

Vent and seep activity inferred from the dispersals and genetic structures of animals in the chemosynthetic communities

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On the seafloor, there are hydrothermal vent fields along ridges and arc-backarc systems, and cold seepage along subduction zones and faults. In each environment, animal communities depending on chemosynthesis have been constructed. Most animals in the communities are endemic to such environments and some species seems to have been strongly influenced by the activity of vents and seeps. Therefore, we tried to find out stability of vents and seeps from population dynamics of animals endemic to chemosynthetic-based communities.

For typical animals in the Western Pacific hydrothermal vent fields, such as tubeworms, vesicomylid clams, provaniid snails and neoverrucid barnacles, molecular phylogenetic and population genetic analyses (including mismatch analysis) were performed on the partial mitochondrial DNA sequences for the COI gene. The analyses of DNA sequences from each population showed that there are at least two types of animal dispersal patterns; 1) animals of which dispersals are restricted within backarc basins by arc (e.g. some provaniid snails and neoverrucid barnacles), and 2) animals of which distributions are restricted within particular depth range (e.g. some vestimentiferan tubeworms and vesicomylid clams). Phylogenetic analyses of the animals showing the first dispersal pattern suggested historical dispersal process and those patterns were consisted with directions of surface circulation systems of the ocean. However, the animals showing the latter dispersal pattern did not show clear direction of historical dispersal. The characteristics of larvae and gamete, such as length of planktonic period and tolerance to temperature, are thought to be important factors to dispersal of those animals. On the other hand, the results of population genetic analyses were consisted with the results of phylogenetic analyses, that is, the populations on the younger branch of phylogenetic trees were thought to have recently expanded. When the rates of nucleotide substitution for shallow water animals were applied, the dates of population expansions for each analyzed populations were calculated as less than several million years. Furthermore, most populations seem to be expanded from a few immigrated animals, and most lineages of animals in chemosynthesis-based communities were thought to be derived within several thousands of years ago. Therefore, each population seems to have repeated immigration, expansion and decline or extinction corresponding to activities of vents and seeps. Thus, genetic information of the animals is thought to record the most recent activities of vents and seeps.

As shown in above, biological information sometimes provides detailed information about activities of vents and seeps. We hope that biological studies on the chemosynthetic-based communities will connect more tightly with geological studies on the vents.