

## **Comparative genomics reveal symbiont-host evolution of deep-sea tubeworms**

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Annelid tubeworms, Siboglinidae, represent keystone species in deep-sea chemosynthetic communities (e.g. hydrothermal vents, cold seeps, mud volcanoes, large organic falls). Dominance of tubeworms in these chemosynthetic habitats is facilitated by endosymbiotic bacteria which provide energy, making them of evolutionary and physiological interest. To date, approximately 200 species have been described within 4 major siboglinid lineages: Vestimentifera, Sclerolinum, Osedax and Frenulata. Three of main lineages of siboglinids (vestimentiferans, frenulates, and Sclerolinum) house chemoautotrophic gammaproteobacteria, whereas Osedax houses heterotrophic Oceanospirillales. In this study, we have sequenced transcriptomic data from host and genomic data from symbionts to further explore the host-symbiont evolution of this group. Recent phylogenomic and mitogenomic studies suggested Osedax being most closely related to the Vestimentifera and Sclerolinum clade. Furthermore, in order to compare whether symbiont-host metabolic machineries (e.g. sulfur metabolism, carbon fixation and secondary metabolite) are conserved across different taxa, we have sequenced four endosymbiont genomes from *Lamallibrachia luymesii*, *Escarpia spicata*, *Seepiophila jonesi*, *Galathealinum brachiosum* as well as using public bacterial genomes from *Riftia pachyptila*, *Tevnia jerichonana* and *Ridgeia piscesae*, to conduct comparative genomics to assess genomic pathways that may facilitate interaction between host and symbiont. Preliminary analyses suggested that the primary and secondary metabolic pathway were relatively conserved across taxa, although variations have been observed in endosymbiont genome of *Galathealinum* (e.g. rTCA cycle). More importantly, we identified the potential molecular mechanisms including