

## **Adaptation of deep-sea mussels to chemosynthetic environments revealed by full genome analysis**

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Hydrothermal vents and methane seeps support dense populations of specialised macrobenthos such as mussels. But lack of genome information hinders understanding of the adaptation of these animals to such inhospitable environment. Here we report the genomes of a vent/seep mussel *Bathymodiolus platifrons* and a shallow-water mussel *Modiolus philippinarum*. Phylogenetic analysis shows that these mussel species diverged approximately 110.4 MYA. Many gene families, especially those for stabilising protein structures and removing toxic substances, 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, 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. Metaproteomic analysis of the gill of *B. platifrons* found the symbionts could provide energy and nutrients to allow the host to thrive. Our study of the genomic composition allowing symbiosis in extremophile molluscs gives wider insights into the mechanisms of symbiosis in other organisms. To better understand molecular mechanisms of adaptation, evolution and population connectivity of deep-sea organisms in chemosynthetic habitats, China Ocean Mineral Resource R&D Association aims to launch a large-scale program to study vent ecosystems along the Mid-Ocean Ridge of both South Atlantic and Southwestern Indian Ocean. To ensure its success, COMRA welcomes scientists from overseas to actively participate in this international collaborative program in next 15 years.