

MINIMIZATION OF GENETIC DIVERSITY LOSS OF FUTURE GENERATIONS IN THE STOCK ENHANCEMENT PROGRAM OF RARE FISH SPECIES

Nobuhiko Taniguchi *, María del Mar Ortega-Villaizán Romo,
and Daiki Noguchi
Graduate School of Agricultural Science, Tohoku University,
Tsutsumidori, Aobaku, Sendai, 981-8555, Japan
nobuhiko@bios.tohoku.ac.jp

Background

In Japan, resource enhancement is done by releasing artificially bred seed of several economically important fish and shellfish species. It is well known that artificial seedling is usually performed using a relatively small number of brood fish, which will therefore lead to the loss of genetic variability. The loss of genetic variability of the artificially bred seed population carries the possible risk of reducing the fitness of the hatchery stock and of the wild population when hatchery bred fish are released. This risk may be managed by using a high number of contributing brood fish, more than $N_c=50$ in the case of short term activities and more than $N_c=500$ for long term activities. This rule can be applied without difficulty to the artificial reproduction of non-endangered fish species such as the red sea bream or the Japanese flounder, but it is not easily applicable to the artificial reproduction of endangered fish species. In the present study, we assessed, with the aid of computer simulation, how to maximize genetic diversity in the broodstock management of endangered or rare fish species, which are highly important for Japanese aquaculture and stock enhancement.

Specific problems with the stock enhancement of endangered populations:

1. Poor existing biological information, such as distribution, migration, spawning, resource management, and population structure.
2. Difficulty in performing population genetic analysis for identification of ESU and MU.
3. Difficulty in establishing captive and founder broodstocks to reproduce hatchery population.
4. Difficulty in avoiding inbreeding in the artificial reproduction and consequent loss of genetic variation in descendants.
5. Difficulty in avoiding genetic impacts of the hatchery bred fish in the wild population.

Risk evaluation. The following are needed for risk evaluation:

1. Genotyping of the wild and hatchery populations by means of DNA markers, in order to evaluate their genetic variability.
2. Population structure and genetic diversity evaluation, in order to identify ESU and MU.
3. Estimation of the gene flow among subpopulations, calculation of the inbreeding coefficient and the effective population size.
4. Estimation of the effective number of contributing parents to the hatchery population.
5. Simulation of the genetic variability of the hatchery population descendants.
6. Estimation of the impact of releasing hatchery bred fish on the genetic variability of wild population.

Losses in genetic variability can be recovered in future generations by minimal kinship selective breeding:

1. The genetic variability of future hatchery generations can be calculated by computer simulation. After genotyping the brood fish, the index of relatedness between each pair of brood fish can be estimated.
2. Selecting pairs which show less genetic relationship (minimal kinship selective breeding), will enable us to maintain higher genetic variability in the hatchery broodstock.
3. We evaluated the efficiency of minimal kinship selective breeding for minimizing the loss of genetic diversity in future generations, even in the case when we do not have the minimum number of recommended contributing brood fish of $N_c=50$ and 500, as introduced above.