Geographical structure of endosymbiotic bacteria hosted by Bathymodiolus mussels at eastern Pacific hydrothermal vents

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Deep-sea hydrothermal vent and cold seep chemoautotrophic bacteria play a pivotal role in sustaining chemosynthetic communities, particularly through their intracellular symbiotic relationships with host invertebrates along the global mid-ocean ridge system and back-arc basins. In vent Bathymodiolus mussels, the nature of horizontal transmission of free-living endosymbionts from environments enables us to investigate their distribution and evolution along the mid-ocean ridge axes. Here, we present evidence for the role of past tectonic event in the divergence of vent symbiotic bacteria of two mussel species, B. thermophilus and B. antarcticus along the East Pacific Rise, Galápagos Rift, and Pacific Antarctic Ridge. PCR amplicons of 16S rRNA encoding gene and six functional genes from endosymbiotic bacteria of each host individual were sequenced through parallel 454-pyrosequencing. Analyses of 16S confirmed that a single dominant y-proteobacterial species makes up most of the intracellular symbiotic bacteria without any genetic differentiation in the studied area. In contrast, analysis of molecular variance of functional genes revealed two divergent geographic groups across the previously well-known phylogeographic boundary at the Easter Microplate for their host and other vent invertebrate species. Estimation of synonymous substitution rates of functional genes between the divergent groups using the age of EM (~5.3-2.5 million years ago) was 0.77-1.62% per nucleotide per million years, remarkably similar to other rare estimates of synonymous substitution rates in E. coli and endosymbionts of aphids. This evidence strongly suggests that the geologic evolution of EM have acted as a physical barrier for the vicariance of symbiotic bacteria of Bathymodiolus mussels.