

Impacts of transmission mode on chemosynthetic symbiont genome evolution: A population genomic perspective

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Chemosynthetic symbioses are widespread in nature, and are responsible for much of the primary productivity of reducing habitats such as hydrothermal vents. To ensure the stability of symbioses over time, reliable symbiont transmission is necessary, occurring vertically from parents, horizontally from the environment, or via a combination of both. The modes(s) of transmission are known to affect genome evolution over long periods of time, and may also impact symbiont population structure on short time scales, as each host contains an entire population of symbionts. However, the genetic diversity of symbionts within a single host remains largely unexplored. Using population genomics, we investigated symbiont diversity in a model chemosynthetic symbiosis, the protobranch bivalve *Solemya velum* which exhibits evidence of both vertical and horizontal transmission. Symbiont populations were sequenced to high coverage (200-1000x), permitting detection of symbiont genetic variants both between and within hosts. Whole-genome analyses revealed signatures of frequent horizontal transmission of symbionts between hosts, including discordant mitochondrial-symbiont genealogies, widespread recombination, and a dynamic symbiont genome structure, with ~20% of specimens containing mixed populations of symbiont haplotypes. These results highlight the importance of mixed infections and recombination in the evolution and maintenance of symbiotic associations. Furthermore, these findings provide insights into why so many chemosynthetic symbioses are horizontally transmitted despite the obligacy of the association and the patchiness and ephemeral nature of reducing environments such as hydrothermal vents.