Reaching trace level protein detection to study archaeological artefacts and museum objects: new proteomics methods based on high resolution mass spectrometry

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Structural proteins such as collagens are well preserved in mineralised tissues such as bones, teeth, and ivory, and can remain a source of genetic information long after the degradation of DNA. For this reason, the analysis of ancient proteins is often used to enable species identification of morphologically unidentifiable bone fragments and to uncover new evolutionary relationships between hominid species. We are optimizing proteomic techniques to perform species identification on ivory and bone objects using minimally invasive procedures, specifically for use with museum and art objects.

In order to perform successful minimally invasive analysis, it is necessary to miniaturise and simplify both the sample preparation and data acquisition methods. This is done, for example, by integrating different chemical treatments into a single or few step, or using miniaturized analytical workflows, both of which have already proven to improve recovery in the most challenging ancient samples. Such approaches contribute to minimizing the amount of starting material needed for palaeoproteomic analysis. In addition to this, the use of de novo sequencing of amino acid protein sequences will be necessary for the samples of interest, as they are expected to be derived from animals that have not had their genomes or proteomes fully sequenced. While de novo sequencing is commonly required in the field of palaeoproteomics, it has, as of yet, rarely been applied to cultural heritage objects to identify the species of origin.

Here, we focus on the analysis of collagen proteins in ancient bones, teeth and ivory. The poster will present innovative minimally invasive methods, which will enable access to precious museum and archaeological collections, where previous analysis has not been permitted due to the large amount of sample required. It will show how the method can shed light on protein structure despite the very small sample amounts taken using microgrit polishing films. Along with sample preparation optimization, we are studying the possible degradation induced during this process, such as protein breakdowns and chemical modifications (oxidation, deamidation…), using bottom-up proteomics, digestion-free methods and top-down proteomics. In the next steps, the results of this sample preparation optimisation will be applied to the case study of historic ivory and bone objects from the collections at The Metropolitan Museum of Art. Here, the goal of the research is to identify the species from which the objects originate, in order to better understand the context of the production and provenance of historic pieces.