Interaction relationship between a chemosymbiotic Calyptogena clam and its vertically-transmitted endosymbiont revealed through meta-transcriptome sequencing

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Hydrothermal vents and methane seeps are deep-sea habitats rich in reduced chemicals, such as sulfide and methane, and support dense communities of megafauna. Many endemic species harbor chemosynthetic symbionts for nutrition. Vesicomyid clams in the genus Calyptogena is one such case, and especially notable as they obtain endosymbionts through vertical transmission. The present study aims to understand the host-symbiont relationship in an undescribed Calyptogena species recently discovered from a cold seep in the South China Sea. The gill, mantle, adductor muscle, and foot tissue were dissected from one individual and subjected to RNA-Seq in an Illumina HighSeq platform. De novo assembly of the reads resulted in 246,150 contigs, among them 25,530 were translated into protein sequences. Comparing the expression level of the host proteins in the four different tissues revealed that Ras protein family, especially the Rab proteins that play an important role in the fusion of endosome and lysosome during endocytosis, are highly expressed in the gill. This indicate that rate of lysis is increased in the gill, where the endosymbionts are housed. Meanwhile, mapping the sequencing reads from the gill to the closest sequenced endosymbiont genome that is from Calyptogena okutanii, revealed high expression of genes involved in sulfur oxidizing and ATP synthesis in the symbiont. These results show that the new Calyptogena species also rely on sulfur-oxidizing symbionts for energy, and the high expression level of Rab proteins may help the host control the symbiont population.