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PG-3 **Diversity and Evolution of Chemoautotrophic Symbioses in Deep-Sea Vent and Seep Invertebrate Animals**

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Symbioses between bacteria and eukaryotes impact the physiology, ecology and evolution of all organisms. Proteobacteria and invertebrates are ubiquitous in marine-reducing environments and are particularly well-characterized in the unique ecosystems structured around deep-sea hydrothermal vents and cold seeps. Unlike all other major ecosystems on the earth, which are driven by photosynthesis, hydrothermal vent and seep ecosystems rely on chemosynthesis. Although free-living chemosynthetic prokaryotes serve as the base of the food chain for some vent and seep organisms, reliance on symbiotic chemosynthetic bacteria is the primary nutritional strategy for many vent and seep invertebrates. In recent years, molecular phylogenetics has enabled exploration of the world of symbiotic bacteria in vent and seep invertebrates. We here report our molecular phylogenetic studies using vent and seep invertebrates collected within the Hatoma and Kuroshima Knolls, off the Ryukyu Islands.

Polychaetes of the family Polynoidae (scale-worms) are well-represented at deep-sea vents and seeps. Nevertheless, little is known about lineages of symbiotic bacteria of scale-worms or even about the presence. We performed PCR-based detection and phylogenetic analysis of the bacteria associated with a free-living scale-worm. The scale-worm, related to the genus *Branchipolynoe*, harbored the significant bacterial population dominated by the novel phylotype that is tightly clustered with thioautotrophic endosymbionts of vesicomid bivalves within gamma-proteobacteria. Our results strongly suggest that some scale-worms have established symbiotic relationships with thioautotrophic symbionts of gamma-Proteobacteria.

Mussels of the genus *Bathymodiolus* are ubiquitous over the world vent and seep sites and hosting either thioautotrophic or methanotrophic symbionts or both. Although the ratio of methane to hydrogen sulfide has been supposed to impact the type of the hosted symbionts, it is still obscure. Furthermore, one of the most intriguing aspects of these three different symbioses concerns their evolutionary origins. On the basis of our molecular phylogenetic and ancestral-state analyses, it is strongly suggested that the most recent common ancestor of the *Bathymodiolus* possessed both of the two types of symbionts and have often lost and reacquired either one symbiont resulting in the present distribution of the types of the hosted symbionts.