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Editorial

Overview of Paleoproteomics

Myron Szewczuk*

Department of Biomedical and Molecular Sciences, Queen's University, Quebec, Canada

EDITORIAL NOTE

Paleoproteomics is a relatively new and fast expanding branch in which ancient taxa's species identity and evolutionary connections are resolved using proteomics-based sequencing technologies. Due to the greater durability of amino acids in proteins compared to nucleic acids in DNA, the study of ancient proteins, although complimentary to paleogenomics in application, has the potential to uncover earlier, more complete phylogenies. The kinds and origins of recovered tissues, as well as the developmental phases of petrified specimens, can all be revealed by ancient protein investigations. Paleoproteomics can be used to textiles, animal skins, food remnants, and ceramics, among other ancient artefacts. In 1955, Philip Abelson described the discovery of ancient amino acid residues in fossilised materials, claiming that the peptide bonds of proteins may have lasted millions of years. Because existing techniques restricted these early discoveries, protein sequencing remained an elusive concept for over four decades. The discovery of osteocalcin in ancient bone samples by mass spectrometry in 2000 sparked fresh interest in the protein's potential as a tool for molecular palaeontology. The introduction of higher-resolution equipment improved the efficiency and depth of ancient protein recovery even more. The first extensive fossil bone proteome from a Pleistocene mammoth femur was successfully recovered and identified in 2012, bolstering paleoproteomics research's prospects.

Collagen Type I

The discovery of collagen type I, the major protein identified in mineralized tissues, has been the focus of ancient bone proteome research. Collagen is extensively conserved across species and accounts for around 90% of all organic bone components. Fibrillar collagens, like COL1, are considered to have developed from a shared metazoan ancestor, which explains their prevalence and importance in the fossil record. Collagen has also been discovered to last considerably longer in fossilised specimens than other non-collagenous proteins, and the protein is unaffected by ancient DNA breakdown. This protein's tightly coiled triple-helical shape and hydrophobic composition make it an ideal contender for longevity, especially in temperate and humid settings where organic molecules degrade quickly. Collagen's taxonomic resolution has been widely examined, and it is known that amino acid changes in most medium and large animals may be resolved to the genus level. Even with tiny animal remains from high temperature regimes, species-level identification is achievable. For these reasons, COL1 is still a crucial protein in paleoproteomics and phylogenetic studies.

Non-collagenous proteins

Non-collagenous proteins make up the remaining 10% of organic bone molecules. Osteocalcin, the most abundant NCP, is a bone and dentin protein involved in bone assembly that is frequently employed as a bone development marker. Preserved osteocalcin was initially discovered in 10,000-year-old bison bone and a 53,000-year-old walrus bone using mass spectrometry (MALDI-MS), indicating phylogenetic reconstruction capability beyond the temporal constraints of aDNA. Additional NCPs found in the bone extracellular matrix have been investigated using more powerful proteomic methods. Despite the fact that type I collagen is the longest-lived protein found in ancient bone specimens, NCP identification and sequencing may provide for better taxonomic precision than collagen-based techniques. Other petrified and ancient materials have also been subjected to proteomic analysis. Researchers have been able to distinguish between horn and hoof remnants of significant species employed at ancient sites by sequencing their keratin peptides on damaged objects. Peptide mass fingerprinting was used to identify the keratin of textiles and animal skins used by Otzi, the Iceman, from ancient samples and reference species. Multiple investigations of mummified human remains have shown the presence of illnesses and disorders using immune response proteins.

Corresponding to: Myron Szewczuk, Department of Biomedical and Molecular Sciences, Queen's University, Quebec, Canada, E-mail:szewczuk@queensu.ca

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