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Abstract

Introduction: How microorganisms interact with each other, with their hosts, and with their environment are key questions addressed by metaproteomics (Armengaud 2023). The study of proteins from these particularly complex samples provides four types of answers: 1) identification of the taxa present, 2) quantification of the biomass of these organisms, 3) identification of the proteins of these taxa and their function, and 4) overall functional representation of the biological system. Paleoproteomics is the science of ancient samples. The best of both worlds is needed for characterizing ancient and complex samples that are only available in minute quantities.

Methods: For some historical artifacts, metagenomics cannot be performed due to the limited amount of material and the level of degraded DNA. To circumvent this time-consuming step, the list of organisms actually present in the sample can be established on the basis of the most reliable taxon-specific peptides. To do so, our proposal relies on an unbiased search of an extensive generic database, followed by a peptide search restricted to the most representative organisms.

Results: This forensic style approach will be illustrated by very "unique" samples such as dental remains of monks from the 16th century for which traces of coronavirus were identified (Oumarou Hama et al., 2023), cardiac relics of a blessed woman for which no trace of embalming were evidenced (Bourdin et al., 2023), as well as with samples from very hostile environments such as nuclear storage pools (Pible et al., 2023). The challenges in terms of mass spectrometry, interpretation and exploitation of the results will be discussed.

References:

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Bourdin V, Charlier P, Crevat S, Slimani L, Chaussain C, Kielbasa M, Pible O, Armengaud J (2023) Deep paleoproteotyping and microtomography revealed no heart defect nor traces of embalming in the (cardiac relics of Blessed Pauline Jaricot. *International Journal of Molecular Sciences*, 24(3):3011.