

Population genetic connectivity and natural selection in deep-sea mussels: insights from mitochondrial genes and genome-wide SNP markers

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Understanding the genetic connectivity among hydrothermal vent and methane seep ecosystems can help to develop informed-management for these deep-sea resources. Nevertheless, little is known about the genetic connectivity of these special chemosynthesis-based ecosystems in the Western Pacific Province. Here, we applied a combination of three mitochondrial genes (i.e., *cox1*, *nad4* and *atp6*) and 7227 genome-wide SNPs identified based on restriction site-associated DNA genotyping-by-sequencing (RAD-seq) approach, to study the genetic connectivity of seven *Bathymodiolus platifrons* populations totaling 130 individuals in the Northwestern Pacific. These populations are distributed over a distance of 3486 km, and are between 858 m and 1482 m in water depth. Among them, two populations in the South China Sea (SCS) and one in Sagami Bay inhabit methane seeps, and four populations in Okinawa Trough inhabit vent fields. The mitochondrial markers showed that these populations were clustered into two genetic groups with one represented by the South Hainan (SH) population and another represented by the rest. In contrast, the genome-wide SNP markers showed that these populations were clustered into three distinct groups represented by the SH, the Jiaolong Ridge (JR) and the Okinawa Trough-Sagami Bay (OT-SB) populations. This pattern of genetic divergence revealed the importance of the Kuroshio Current and its intrusion into the SCS from the Luzon strait, rather than the water depth or types of habitat (vents vs. seeps), in shaping the genetic structure of this deep-sea mussel with a long pelagic larval period. Furthermore, an analysis of the SNP outliers detected 162 genes under natural selection, including genes with detoxification, endocytosis and apoptosis functions. Overall, our study has revealed the key role of the Kuroshio Current in maintaining the high genetic connectivity of the deep-sea mussel populations along its main course, the importance of the SCS as a marginal sea in promoting genetic divergence of deep-sea mussels, and highlighted the potential of high-throughput SNP discovery in resolving the fine genetic structure of deep-sea invertebrates with long-distance larval dispersal capabilities.

Keywords: Genetic connectivity, natural selection, hydrothermal vent, methane seep, *Bathymodiolus*, RAD-seq