

DNA sequence analyses to elucidate the evolutionary history of chemosynthetic animals

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Recent developments in sequencing technology allow us to obtain DNA sequences easily from organisms and estimate many aspects of their evolution based on analyses of the sequence datasets. Our presentation reviews studies based on molecular taxonomy and phylogeny and population genetics of chemosynthetic animal communities. All organisms on earth contain the same quality of DNA, enabling comparisons of morphologically diverse animals.

For example, molecular taxonomic studies showed that tube worms belong to the Annelida. Molecular phylogenetic research results suggested the time of adaptive radiation/divergence of alvinocaridid shrimps in vent environments. In vesicomid clams and Alviniconcha snails, molecular differences without clear morphologic differences have been found, suggesting the existence of sibling species. Recently, a morphologic difference has been found between two genetically different Alviniconcha with observations of new individuals. On the other hand, there is no genetic differentiation between morphologically different populations of Paralvinella polychaetes found in the Okinawa Trough and Izu-Bonin Arc. Environmental bimorphy may thus occur in Paralvinella. Molecular taxonomy and phylogenetics have provided hypotheses on the evolution of chemosynthetic animal communities and suggested taxonomic criteria based on morphology.

In addition, population-level genetic diversity can be analyzed and dispersal or other ecological aspects of animals can be estimated based on DNA sequences. In the tube worm *Lamellibrachia satsuma*, the genetic diversity of populations in closed Kagoshima Bay was much less than that in populations in the open ocean, suggesting a restricted larval supply to Kagoshima Bay. Among Alviniconcha snails, a newly established population shows the greatest genetic diversity among all discovered populations, which indicates that an as yet undiscovered mother population of these snails exists.

Although it is impossible to observe all chemosynthetic populations worldwide, analyses of DNA sequences yield useful information on present and recent chemosynthetic animal communities including undiscovered ones.