**Iberian dogs – a diachronic genomic analysis**

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**Objectives:** Dogs are an important genetic patrimony and in Portugal several functional breeds have been developed. The analysis of their genomes including those from ancient samples can provide a good opportunity to understand the origins and evolution of dogs from more peripheral regions, as well as to infer some of the morphological characteristics exhibited by past individuals.

**Materials and Methods:** We employed well-established molecular biology methods, such as high-throughput sequencing and a nuclear capture assay, in order to recover endogeneous ancient DNA (aDNA) and SNP data from 14 ancient specimens dated from Mesolithic (~8,000 yBP) through the Middle Ages. Whole genomes from present-day Iberian dogs (n=46) and Iberian wolves (n=2) were also retrieved for a comprehensive study of dog diversity. Regarding data analysis some specific scripts were improved by our team and adjusted to either modern or ancient samples.

**Results:** Although poorly preserved, aDNA was recovered. The endogenous content (%) is not correlated with the antiquity of each sample (r=-0,42, ns). Ancient dog mitogenomes (>90%, 3x coverage) are distributed within the variability of the A and C clades, while present-day dogs show a wider range of variability: clades A to D. WGS allowed the identification of 12 dogs (9 males, 3 females) and 3 ancient wolves (2, 1). Based on autosomal markers, ancient dogs show either a single or a mixed ancestry, while present-day dogs show a single ancestry/breed meaning they are genetically well-defined breeds. From 3 Roman dogs (Spain), 3-7 SNPs involved in determining the morphology were recovered whereas for one of the ancient wolves, only a single *locus* was recovered **Conclusions:** DNA (mitochondrial and nuclear) was recovered from *Canis* archaeological samples, and it helped in documenting the presence of dogs and describe their genomic composition in Iberia.

**Keywords:** Archaeogenomics; Dog; Evolution; Breeds.

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