the metric characteristics of the respective holotypes, and thus inevitably probabilistic in nature and often inconsistent with each other. The existing studies are focused on the relationship between species, while the connections between their respective genera are not taken into account. This contradicts the classification posited by C. Linnaeus which assigns the category of a genus to the initial form, while a species is a category of its current state, changed over time in response to various external conditions [2].

Methods

In phylogeny, a genus is understood to be equivalent to a species, though reproductively maternal to the one under study. Therefore, if we are to reconstruct the species system, what we need is a characteristic that would reflect the current state of the species and at the same time indicate its phyletic relationship with the parent one. It is hereby proposed to use adaptability to the environment as the sought-for characteristic. It encompasses a set of functional adaptive characters, both newly acquired and inherited from ancestors [3]. The proposed method consists of adaptive differentiation of the paleoanthropological material into sympatric reproductive lines which are further divided into intervals where sets of adaptive characters remain unchanged. This can be achieved, firstly, by studying the value fields of metric features of fossils. If any feature shows two fields of values on the paleontological scale, this will mean that the material includes individuals featuring dichotomously different adaptability to the environment. Therefore, such individuals can be distributed into different adaptive lines showing sympatric coexistence. Secondly, the medians of the value fields on these lines clearly indicate that they represent continuous piecewise linear functions which consist of linear intervals connected by changepoints. The linear part of the median, limited by two changepoints, points at constant sets of adaptive characters of its individuals and thus serves as a basic adaptive phyletic element of the phylogeny, which in the Darwin's genealogical classification can be assigned the category of an adaptive paleospecies. Each changepoint between two paleospecies establishes their mutual mother-filial hierarchy in the genealogical classification. If the said adaptive paleospecies are arranged as segments on a paleontological scale and form a hierarchy with their maternal species, then we can obtain a phylogenetic (genealogical) system of paleospecies.

Results

When applied to samples of African bipedal primates from 6.0-1.0 Mya deposits, the method of adaptive differentiation allowed us to construct a phylogenetic scheme that revealed the coexistence of two sympatric adaptive paleospecies. One of them became extinct 1.34 Mya, while the other died out 2.6 Mya having formed a filial paleospecies 2.5 Mya. In addition, extrapolation of the median lines of features into deeper sediments showed their possible origin from a certain hypothetical mother paleospecies that already had bipedalism in the interval of 9.0-8.0 Mya.

Conclusion

The proposed method of adaptive differentiation has proved efficient in reconstructing the phylogeny (Darwin's genealogical classification) of African bipedal primates from 6-1 Mya deposits. The method can be applied in other areas of paleontology. Moreover, further study of bipedal primates from deeper deposits will allow us to assess the predictive value of the proposed method.

References: [1] Darwin ChR (1859) On the origin of species by means of natural selection, or the preservation of favoured races in the struggle for life. London: John Murray, Albemarle Street.
[2] Linnaeus C (1751) Caroli Linnaei, Botanicorum Principis, Philosophia Botanica, Matriti: ex Typogr. Viduae, et Filii Petri Marin. Anno M.Dcc.Xcii. [3] Vyrskiy, S. 2021. Reconstruction of African Bipedal Primates' Phylogeny Based on the Adaptive Species Axiom. J Anthro & Archeo Sci 5(2). JAAS.MS.ID.000207. DOI: 10.32474/JAAS.2021.05.000207.

Poster Presentation Number 116, Session 2, Friday 17:00 – 18:30

Examining human-animal interaction of the Late Pleistocene and early Holocene in Zagros Mountains using ZooMS

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The Zagros Mountains, situated to the east of the Fertile Crescent, serve as a key locus for investigating Paleolithic economies and the origins of agriculture. Excavations at sites such as Ganj Dareh, Ali Kosh, and Sheikh-e Abad have yielded invaluable insights into Neolithic lifeways and the processes of animal and plant domestication.

Our comprehension of Stone Age economies undergoes continuous refinement with advancements in excavation techniques and zooarchaeological methodologies. Researchers have developed Zooarchaeology by Mass Spectrometry (ZooMS) as a new technique, offering a biomolecular approach to identifying faunal remains. The method is particularly adept at identifying previously unidentifiable bones that contain collagen. The method has numerous applications in Paleolithic and Neolithic contexts. In the deep deposits characteristic of the aceramic Neolithic sites in the Zagros like Chogha Golan, roughly 3% of the faunal remains could be identified using morphological criteria, hindering interpretations that rely on changes in species representation and relative abundances [1]. Similarly, ZooMS can help to augment our knowledge of Paleolithic economies at sites like Ghar-e Boof [2]. Furthermore, ZooMS analyses have revealed that classifications of body sizes of unidentifiable bones can be problematic [3], particularly in regions like the Zagros where gazelles, cervids and caprines share similar body sizes. Given that changes in body size can serve as proxies for domestication, the application of ZooMS in this context holds promise for enhancing our understanding the dynamics of animal domestication.

While a successful ZooMS attempt has been reported at the Neolithic open-air site in Iran [4], another endeavour in the Zagros Initial Upper Paleolithic Palaeolithic proved unsuccessful [5]. More studies in Paleolithic contexts are needed to check the utility of the ZooMS in the Zagros region. Recent strides in high-throughput protocols present renewed opportunities for large-scale ZooMS analyses. By integrating ZooMS taxonomic identifications with morphometric data, we can trace nuanced morphological changes and elucidate site-specific patterns of human-animal interaction and refine our understanding of faunal dynamics during the Late Pleistocene and early Holocene.

We thank the team of Tübingen-Iranian Stone Age Research Project (TISARP) and the Iranian colleagues, for their support during fieldwork.

References: [1] Starkovich, B.M., Riehl, S., Zeidi, M. and Conard, N.J., 2016. Subsistence strategies in the aceramic Neolithic at Chogha Golan, Iran. Bones and Identity Zooarchaeological Approaches to Reconstructing Social and Cultural Landscapes in Southwest Asia. 45-71. [2] Mata-González, M., Starkovich, B.M., Zeidi, M., Conard, N.J., 2022. New zooarchaeological perspectives on the early Upper Paleolithic Rostamian sequence of Ghar-e Boof (southern Zagros Mountains, Iran). Quaternary Science Reviews. 279, 107350. [3] Torres-Iglesias, L., Marín-Arroyo, A.B., Welker, F., de la Rasilla, M., 2024. Using ZooMS to assess archaeozoological insights and unravel human subsistence behaviour at La Viña rock shelter (northern Iberia). Journal of Archaeological Science. 161, 105904. [4] Seabrook, M., 2024. Balancing methods of Caprine identification: integrating morphological and zooms analyses. Available at SSRN: https://ssrn.com/abstract=4792693 [5] Shoaee, M.J., Vahdati Nasab, H., Storozum, M., Frenzel, P., Akhavan Kharazian, M., Fernandes, R., Hashemi, S.M., Jayez, M., Amano, N., Marzban Abbasabadi, B., Aalipoor, M., Lucas, M., Marzo, S., Ilgner, J., Patalano, R., Roberts, P., Boivin, N., Petraglia, M., 2024. Initial Upper Paleolithic in the Zagros Mountains. Frontiers in Earth Science. 12.

Pecha Kucha Presentation, Session 2, Thursday 11:20 – 12:50

Hip hip hooray! A complete virtual reconstruction of Sterkfontein's Sts 65 hipbone

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The adult Sts 65 hipbone from Member 4 of Sterkfontein, South Africa, presents a nearly undistorted right ilium and partial superior pubic ramus, as well as a fragment of the iliac crest. It has been dated to between ca. 2.6 – 2.1 million years and is attributed to *Australopithecus africanus*. Due to its fragmentary preservation, Sts 65 is among one of the most understudied hominin hipbones. In terms of size, it appears to be intermediate between the other pelvic remains recovered from Sterkfontein; specifically, the subadult Sts 14 and the StW 431 pelvis, a presumed female and male respectively. Based on the acetabulum size of Sts 65, a body mass 20-30% larger than that of Sts 14 has been estimated, whereas the inferred body mass of StW 431 is about 80% larger than Sts 14 [1]. Due to a possibly narrower greater sciatic notch and increased robusticity, Sts 65 was originally classified as male [2], although the true shape of the greater sciatic notch cannot be reliably inferred due to its preservation state. A faint depression in the preauricular region has also been interpreted as a preauricular sulcus, a characteristic usually found in females, which initiated a subsequent obstetric analysis of the Sts 65 birth canal [3]. However, this depression could alternatively represent a paraglenoid groove which would then be characteristic of males [4]. Contextualizing the enigmatic morphology of Sts 65 is therefore important given the aforementioned morphological inconsistencies and the recent claims of notable locomotor and taxonomic diversity at Sterkfontein [1,4-5].

Here we perform a novel virtual reconstruction of the right Sts 65 hipbone to assess the shape of the greater sciatic notch and the size disparity as well as to re-evaluate its taxonomic status. To approximate missing regions, a thin plate spline extrapolation method was performed utilizing different configurations of homologous landmarks using Sts 14 and StW 431 as reference warping templates. To optimize alignment between the target and various reference meshes, Sts 14 was scaled up by 8% to accommodate the size discrepancy between them, which is in accordance with previous suggestions of a significantly larger body size in Sts 65 [4].

In contrast to previous interpretations [3], our results demonstrate that the superior pubic ramus is incomplete, indicating a significant elongation of the pubis, which corresponds with aspects of the morphology observed in Sts 14. We also found that the greater sciatic notch forms a double arch with the outline of the sacro-iliac joint surface (the auriculum), supporting a male sex attribution. In addition, Sts 65 exhibits a distinct sigmoid curvature of the iliac crest that is unlike both Sts 14 and StW 431. In terms of general morphology, however, the partial hipbone Sts 65 seems to more closely resemble Sts 14. This unexpectedly high morphological heterogeneity revealed by our reconstruction adds to the ongoing discussion of the potential taxonomic heterogeneity observed at Sterkfontein.

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References: [1] Fornai, C., Krenn, V.A., Mitteroecker, P., Webb, N.M., Haeusler, M., 2021. Sacrum morphology supports taxonomic heterogeneity of "*Australopithecus africanus*" at Sterkfontein Member 4. Communications Biology. 4, 347. [2] Robinson, J.T., 1972. Early hominid posture and locomotion. University of Chicago Press, Chicago. [3] Claxton, A.G., Hammond, A.S., Romano, J., Oleinik, E., DeSilva, J.M., 2016. Virtual reconstruction of the *Australopithecus africanus* pelvis Sts 65 with implications for obstetrics and locomotion. Journal of Human Evolution. 99, 10–24. [4] Haeusler, M, Ruff, CB, 2020. Pelves. In: Zipfel, B, Richmond, BG, Ward, CV (Eds.) Hominin Postcranial Remains from Sterkfontein, South Africa, 1936–1995. Oxford University Press, Oxford, pp. 181–201. [5] Georgiou, L., Dunmore, C.J., Bardo, A., Buck, L.T., Hublin, J.-J., Pahr, D.H., Stratford, D., Synek, A., Kivell, T.L., Skinner, M.M., 2020. Evidence for habitual climbing in a Pleistocene hominin in South Africa. Proceedings of the National Academy of Sciences. 117, 8416–8423.

Pecha Kucha Presentation, Session 7, Friday 13:30 – 15:00

It's a boy? A machine learning and deformation-based morphometric approach to evaluating pelvic sexual dimorphism in the Kebara 2 Neanderthal pelvis

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The Kebara 2 Neanderthal specimen from the Kebara limestone cave in Israel includes a remarkably well-preserved, albeit crushed, pelvis dated to 59–64 ka. With two relatively complete associated hipbones and an associated sacrum, Kebara 2 provides important information regarding the functional capacity of the Neanderthal pelvis; specifically, shedding light on locomotor biomechanics, sexual dimorphism, and by inference, the potentially unique birth pattern of these late archaic humans. Most notably, Kebara 2 has a distinctly elongated superior pubic ramus that could significantly influence the configuration of the bony birth canal in female Neanderthals. Nevertheless, Rak and Arensburg [1] demonstrated that the size of the inlet is still comparable to modern humans, thus obscuring the true functional relevance of this feature.

The current study introduces a new landmark-based digital reconstruction of the more complete right Kebara 2 hipbone, thus complementing previous attempts [2-3]. Our analyses utilize novel methodological approaches employed on a comparative sample of modern humans consisting of both juveniles and adults (n=147). Diffeomorphometrics, a landmark-free deformation-based approach, was performed using the Deformetrica software and in combination with both unsupervised and supervised machine learning classification algorithms (i.e., K-means clustering and support vector machines) to recover clusters representative of biological sex within the sample and to classify our Kebara 2 reconstruction. The advantage of a landmark-free approach is its ability to quantitatively consider the complete hipbone morphology without the need to establish individual homologous landmarks, a procedure susceptible to observer bias. The subsequent machine learning classification effectively partitioned the data into discrete clusters with and without a priori category assignment. Specifically, our supervised classification model achieved a high level of accuracy, correctly classifying over 90 % of the modern human sample. The within-cluster sum of squares (WCSS) was also lowest when two groups were defined, reiterating the presence of two morphological clusters. Kebara 2's classification as either male or female was highly dependent on the specific algorithm used. However, its elongated pubis places it at the extremes of human male variation, and the Deformetrica analysis places it along the periphery of the female cluster, which is a result that we have independently corroborated via traditional geometric morphometrics performed using a full pelvic landmark configuration (n=114) and similar comparative sample (n=167).

This work successfully demonstrates that our approach is a reliable and time efficient method that produces results comparable to the more intensive methodological alternatives commonly used to assess morphology. The notably long and slender pubis observed in Kebara 2, a feature shared among Neanderthals, could represent the primitive condition as inferred from australopithecines and the Gona pelvic material or relate to differences in locomotor biomechanics, thus representing a derived characteristic [1]. Such insights remain critical for directly testing whether Neanderthals had a more primitive birth pattern, given these unique features [4]. Our study suggests that the almost intermediate placement of Kebara 2 between males and females recovered in our shape analyses, driven by the unusual pubis, makes the consistent sexing of the specimen difficult, attesting to the importance of this feature for sex classification in anatomically modern human samples. However, it remains reasonable to assume a similar pattern overall of sexual dimorphism for Neanderthals as in modern humans and, by extension, a comparably difficult birth process given the fact it is namely one feature (the pubis) that is impeding reliable sex classification and that previous work [1] demonstrated that the elongated pubis does not contribute to a larger pelvic canal in Neanderthals. We thereby predict that female Neanderthals will similarly fall within the modern human range, albeit possibly at the extremes like Kebara 2, and this assumption should be used to guide future reconstructions and their interpretations.

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References: [1] Rak, Y., Arensburg, B., 1987. Kebara 2 Neanderthal pelvis: First look at a complete inlet. American Journal of Physical Anthropology. 73, 227-231 [2] Rmoutilová, R., Haeusler, M. 2023. The shape of the Neanderthal pelvis: implications of a new reconstruction of Kebara 2 for childbirth. American Journal of Biological Anthropology 180, 149–150. [3] h Adegboyega, M.T., Stamos, P.A., Hublin, J.-J., Weaver, T.D., 2021. Virtual reconstruction of the Kebara 2 Neanderthal pelvis. Journal of Human Evolution. 151,102922. [4] Weaver, T.D., Hublin, J.-J., 2009. Neandertal birth canal shape and the evolution of human childbirth. Proceedings of the National Academy of Sciences. 106, 8151-8156.

Podium Presentation, Session 3, Thursday 14:20 – 16:00

Zooarchaeological and palaeoproteomic analysis of the Baishiya Karst Cave faunal assemblage reveals Denisovan occupation history and subsistence strategies on the Tibetan Plateau

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Genetic and fragmented palaeoanthropological data suggest that Denisovans were once widely distributed across eastern Eurasia [1-3]. From this limited archaeological data it has been suggested that Denisovans were capable of adapting to a highly diverse range of environments. To further address this question and better understand Denisovan subsistence strategies, we conducted an integrated proteomic and zooarchaeological analysis of the faunal assemblage recovered from Baishiya Karst Cave (China). Located on the lower ranges of the Tibetan Plateau, previous research identified a Denisovan mandible, Xiahe 1, as well as Denisovan sedimentary mtDNA throughout the stratigraphy [3-4]. We studied over 2,500 faunal specimens using traditional zooarchaeological methods. Of these, just under 2,000 specimens were analysed using ZooMS (Zooarchaeology by Mass Spectrometry) to assign taxonomic identities. In combination, this approach allowed taxonomic and bone surface modification analysis to be successfully conducted on the majority of the faunal assemblage.

ZooMS screening resulted in the identification of one new hominin specimen, Xiahe 2. Based on its stratigraphic position within layer 3 and previous radiocarbon dating of bone specimens from this layer [4], the Xiahe 2 specimen dates to approximately 48-32 thousand years ago. Shotgun proteomic analysis assigns this specimen to the Denisovan lineage, extending their fossil presence at Baishiya Karst Cave well into the Late Pleistocene. This result is in agreement with previous ancient mtDNA results obtained from sediments deposited within the cave [4].

Integrating ZooMS taxonomic identifications into a zooarchaeological analysis framework allows us to significanly improve taxonomic and behavioural insights obtained from the faunal assemblage. Throughout the stratigraphic sequence, the faunal assemblage is dominated by bovids, particularly Caprinae. In addition, we identify the presence of megaherbivores, carnivores, small mammals and birds. The high proportion of the bharal (*Pseudois nayaur*), the goa (*Procapra* cf. *picticaudata*), the wild yak (*Bos* cf. *mutus*) and equids (*Equus* sp.) indicates a grass-dominated landscape within Ganjia Basin. The presence of, for example, red deer (*Cervus elaphus*) and musk deer (*Moschus* sp.) suggests the presence of small-scale forest-shrub landscapes as well.

The high intensity of anthropogenic modifications on the bone surfaces suggests that Denisovans were the primary agent of faunal accumulation. The type and bone element location of these anthropogenic modifications suggests that the complete *chaîne opératoire* of carcass processing is represented at Baishiya Karst Cave, including meat, marrow and hide exploitation, but also the use of bone as tool-making materials. Anthropogenic modifications are also present on carnivore, small mammal, and avian remains. Our results therefore provide new and unique insights into Denisovan behaviours and their adaptations to the challenging environmental conditions of the Tibetan Plateau.

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References: [1] Reich, D., Green, R.E., Kircher, M., Krause, J., Patterson, N., Durand, E.Y., Viola, B., Briggs, A.W., Stenzel, U., Johnson, P.L.F., Maricic, T., Good, J.M., Marques-Bonet, T., Alkan, C., Fu, Q., Mallick, S., Li, H., Meyer, M., Eichler, E.E., Stoneking, M., Richards, M., Talamo, S., Shunkov, M.V., Derevianko, A.P., Hublin, J.-J., Kelso, J., Slatkin, M., Pääbo, S., 2010. Genetic history of an archaic hominin group from Denisova Cave in Siberia. Nature. 468, 1053-1060. [2] Demeter, F., Zanolli, C., Westaway, K.E., Joannes-Boyau, R., Duringer, P., Morley, M.W., Welker, F., Rüther, P.L., Skinner, M.M., McColl, H., Gaunitz, C., Vinner, L., Dunn, T.E., Olsen, J.V., Sikora, M., Ponche, J.-L., Suzzoni, E., Frangeul, S., Boesch, Q., Antoine, P.-O., Pan, L., Xing, S., Zhao, J.-X., Bailey, R.M., Boualaphane, S., Sichanthongtip, P., Sihanam, D., Patole-Edoumba, E., Aubaile, F., Crozier, F., Bourgon, N., Zachwieja, A., Luangkhoth, T., Souksavatdy, V., Sayavongkhamdy, T., Cappellini, E., Bacon, A.-M., Hublin, J.-J., Willerslev, E., Shackelford, L., 2022. A Middle Pleistocene Denisovan molar from the Annamite Chain of northern Laos. Nature Communications. 13, 2557. [3] Chen, F., Welker, F., Shen, C.-C., Bailey, S.E., Bergmann, I., Davis, S., Xia, H., Wang, H., Fischer, R., Freidline, S.E., Yu, T.-L., Skinner, M.M., Stelzer, S., Dong, Guangrong, Fu, Q., Dong, Guanghui, Wang, J., Zhang, D., Hublin, J.-J., 2019. A late Middle Pleistocene Denisovan mandible from the Tibetan Plateau. Nature. 569, 409-412. [4] Zhang, D., Xia, H., Chen, F., Li, B., Slon, V., Cheng, T., Yang, R., Jacobs, Z., Dai, Q., Massilani, D., Shen, X., Wang, J., Feng, X., Cao, P., Yang, M.A., Yao, J., Yang, J., Madsen, D.B., Han, Y., Ping, W., Liu, F., Perreault, C., Chen, X., Meyer, M., Kelso, J., Pääbo, S., Fu, Q., 2020. Denisovan DNA in Late Pleistocene sediments from Baishiya Karst Cave on the Tibetan Plateau. Science. 370, 584-587.

Poster Presentation Number 117, Session 2, Friday 17:00 – 18:30

Sexual dimorphism in the enamel-dentine junction of permanent canines of European modern humans

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Determining the sex of an individual to create a biological profile is one of the main challenges that biological anthropology must face, especially with non-adult individuals, where determining sex with classical methods is near impossible [1]. Dental anthropological investigations into sexual dimorphism have conventionally concentrated on evaluating the dimensions and configuration of the enamel cap of canines. However, the morphology of the crown dentine surface can be closely linked to that of the enamel surface [2], which can make it easier to examine the morphology of the crowns even when the enamel surface is worn [3-4]. This work analyzes the surface of the enamel-dentine junction (EDJ) of permanent canines of males and females from a contemporary human population of Europe (Spain), assessing the differences that exist between males and females as well as between maxillary and mandibular canines. Micro-CT and 3D geometric morphometry techniques were used, gathering the morphological data of the EDJ with a template comprising a total of 96 landmarks and semilandmarks, followed by Procrustes registration [4], space principal component analysis (PCA) and comparison of centroid sizes. Significant differences in the morphology of the EDJ were observed between the sexes, particularly concerning the overall shape of the crown, the symmetry of the mesial and distal edges, and the development of the distal accessory ridge. Our results indicate a) that they could partially relate to retention of the canine-premolar honing complex in males thanks to the conservative properties of the dentine, which was presumed lost by this point of the human lineage, and b) that analyses of the permanent canine EDJ may potentially provide a novel method for estimating the sex of adult and non-adult skeletons, which would be especially useful in both the study of human evolution and concrete fossils as well as in forensic sciences.

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References: [1] Weiss, K.M., 1972. On the systematic bias in skeletal sexing. American Journal of Physical Anthropology. 37, 239–249. [2] Smitha, T., Sheethal, H., Hema, K., Franklin, R., 2019. Forensic odontology as a humanitarian tool. Journal of Oral and Maxillofacial Pathology. 23, 164. [3] García-Campos, C., Martinón-Torres, M., Martín-Francés, L., Martínez de Pinillos, M., Modesto-Mata, M., Perea-Pérez, B., Zanolli, C., Labajo González, E., Sánchez Sánchez, J.A., Ruiz Mediavilla, E., Tuniz, C., Bermúdez de Castro, J.M., 2018. Contribution of dental tissues to sex determination in modern human populations. American Journal of Physical Anthropology. 166, 459–472. [4] García-Campos, C., Martinón-Torres, M., Martínez de Pinillos, M., Modesto-Mata, M., Martín-Francés, L., Perea-Pérez, B., Zanolli, C., Bermúdez de Castro, J.M., 2018. Modern humans sex estimation through dental tissue patterns of maxillary canines. American Journal of Physical Anthropology. 167, 914–923. [5] Zelditch, M., Swiderski, D., Sheets, H. D., 2012. Geometric morphometrics for biologists: a primer. Academic press.

Poster Presentation Number 118, Session 2, Friday 17:00 – 18:30

A terminal Pleistocene demographic cycle at Natufian el-Wad Terrace, Israel

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It is increasingly acknowledged that some intensive and prolonged human settlements at the end of the Pleistocene had strongly affected their environments in myriad ways before any reliance on food production. This included intensified subsistence practices that could have depressed game populations, niche-constructing activities that altered the abundances of animal and plant taxa (both intentionally and inadvertently), and synanthropic relations whereby certain taxa benefited from the refuse or shelter provided by the habitation. The intertwined nature of these effects and their equivocal archaeological signals require a detailed, high-resolution and multi-proxy record to tease out. Here, we present such a case-study from the earliest hunter-gatherer "built environment", the Natufian Culture of the terminal Pleistocene Levant. The deep Early Natufian sequence of el-Wad Terrace (Mount Carmel, Israel), provides a rich record (ca. 14.9–13.2 ka) that includes an initial phase with little architecture, followed by an intensive architectural phase with ten stratified construction levels, in turn capped by more ephemeral habitation levels. The sequence ends with an even more ephemeral-looking Late Natufian deposits (ca. 13.2–12 ka). Using the rich zooarchaeological samples from each stage, and controlling the environmental parameters by independent proxies (plant carbon isotopes and microvertebrate accumulations), we propose that the different modes of habitation had different effects on subsistence intensification and diversification, as well as proliferation of synanthropic taxa. We test how hunting patterns changed with the mode of occupation, revealing the human response to the impact a growing sedentary habitation had on the site's environment. Since our sequence's duration is comparable to ethnographically known demographic cycles, we further investigate the possibility that these developments correspond to a Malthusian cycle, whereby gradual demographic growth in this early sedentary hamlet eventually led to an overpopulation crisis, which was mediated first by adjusting the subsistence patterns, and later possibly entailed the partial abandonment of the site and reorganization elsewhere.

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Podium Presentation, Session 1, Thursday 9:20 – 11:00

Could the Rising Star hominins represent relictual australopiths?

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Since 2013, the Dinaledi and Lesedi Chambers of the Rising Star cave system yielded hundreds of hominin remains attributed to *Homo naledi*, and dated to 335–236 ka [1-3]. This extraordinary assemblage represents a minimum of 15 individuals of various ontogenetic stages, all showing a surprisingly low degree inter-individual variation [4]. The estimated stature, body mass and endocranial volume of the Rising Star hominins are on par with those of *Australopithecus* and *Paranthropus* [1-2]. Most of the anatomy of this species is known, but counterintuitively, this led to an increasing number of questions regarding its evolution and phylogenetic relationships [1-4].

The rounded cranium of the Rising Star hominins was described as most similar to that of *H. erectus*/*ergaster* [1]. In addition, the absence of sagittal crest was described to be distinct from species of the genus *Paranthropus* [1], but some *Paranthropus robustus* specimens, like DNH 7 from Drimolen, display a rounded cranium without sagittal crest [5]. The maxilla and mandible of the Dinaledi and Lesedi hominins are prognathic and the teeth of the Rising Star hominins exhibit distinct australopith traits [1–3]. The postcranial remains of the Rising Star hominins show a mixture of australopith- and early *Homo*-like features, together with later *Homo*-like traits [1-2]. However, the scarcity of comparative material clearly attributed to *Paranthropus* and early *Homo* makes taxonomic interpretations of the postcranial elements challenging.

Morphological features of the cranium and teeth of the Rising Star hominins are revised here and new analyses of craniodental structures are conducted to re-evaluate their taxonomy and phylogenetic relationships. Several metric and non-metric traits were computed for the Rising Star hominins and compared with other hominin taxa (e.g., index of palate protrusion, mandibular corpus shape index, crown occlusal area of postcanine teeth). Using the surface models of the Rising Star hominins available on MorphoSource, bidimensional geometric morphometric analyses of the neurocranium lateral and posterior profile, maxilla lateral profile, and of the cross-sectional mandible symphysis shape were conducted in comparison with published and original data of specimens belonging to *Australopithecus*, *Paranthropus*, and Early to Middle Pleistocene *Homo*. The crowns of the mandibular M3s of DH1 (the least worn teeth) were virtually cropped and compared with the external surface files of original fossils and cast of unworn to slightly worn specimens attributed to *Australopithecus*, *Paranthropus*, and Early–Middle Pleistocene *Homo*.

The revision of craniodental metric and non-metric traits of the Rising Star hominins point toward an australopith-like condition (some traits being not diagnostic between genera, and a number of features being autapomorphic of *naledi*). This is supported by the geometric morphometric analyses of the neurocranium, maxilla, mandible symphysis and M3 crown shape that statistically attribute the Rising Star specimens to either *Australopithecus* or *Paranthropus*.

The Rising Star hominins lived toward the end of the Middle Pleistocene, at a time when it is commonly assumed that among hominin genera, only *Homo* existed, while the australopiths were long extinct. However, the African fossil record for this time period is extremely scarce, with only a few Middle Pleistocene fossils available for all of the continent. The present study of the Rising Star hominins suggest that they most likely represent the terminal stage of an australopith (possibly *Paranthropus*-related) evolutionary branch.

For access to three-dimensional surfaces of the Rising Star specimens and comparative data, I am grateful to the following colleagues, institutions and online databases: J. Braga, G. Chinamatira, A. S. Hammond, K. Jakata, S. Jirah, L. Kgasi, A. Mazurier, R. Macchiarelli, L. Pan, M. Tawane, R., A. Vecino Gazabón, S. Xing, B. Zipfel, Evolutionary Studies Institute, University of Witwatersrand, Ditsong National Museum of Natural History, American Museum of Natural History, https://africanfossils.org, https://www.morphosource.org. For scientific discussion, I sincerely thank J. K. Brophy, M. Cazenave, Z. Cofran, T. W. Davies, H. S. Groucutt, J. Hawks, S. D. Hurst, R. Joannes-Boyau, O. Kullmer, R. Macchiarelli, C. M. Orr, D. Reed, F. Schrenk, L. Schroeder, M. M. Skinner, A. Urciuoli, B. A. Wood, B. Zipfel. This study received financial support from the French government in the framework of the University of Bordeaux's IdEx "Investments for the Future" program / GPR "Human Past".

References: [1] Berger, L.R., Hawks, J., de Ruiter, D.J., Churchill, S.E., Schmid, P., Delezene, L.K., Kivell, T.L., Garvin, H.M., Williams, S.A., DeSilva, J.M., Skinner, M.M., Musiba, C.M., Cameron, N., Holliday, T.W., Harcourt-Smith, W., Ackermann, R.R., Bastir, M., Bogin, B., Bolter, D., Brophy, J., Cofran, Z.D., Congdon, K.A., Deane, A.S., Dembo, M., Drapeau, M., Elliott, M.C., Feuerriegel, E.M., Garcia-Martinez, D., Green, D.J., Gurtov, A., Irish, J.D., Kruger, A., Laird, M.F., Marchi, D., Meyer, M.R., Nalla, S., Negash, E.W., Orr, C.M., Radovcic, D., Schroeder, L., Scott, J.E., Throckmorton, Z., Tocheri, M.W., VanSickle, C., Walker, C.S., Wei, P., Zipfel, B., 2015. *Homo naledi*, a new species of the genus *Homo* from the Dinaledi Chamber, South Africa. eLife. 4. [2] Hawks, J., Elliott, M., Schmid, P., Churchill, S.E., Ruiter, D.J. de, Roberts, E.M., Hilbert-Wolf, H., Garvin, H.M., Williams, S.A., Delezene, L.K., Feuerriegel, E.M., Randolph-Quinney, P., Kivell, T.L., Laird, M.F., Tawane, G., DeSilva, J.M., Bailey, S.E., Brophy, J.K., Meyer, M.R., Skinner, M.M., Tocheri, M.W., VanSickle, C., Walker, C.S., Campbell, T.L., Kuhn, B., Kruger, A., Tucker, S., Gurtov, A., Hlophe, N., Hunter, R., Morris, H., Peixotto, B., Ramalepa, M., Rooyen, D. van, Tsikoane, M., Boshoff, P., Dirks, P.H., Berger, L.R., 2017. New fossil remains of *Homo naledi* from the Lesedi Chamber, South Africa. eLife. 6. [3] Delezene, L.K., Skinner, M.M., Bailey, S.E., Brophy, J.K., Elliott, M.C., Gurtov, A., Irish, J.D., Moggi-Cecchi, J., de Ruiter, D.J., Hawks, J., Berger, L.R., 2023. Descriptive catalog of *Homo naledi* dental remains from the 2013 to 2015 excavations of the Dinaledi Chamber, site U.W. 101, within the Rising Star cave system, South Africa. Journal of Human Evolution. 180, 103372. [4] Delezene, L.K., Scott, J.E., Irish, J.D., Villaseñor, A., Skinner, M.M., Hawks, J., Berger, L.R., 2024. Sex-biased sampling may influence *Homo naledi* tooth size variation. Journal of Human Evolution. 187, 103490. [5] Rak, Y., Kimbel, W.H., Moggi-Cecchi, J., Lockwood, C.A., Menter, C., 2021. The DNH 7 skull of *Australopithecus robustus* from Drimolen (Main Quarry), South Africa. Journal of Human Evolution. 151, 102913.

Poster Presentation Number 119, Session 2, Friday 17:00 – 18:30

Reconstructing Sandrone: digital investigation of *Oreopithecus bambolii*

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It has been 150 years since *Oreopithecus bambolii* Gervais, 1872, a Miocene primate species, was discovered. This species inhabited the Tusco-Sardinian archipelago approximately 8.3 to 6.7 million years ago. The most complete specimen of *O. bambolii*, known as "Sandrone" (IGF 11778), was unearthed in a Late Miocene lignite mine in Baccinello (Grosseto, Italy). Despite its completeness and anatomical articulation, Sandrone exhibits significant fragmentation and deformation resulting from taphonomic processes.

Oreopithecus bambolii is a species that has sparked debate over more than a century with some researchers considering it as a potential milestone for investigating the origins of bipedalism. Previous analyses of the lumbar region, pelvis, foot, and inner ear of IGF 11778 have indeed suggested bipedal locomotion, although interpretations of pelvic morphology are not fully consistent with this hypothesis [1].

Here we introduce the project SANDRONE (Scientific investigation, virtual reconstruction AND musealization of OReO*pithecus bambolii*: locomotor and manipulative adaptations before humaN Evolution). Our goal is to digitally restore the iconic fossil using cutting-edge techniques and protocols in virtual anthropology tailored to the status of preservation of each bone element. Then, we will focus on the morphological and functional analyses of its locomotion and manipulative capabilities in the frame of its (paleo)environment. The upper and lower limbs of IGF 11778 will be digitally studied through cross-sectional geometric and three-dimensional geometric morphometric analyses using the R package *morphomap* [2].

In the present work, we report the tomographic investigation of the fossil from Baccinello and the preliminary results of restoration protocols including retrodeformation [3], surface warping [4] and target deformation [5]. The methodological design of the virtual restoration will allow us to estimate the missing parts and the digital reconstruction based on multivariate analysis. Beyond the scientific aspect, the project aims to enhance the fossil, renewing the museum exhibition in the Geological and Paleontological Museum of Florence with a hyper-realistic body reconstruction of Sandrone, and several panels illustrating the paleoenvironmental features of the Baccinello area during the Miocene.

Additionally, the project aims at using only open-source software, to ensure that the methodologies employed can be replicated and further developed by other researchers in the field. The expertise gathered in this project will be utilised to organise training courses for students and early researchers about virtual anthropology.

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References: [1] Hammond, A.S., Rook, L., Anaya, A.D., Cioppi, E., Costeur, L., Moyà-Solà, S., Almécija, S., 2019. Insights into the lower torso in late Miocene hominoid *Oreopithecus bambolii*. Proceedings of the National Academy of Sciences. 117:278–284. [2] Profico, A., Bondioli, L., Raia, P., O'Higgins, P., Marchi, D., 2020. Morphomap: An R package for long bone landmarking, cortical thickness, and cross-sectional geometry mapping. American Journal of Physical Anthropology. 174, 129–139. [3] Schlager, S., Profico, A., Di Vincenzo, F., Manzi, G., 2018. Retrodeformation of fossil specimens based on 3D bilateral semi-landmarks: Implementation in the R package "Morpho." PLOS ONE. 13, e0194073. [4] Gunz, P., Mitteroecker, P., Neubauer, S., Weber, G.W., Bookstein, F.L., 2009. Principles for the virtual reconstruction of hominin crania. Journal of Human Evolution. 57, 48–62. [5] Cirilli, O., Melchionna, M., Serio, C., Bernor, R.L., Bukhsianidze, M., Lordkipanidze, D., Rook, L., Profico, A., Raia, P., 2020. Target deformation of the *Equus stenonis* holotype skull: a virtual reconstruction. Frontiers in Earth Science. 8, 247