

Palaeoproteomics: state of the art and perspectives



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The revolutionary impact of ancient DNA analysis in many different research areas cannot be understated. Nevertheless the most ancient DNA sequences recovered from temperate and high-latitude environments are dated at ~ 0.5 and ~ 0.8 Ma, respectively, despite the exceptional efforts thrown into methodological development. Recent experimental evidence and theoretical models agree in indicating that ancient protein residues can be retrieved from epochs and geographic areas that are unsuitable for aDNA recovery at the moment. This is not the only advantage ancient proteins present over ancient DNA. Being the products of gene expression, protein sets, i.e., proteomes, vary between different tissues, organs, or developmental stages. Also, ancient proteomes can provide direct evidence of physiological and pathological processes that occurred in the past. Admittedly, ancient proteins are less useful than aDNA as a source of genetic information and, as such, they are not the evidence of choice for reconstruction of ancient population dynamics. In the past few years, investigation of ancient proteomes, i.e., palaeoproteomics, has demonstrated the value of this approach in palaeontology and human evolution studies. In the future, palaeoproteomics has the potential to enable access to genetic evidence from epochs and geographic areas incompatible with ancient DNA preservation, and facilitate investigation into deep time evolution that has been intractable for molecular phylogenetics.

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