

Meta-transcriptomic analysis unveils the symbiotic relationship between methane seep tubeworm and its symbiont

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Deep-sea chemosynthetic ecosystems are known for abundant reduced chemicals and thus support extensive megafauna including tubeworms (Annelida, Siboglinidae) which are mouthless and gutless and reliant on their symbiotic sulphide-oxidizing bacteria (SOB) as an energy and nutrient source. Most studies of chemosynthetic tubeworms have focused on *Riftia pachyptila* and *Lamellibrachia* spp., while other tubeworms have received little attention. We analyzed the meta-transcriptome of *Paraescarpia echinospica* collected from a newly discovered methane seep in the South China Sea to understand the molecular mechanisms of symbiosis between the tubeworm and its symbionts by sequencing three tissues, i.e. plume (a gill-like organ), vestimentum and trophosome (the organ that harbors the symbionts). The transcriptome sequences were assembled, annotated, and species sorted. The bacterial transcripts were involved in chemoautotrophy activities which were characteristics of SOB, such as sulphide oxidation, ion-regulation, and sulfurtransferase activity, etc. Host genes that were highly expressed in trophosome were represented by chitin metabolism, oxygen transport, hemoglobin complex and cell adhesion. These results suggest mutual benefits between *P. echinospica* and its symbionts. Our study has revealed the importance of thioautotrophy regulatory pathways in the symbionts, the dominant regulatory pathways in the host, and demonstrated the utility of meta-transcriptome sequencing in unveiling the relationship between deep-sea invertebrate hosts and their uncultured symbionts.

Keywords: Deep-sea, Chemosynthetic, Tubeworm, Symbionts