

Significance of intensive and extensive genetic analyses of natural populations in evolution and conservation(Sustainable Yield and Population Conservation for Marine Organisms from the Point of View of Genetic Resources, International Workshop in Faculty of Agricultural Science and Field Science Center in Tohoku University 2008)

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Significance of intensive and extensive genetic analyses of natural populations in evolution and conservation

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For achieving conservation and reasonable management of biological resources in marine and inland waters, it is very important to understand various aspects of their diversity, such as their evolutionary relationships, population structure and genetic diversity of species. Intensive and extensive genetic analyses of groups of species and natural populations of a species are essential for this. In the present workshop, I would like to discuss on this subject on the basis of our research experiences.

One of goals of our research team has been clarifying phylogenetic relationships of fishes, which are important components of aquatic ecosystems, aiming to understand their evolution at the gene and genome level. We would emphasize that reliable phylogenetic frameworks are indispensable bases for biologically meaningful comparisons, which are necessary for evolution and management studies. Reliability of traditional phylogenies is not so high, nonetheless, because they have been based on a limited amount of information. We have begun therefore to study molecular phylogenies on the basis of large amounts of nucleotide sequence data from complete mitochondrial genomes. We have mostly completed sequencing and analyzing of representative species from major families of ray-finned fishes, and have succeeded to provide a rather comprehensive phylogeny of them. Here, firstly I present an outline and some relevant examples of our results of this line of studies.

Another aim of our research team is to understand nature of species including genetic population structure of species. Through studies for this purpose, we have become aware that intensive and extensive genetic analyses of natural populations are extremely useful. Therefore, in this workshop, I introduce some examples of our studies showing that extensive sampling of specimens of species concerned from a wide range of distribution area is very useful to improve our understanding of fish species.

One of important direction of future study appears to be population genetic analyses of genes responsible for local adaptation of natural populations. We are trying to establish a methodology for identifying such genes by using a novel molecular biology technique. In the end of my talk, I will present our present stage of this trial and discuss future prospects.