

Biom mineralization Toolkit in Deep-Sea Mussels: Insights from the Mantle Transcriptome and Shell Matrix Proteome of *Bathymodiolus platifrons*

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As calcium carbonate is more soluble at lower temperature and higher pressure, understanding how deep-sea mollusks form their shells through biomineralization can reveal their adaptation to the deep-sea environment. Shell matrix proteins (SMPs) are known to play a key role in the shell formation of shallow water mollusks but so far there is no report of the composition and roles of SMPs in shell formation of deep-sea mollusks. In the present study, we analyzed the mantle transcriptome and shell matrix proteome of the deep-sea mussel *Bathymodiolus platifrons*. GO enrichment analysis of the highly expressed genes of the mantle revealed the enrichment of genes that are related to ion transportation and extracellular regions, indicating that the mantle was active in biomineralization. Nineteen SMPs were identified and their methiothine residues were exclusively oxidized. Among these identified SMPs, homologs of the 2 Chitin-bd-like proteins, 1 Perlwapin-like and 2 MSI60-like proteins have been reported in the shallow-water mussels *Mytilus* spp.. The 19 SMPs also included 3 with homology to proteins from non-mytilid bivalves, 1 from a gastropod, 1 from a nematode, and 9 novel proteins. Protein functional domain analysis showed that domain shuffling and *de novo* generation could be the major mechanisms for the evolution of SMPs in deep-sea mussels.

Keywords: deep-sea, bivalves, shell matrix protein, evolution, proteomics