

ABSTRACT FAUP-003

Enamel proteome of Pleistocene Cave Bears from Sierra de Atapuerca Sites

Speaker: Amanda Gutiérrez Carbajal

National Research Center on Human Evolution, Spain; Universitat Pompeu Fabra, Spain

Co-authors: Elena Santos Ureta^{1,2,3}, Esther Lizano^{4,5}, Tomàs Marquès i Bonet^{4,5}, Juan Luis Arsuaga^{2,6}, José María Bermúdez de Castro^{1,7}, María Martínón Torres^{1,7}

¹ National Research Center on Human Evolution, Spain

² Centro Mixto UCM-ISCIII de Evolución y Comportamiento Humanos, Spain

³ Universidad de Alcalá, Spain

⁴ Universitat Pompeu Fabra, Spain

⁵ Universitat Autònoma de Barcelona, Spain

⁶ Universidad Complutense de Madrid, Spain

⁷ University College London, Spain

Abstract:

This study presents the proteomic characterization of the cave bear lineage based on the dental proteome of several species, each of them representative of a different period of the Pleistocene in Sierra de Atapuerca archaeological sites (Burgos, Spain). A total of n=20 dental enamel samples from fossils assigned to the species *U. dolinensis* and *U. deningeri* have been analyzed. The fossil remains studied were recovered from Gran Dolina (ca. 910ka) and Sima de los Huesos (ca. 430ka) sites, where human presence was documented during the mid-Middle and Early Pleistocene (Bermúdez de Castro, et al. Science 1997; Arsuaga, et al. Science 2014). It is from the TD6 level (ca. 860 ka) of the Gran Dolina site, where proteins have recently been extracted from *Homo antecessor* dental remains (Welker, et al. Nature 2020). Due to the optimal state of conservation, it has been possible to successfully extract peptides from all the cave bear samples, which has allowed us to identify and sequence for the first time the dental proteome of these species. The results obtained reveal that species from Middle and Late Pleistocene cave bear lineage differ at a proteomic level from the brown bear lineage, to which some of the extant bear species belong. Consistent variations at amino acid level in protein sequences suggest such differences. The comparison with an enlarged sample including more cave bear remains from other European sites with similar chronologies will allow us to explore the taxonomy and phylogeny of the cave bear lineage.