Understanding the deep-sea biominerlization tool-kit by comparative proteomic characterization of deep-sea Bathymodiolus and shallow-water Modiolus mussels

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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 and the shallow-water mussel Modiolus philippinarum. GO enrichment analysis of the highly expressed genes of the mantle in both species revealed the enrichment of genes that are related to ion transportation and extracellular regions, indicating that the mantle was active in biomineralization. A total 117 and 59 SMPs were identified in B. platifrons and M. philippinarum, respectively. Protein similarity comparison between these two species revealed very few proteins were share between each other, and a suite of novel SMPs were found in each species, indicating de novo generation of SMPs. Comparison with mantle highly expressed transcripts from other deep-sea mussels as well as SMPs from shallow-water mussels can reveal some of the mechanisms of shell formation in the deep-sea.