

Genetic connectivity and speciation of reef-building coral

*Yasuda Nina¹

1. University of Miyazaki

Coral reef ecosystem is one of the most biologically diverged systems though coral reefs are now threatened by various stresses including local anthropogenic stress by coastal development, terrestrial discharge as well as global climate change. Corals in Japan are distributed near the edge of their distribution. For the last 80 years some coral species are reported to show range expansion toward north while some corals are severely degraded by coral bleaching due to high water temperature in tropical area (Yamano et al. 2011). Therefore, corals in Japanese waters is considered to be a very sensitive area to climate change and is facing dramatic change of coastal ecosystems. Under these circumstances, revealing genetic connectivity and assessing genetic diversity of coral reef organisms along Kuroshio Current provides important implications for mechanism of poleward migration and stability of temperate peripheral populations as compared with tropical “threatened” populations.

In this study, molecular genetic markers such as highly polymorphic microsatellite markers are used to estimate genetic structure of coral reef organisms. On estimating intra-species connectivity of reef-building coral species, hidden speciation if any, is simultaneously estimated by genetic clustering analysis.

Heliopora coerulea is a living fossil whose morphological characteristics has not been changed since ancient times (Cretaceous). *H. coerulea* fertilizes within female polyps and broods their larvae until they become almost competent for settlement. Clustering analysis using microsatellite markers as well as nuclear ITS2 marker revealed two hidden lineages along Kuroshio Current. Each of the lineage is sometimes distributed in the same region but intra-lineage gene flow among distant populations are stronger than inter-lineage gene flow in geographically close populations, indicating reproductive barrier between different lineages. One lineage (HC-A) prefers to distribute in colder area and often predominates outer reef slopes. The other (HC-B) prefer to distribute in warmer area and often found inside reefs. There is almost one month difference of reproductive timing of the two lineages. Northernmost habitat of HC-A is Yakushima while that of HC-B is Okinawa island. Even within the same lineage, gene flow of HC-A and HC-B is limited in accordance with low larval dispersal potential (pelagic larval duration is mostly within a few hours and up to two weeks).

In *Acropora hyacinthus*, possible three different lineages are found along Kuroshio Current. One of the three lineages can be found in both temperate and sub-tropical region while the other two lineages are found in sub-tropical regions, implying coral population in temperate region can act as a refugia at least for one of the three lineages. We found two of the lineages in Sekisei Lagoon. Genetic barrier analysis of the both lineages showed weak barriers among eastern, central and south western Sekisei Lagoon, suggesting these three region should be conserved separately as different management units. Recently appeared northernmost populations (Amakusa, Goto and Shikine) showed no sign of population bottleneck, suggesting these populations reproduce relatively stable since they were newly colonized. However lower genetic diversity (allelic richness) were found in these new populations suggesting more vulnerable to environmental change than other temperate populations. Especially, Goto population showed higher ratio of asexual reproduction and significant differentiation with other populations, local extinction of Goto population would require longer time for recovery.

Keywords: coral reefs, connectivity, gene flow

