

## **The symbiotic relationship between a methane seep tubeworm and its symbiont as revealed through meta-transcriptomic analysis**

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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, they rely on their symbiotic sulphide-oxidizing bacteria (SOB) as an energy and nutrient source. We analyzed 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. trophosome (an organ that harbors the symbionts), plume (a gill-like organ) and vestimentum. The transcriptome sequences were assembled, annotated, and species sorted. Only one symbiont species was found by 16S rDNA clone library approach in trophosome, and its sequence showed over 99% similarity to that of *Escarpia southwardae* symbiont. 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 not only revealed the importance of thioautotrophy regulatory pathways in the symbionts and the dominant regulatory pathways in the host, but also demonstrated the utility of meta-transcriptome sequencing in unveiling the relationship between deep-sea invertebrate hosts and their uncultured symbionts. In addition, the genomes of *P. echinos* symbiont are also being sequenced in order to better understand the symbiosis.