

## **Cryptic diversity and host-symbiont specificity in Pacific deep-sea tubeworms**

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Vestimentiferan tubeworms are key taxa in deep-sea chemosynthetic habitats worldwide. As adults they acquire their nutrition exclusively through their sulfur-oxidizing bacterial endosymbionts, which are taken up from the environment. Although horizontal transmission should favor infections by various symbiotic microbes, traditional 16S rRNA sequence analyses imply that every tubeworm harbors a symbiont population consisting of a single predominant phylotype. The same analyses have shown that different co-occurring host taxa can be infected by the same symbiotic phylotype, indicating that an exclusive association between a symbiont species and a particular host species might not exist. Even so, a few multi-gene studies suggest that genetic variation and host specificity does exist in the symbionts of vestimentiferan tubeworms. To address these aspects in more detail we will analyze symbiotic associations in geographically widespread populations of the tubeworm species *Lamellibrachia barhami*, *Escarpia spicata* and *Ridgeia piscesae* from chemosynthetic ecosystems in the eastern Pacific Ocean. Using metagenomic, 16S amplicon and restriction-site associated DNA sequencing we will identify single-nucleotide polymorphisms in hosts and symbionts to assess the genomic diversity and population structure in both partners. The genotypic data will then be used in multivariate and correlative statistics to determine the degree of host-symbiont specificity. We expect that this study will advance our understanding of symbioses between animals and bacteria in the deep sea and provide a basis for future research on how host-symbiont interactions influence ecological adaptation, genetic population differentiation and evolutionary diversification of both partners.