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Ancient DNA from domestic animal species remains: preliminary approaches

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ABSTRACT

DNA analysis from ancient and old remains offers new tools to answer archaeozoological questions and investigate the origin of the genetic variability in domestic animal species. Molecular genetics techniques contribute to identify the species supporting classical osteological studies and to establish the relationship to modern species and breeds.

Mitochondrial DNA (mtDNA) sequences are useful to reconstruct the history of maternal lineages comparing haplotype variations of present and old DNA samples. Mitochondrial data from modern cattle populations show a high diversity in Anatolia and in the Middle East supporting a near-Eastern matrilineal centre of origin. On the contrary in Europe a single family of mitochondrial haplotypes strongly dominates.

A number of recent studies reported the successful recovery of ancient and old nuclear DNA (nuDNA) sequences. Such studies represent an important breakthrough, as nuDNA can be used for the characterisation of genetic loci directly involved in phenotypic traits, answering challenging questions. A bright example is offered by the study on the single nuclear exon of melanocortin type 1 receptor gene from a ca. 43,000 years old mammoth bone from Siberia, showing that mammoth populations were polymorphic with regard to hair colour, harbouring both dark and light haired animals.

In contrast, these studies on ancient and old DNA sequences need great caution, due to the analytical problems caused by post-mortem damage of DNA, contamination from exogenous sources of mt- and nuDNA, and the consequent reliability of observed polymorphisms.

The present research describes the preliminary analytical approach to DNA study of faunal remains (103 animal bones of different domestic species: Bos taurus 51; Ovis aries/Capra hircus 39; Sus scrofa/Sus domesticus 10; Gallus gallus 1; Equus caballus/Equus sp. 2), collected in seven archaeological sites located within the province of Trento, in the Alpine region of Trentino Alto-Adige (N-E Italy). The chosen sites, dating from the Bronze Age to the late Middle Ages, display different settlement typology and include Iron Age retic houses, votive Bronze Age contexts, a 4th century roman villa and several 13th century medieval buildings. Archaeozoological data will be collected on species, skeletal parts, age of slaughter, method of butchery, evidence of bone working and presence of pale-opathologies. We describe the analytical procedure used in preparing and collecting samples and in extracting and analysing DNA from a subset of the bones previously described.