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# Book of abstracts

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### **Visibility of epigenetic cranial traits on multi-slice computed tomography (MSCT) scans and dry bones**

**E**pigenetic traits are defined as the expression of genes affecting development. In the fifties of the 20th century, genetic studies conducted on mice showed the epigenetic traits to be the most convenient for determining family relationships and population affiliation as they show high heritability even though they are partly influenced by the environment. Various studies on human crania showed that the frequencies of epigenetic traits could be used for studying biological distances between populations. To examine if multi-slice computed tomography (MSCT) images could be used as a reference for the study of the modern population, we conducted a pilot study in which we compared the visibility of the same 80 epigenetic traits on 40 dry archaeological skulls from two medieval sites, 32 from Velim Velištak (21 males, 11 females) and 8 from Radašinovci (4 males, 4 females) and their MSCT scans. From a total of 80 traits analyzed, we identified 54 (67.5%) of them in the sample. When Cohen's kappa was calculated, 24 traits showed almost perfect or perfect agreement ( $K=0.81-0.919$ ), 19 traits showed substantial agreement ( $K=0.611-0.794$ ), one showed moderate agreement ( $K=0.588$ ), 5 showed fair agreement ( $K=0.281-0.557$ ), and 5 showed slight agreement ( $K=0.003-0.17$ ).

The study showed that most identified traits could be analyzed on dry bones and CT images interchangeably. However, some traits showed lower agreement levels, and their application should only be restricted to dry bones. Future studies are required to prove consistency between the two scoring modalities because the prevalence of some traits can be extremely low, thus disabling the comparison.

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### **Filling in the blanks: the application of palaeoproteomics in faunal analysis**

**F**aunal assemblages from archaeological contexts are often abundant in the form of highly fragmented osseous remains which can be a limiting factor for the purposes of standard archaeozoological analysis. Therefore, the number of identified specimens (NISP), the minimum number of individuals (MNI), the minimum number of anatomical elements (MNE), age profiles etc. can be misrepresented. Because of this, efforts to further improve our knowledge of human-animal relationships in the past have been intensified in the last few decades. Apart from the already well-established ancient DNA analyses, in the past ten years, the use of palaeoproteomics in archaeology has been increasing. Proteomic studies range from exploring whole proteomes of tissue or substrate



(e.g., bone, enamel, shell) to detecting peptides to identify the taxon of the bone specimen. The latter can be achieved with Zooarchaeology by Mass Spectrometry (ZooMS), a technique of peptide mass fingerprinting (PMF). ZooMS aims at discriminating tissue rich in collagen type I from a taxonomic point of view because the amino acid sequence of COL1 varies across different taxonomic groups. This method analyses collagen, a protein less prone to decay thanks to its high abundance in osseous tissues and its arrangement into a highly stable triple helix. ZooMS is a fast and cost-effective method that has been explored and improved rapidly in the past decade and is especially suitable for improving and complementing faunal analysis. Its effectiveness varies based on the taphonomic processes and the age of the sample itself but, generally, it has a significantly higher success rate than the DNA analysis. Here, we present the possibilities and limitations of proteomic studies in archaeology and preliminary results of the analysis conducted on Palaeolithic sites in Istria, Croatia as a part of the PREHISTRIA project (IP-2019-04-7821) and iNEAL Cost Action (CA-19141).

### **Kyriaki Tsirtsis & Evi Margaritis**

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### **Plants and people in Classical/early Hellenistic Sikyon: what we got through the analysis of archaeobotanical material**

**D**aily activities related to food production or procurement and storage, as well as cooking stages, reflect important scheduling decisions and ancient economic models which can be deciphered through the study of archaeobotanical remains. This presentation attempts to showcase the need of applying archaeobotanical research in archaeological sites, as both macrobotanical (carbonized grains) and microbotanical (such as starch granules) remains have the potential to decode the agricultural and cooking activities that took place in a site, and eventually unfold snapshots of daily agrarian life. While macrobotanical remains can shed light on a wide range of human-plant interactions, from resource management and environmental impact to cultural modification of plant products and the plants themselves (such as specific olive tree varieties), starch granules are a source of information concerning plant use and human dietary behaviour. For the needs of this paper and in order to address the different proxies, in particular macrobotanical analysis, starch granule analysis, geometric morphometric analysis and SEM analysis that can be integrated, the Classical-Early Hellenistic site of Sikyon (Peloponnese) will be used as a case study, in which all these disciplines have been so far applied allowing to trace not only the exploited plant resources but also the relationships between people and plants during the Classical-Early Hellenistic periods in NE Peloponnese (Greece).

### **Andreja Sironić<sup>1</sup>, Alexander Cherkinsky<sup>2</sup>, Damir Borković<sup>1</sup>, Jadranka Barešić<sup>1</sup> & Ines Krajcar Bronić<sup>1</sup>**

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### **International radiocarbon mortar dating intercomparison – MODIS2**

**I**n 2020 three mortar samples from different sites and chronologies were distributed among 11 radiocarbon laboratories as a part of the Second International Mortar Dating Intercomparison Study (MODIS2). The samples were in form of bulk mortar and particle size fraction smaller than