

Mussel genomes provide insights into adaptation to deep-sea chemosynthetic environments

*Pei-Yuan Qian¹, Jin Sun¹, Jian-Wen Qiu²

1. Hong Kong University of Science and Technology, 2. Hong Kong Baptist University

The environment of deep-sea hydrothermal vents and methane seeps is characterised by darkness, lack of photosynthesis-derived nutrients, high hydrostatic pressure, variable temperatures and high concentrations of heavy metals and other toxic substances. Despite this, these ecosystems support dense populations of specialised macrobenthos such as giant tubeworms, mussels, limpets, clams and shrimps. Lack of genome information hinders understanding of the adaptation of these animals to such inhospitable environment. Here we report the genomes of a deep-sea vent/seep mussel *Bathymodiolus platifrons* Hashimoto & Okutani, 1994 and a shallow-water mussel *Modiolus philippinarum* (Hanley, 1843). Phylogenetic analysis shows that these mussel species diverged approximately 110.4 million years ago (MYA). Many gene families, especially those for stabilising protein structures and removing toxic substances from the cell, are greatly expanded in *B. platifrons*, indicating adaptation to extreme environmental conditions. The *B. platifrons* innate immune system is considerably more complex than that of other lophotrochozoan species including *M. philippinarum*, with significant expansion and high expression of gene families related to immune recognition, endocytosis and caspase-mediated apoptosis in the gill, revealing presumed genetic adaptation of the deep-sea mussel to the presence of its chemoautotrophic endosymbionts. A follow-up metaproteomic analysis of the gill of *B. platifrons* found methanotrophy, assimilatory sulfate reduction, and ammonia metabolic pathways in the symbiont, providing energy and nutrients to allow the host to thrive without dependent on photosynthesis derived food. Our study of the genomic composition allowing symbiosis in extremophile molluscs gives wider insights into the mechanisms of symbiosis in other organisms such as deep-sea tubeworms and shallow-water corals.

In addition, we would also like to take this opportunity to introduce a large-scale program on “U-Shape” area that targets at the vents along the Mid-Ocean Ridge of both South Atlantic and Western Indian Ocean, to be launched by China Ocean Mineral Resource Research and Development Association, for which we call for international collaboration in next 15 years.

Keywords: Genome sequencing, Bathymodiolus, Symbiosis