

Butter clam genome assembly and analysis reveals the historical adaptation of shellfish genome to changes in the marine environment

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Abstract

Purple butter clam (*Saxidomus purpuratus*) is an economically important bivalve shellfish. This species belongs to the subclass Heterodonta that diverged in calcite seas with low magnesium concentrations. We sequenced and assembled its genome and performed an evolutionary comparative analysis. A total of 911 Mb assembly of *S. purpuratus* was anchored into 19 chromosomes and a total of 48,090 protein-coding genes were predicted. We identified its repeat-based expanded genes that are associated with the sodium/potassium-exchange ATPase complex. In addition, different types of ion transporters were enriched in the common ancestor of Heterodonta (calcium, sulfate, and lipid transporters) and the specific evolution of *S. purpuratus* (calcium and sodium transporters). These differences seem to be related to the divergence times of Heterodonta (calcitic sea) and Veneraidea (aragonitic sea). Furthermore, we analyzed the evolution of scavenger receptor (SR) proteins in *S. purpuratus*, which are involved in a wide range of immune responses, and compared them to the closely related *Cyclina sinensis*. We showed that a small number of SR proteins, exhibited collinearity between the two genomes, which is indicative of independent gene evolution. Our genomic study provides an evolutionary perspective on the genetic diversity of bivalves and their adaptation to historical changes in the marine environment.

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