

Dual gene repertoires for larval and adult shells reveal key molecules for molluscan shell formation

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Molluscan shells, mainly composed of calcium carbonates, contain organic components such as proteins and polysaccharides. The shell organic matrices construct frameworks of shell structures and regulate crystallization processes during shell formation. To date, a number of shell matrix proteins (SMPs) have been identified, and their functions in shell formation processes studied. However, previous studies focused only on SMPs extracted from adult shells, which are secreted after metamorphosis.

Here, by proteomic analysis combined with genomic and transcriptomic analyses, we have identified 31 and 111 SMPs from the larval shells of the pearl oyster *Pinctada fucata* and the Pacific oyster *Crassostrea gigas*, respectively. The larval SMPs are almost totally different from adult ones in both species. RNA-seq data also confirmed that gene expression profiles regarding larval and adult shell formation are nearly completely different. Therefore, the bivalves have two repertoires of shell matrix protein genes to construct larval and adult shells.

Despite the considerable difference between larval and adult SMPs, there are some functional domains shared by both SMP repertoires. The conserved domains include carbonic anhydrase (CA), von Willebrand factor type A (VWA), chitin binding (CB), and acidic domains. These domains may play crucial roles for shell formation.

Furthermore, comprehensive genomic survey revealed that the CA and VWA-CB-domain-containing protein families expanded in molluscs among metazoans and that some family members were co-opted to shell biomineralization.

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