## Molecular evolution of shell matrix proteins

# Kazuyoshi Endo[1]; Isao Sarashina[2]

[1] Earth Evolution Sci., Tsukuba Univ.; [2] Life and Environmental Sciences, Tsukuba Univ.

Shell matrix proteins are important not only in the regulation of mineral precipitation but also in deciphering evolutionary histories of shell biomineralization. The amino acid sequences unveil the histories when compared among different taxa. To this end, we characterized the amino acid sequences of some shell matrix proteins, including Nacrein, Aspein/Asprich, Shematrin, and Dermatopontin, and compared each of them with known sequences of closely related molluscan taxa. Phylogenetic distributions indicated that Nacrein could have been present as a shell matrix protein in early Cambrian when the first shells originated, but all the other proteins were deployed in the shell matrix more recently. In general, the extent of sequence variations of shell matrix proteins is surprisingly high even between congeneric species, suggesting that those proteins experienced dynamic, and possibly adaptive, processes of evolution. The commonalities among those variations may represent functionally important motifs. For instance, residues necessary for carbonic anhydrase activity are conserved in Nacrein, and potential chitin-binding motifs appear to be conserved in Shematrin. Comparisons of Aspein/Asprich proteins, however, did not indicate presence of particularly conserved motifs, suggesting that mere accumulation, rather than specific arrangement, of Asp residues is required for their function.