

A complete genome of *Bathymodiolus thermophilus* thioautotrophic symbiont reveals a unique hydrogenase operon among hydrothermal vent mussel symbionts

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Abstract

The mytilid mussel *Bathymodiolus thermophilus* lives in the deep-sea hydrothermal vent regions due to its symbiotic relationship with chemosynthetic Gammaproteobacteria species which reside inside specialized gill cells. The symbionts in the gill bacteriocytes oxidize the reduced sulfur amply available in the vent environment. Here we sequenced and assembled the complete genome of a gill symbiont sampled from an individual mussel from the East Pacific Rise (EPR9N), using PacBio sequencing technology. The final symbiont assembly consists of a single contig size of 2.83 Mb, with a GC content of 38.6% and encodes for 2,133 protein-coding genes. CRISPR diversity analysis confirmed this genome originated from a single symbiont strain. Comparative analysis revealed 2,554 core gene clusters were shared with other *B. thermophilus* thiotrophic gill symbiont genomes, whereas 125 were unique to this EPR9N strain. In addition, we found that EPR9N strain has a unique hydrogenase operon among *Bathymodiolus* mussels consisting of additional H₂-sensing hydrogenase subunits and a histidine kinase gene. Also, we found methylated regions sparsely distributed throughout the EPR9N genome, mainly in the transposases regions and densely present in the rRNA gene regions. Variation in genome size, gene content and genome re-arrangements across individual hosts suggest multiple symbiont strains can associate with *B. thermophilus*. This complete mussel symbiont genome will be invaluable for further comparative genomic analyses studying structural genome evolution, symbiont population diversity, and symbiont ecology in deep-sea chemosynthetic environments.

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