

Genetic diversity of planktonic foraminifer *Globigerina bulloides* in the Northwest Pacific

Atsushi Kurasawa[1]; Masashi Tsuchiya[2]; Takashi Toyofuku[2]; Hiroshi Kitazato[3]; Hiroshi Nishi[4]

[1] Hokkaido Univ./IFREE4, JAMSTEC; [2] IFREE4, JAMSTEC; [3] IFREE, JAMSTEC; [4] Dept. Earth and Planet. Science, Hokkaido Univ.

The distributions of planktonic foraminiferal species reflect the environmental preferences of each species. Although species descriptions of planktonic foraminifera are almost exclusively based on morphological characters, each morphospecies is considered to represent a genetically continuous population and exhibit ecological features. However, molecular phylogenetic studies of planktonic foraminifera revealed that many planktonic foraminiferal morphospecies exhibit high intra-specific genetic diversity. Presence of genetically discrete populations (genotypes) is confirmed in many morphospecies and growing evidences suggest that cryptic speciations may have occurred even in pelagic circumstances.

In this study, the genetic diversity of *Globigerina bulloides* in the Northwest Pacific was examined in order to reveal (1) the correlation between oceanic environment and genetic diversity and (2) the geneflow between oceanic provinces. Five genotypes are confirmed by partial small subunit ribosomal DNA (SSU rDNA) sequences and the distribution patterns of the genotypes are corresponding to the watermass structure. The difference in distribution patterns among genotypes suggests that there are ecological differences among these genotypes. The subpolar region was dominated by single genotype and other genotypes, including polar/subpolar genotypes in the Atlantic Ocean, are not found in this region. This endemism in the North Pacific subpolar region suggests that the Bering Strait and the Subpolar front act as barrier for *Globigerina bulloides* and the North Pacific subpolar region is an enclosed circumstance. On the other hand, no genetic difference between the marginal seas (the Okhotsk Sea and the Bering Sea) populations was found. This result suggests that gene flow between the marginal seas and Open Ocean prohibits the isolation of marginal sea populations, or the isolation of marginal sea population occurred recently and the genetic variations are not observable in sequenced region.