

琉球大学学術リポジトリ

長膜亜目スナギンチャク類における分子系統、分類
および進化に関する研究

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博士論文の要約

In symbiotic studies, host switching has been considered as one of the main drivers of speciation and leads to diversification of symbiotic systems. However, the amount of research on host switching in marine organisms is low in comparison to that of terrestrial symbiotic relationships. Macrocnemic zoantharians are colonial hexacorallians and commonly occur in a wide variety of marine habitats including extreme environments such as methane cold seeps in the deep sea. Macrocnemic zoantharians commonly associate with marine invertebrates representing seven phyla. Therefore, macrocnemic zoantharians can be a good model to understand the patterns and process of host switching, and how it effects diversification in zoantharians.

The suborder Macrocnemina consists of five families, and symbiotic species belong to three families. It has been suggested that symbiotic species within Macrocnemina are highly diversified. In particular, taxonomic studies focused on the family Parazoanthidae have been actively conducted for the last two decades, and the systematics of this family have been rearranged. On the other hand, systematic studies on the other two families comprising symbiotic species lag behind those of Parazoanthidae. This study conducts integrated taxonomy with molecular phylogeny, morphological observations, and ecological data for three genera associated with marine invertebrates to better understand diversity and evolutionary relationships as well as the diversification patterns of macrocnemic zoantharians by host switching according to the taxonomic information generated in this study.

Investigation of the diversity and taxonomy of macrocnemic zoantharians from families Epizoanthidae, Hydrozoanthidae, and Hydrozoanthidae in this study have resulted in the discovery of one genus and nine species previously unknown to science, and at least four more genera and five more species awaiting formal description. The descriptions from

this study provide a framework for further revision of macrocnemic zoantharians, and improve our knowledge of the evolutionary history of zoantharians. In order to estimate evolutionary transitions of host switching, ancestral state reconstruction was performed based on a molecular phylogenetic tree utilizing six genetic markers. The results of the analyses showed that symbiotic associations with Annelida, Cnidaria, Echinodermata, and Porifera were found in different clades, and host specializations to these phyla have occurred independently in zoantharians, suggesting unique host switching patterns between different animal phyla by zoantharians.