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# Advances in Fish Genetics and Breeding Sciences Topics in Recent Study of Genetics in Aquaculture

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## Summary

Five recent topics in the study of fish genetics and breeding sciences are introduced. Two of these topics relate to the identification and conservation of genetic diversity in fish populations. These two topics include the study of the Mekong giant catfish, which is an endangered fish in the Mekong River, and the computer simulation of the selective breeding to maintain genetic diversity in artificial breeding. The other three topics related to the application of quantitative genetics in fish breeding. The estimation of the heritabilities and genetic correlations in the guppy and masu salmon are discussed, and estimation of the mode of inheritance of thermal tolerance in the guppy.

## Introduction

In the study of fish genetics and breeding sciences, the methods of analysis and tools have advanced remarkably in the current decade. These development mainly involve advances in the technology used to recombinant DNA and computer analysis. The former technique advances the procedures of quick development of DNA markers. DNA markers, such as microsatellite DNA and mitochondrial DNA markers, have been contributed to the study of genetic identification and the evaluation of the genetic diversity of fish populations, including both natural and cultured populations. The latter technology makes the traditional method to estimate genetic parameters treats large amount of data more easily. This technology also makes it easy to simulate several genetic models for the estimation of genetic diversity after a large number of generations in several cases. In the present paper, recent topics in the study of fish genetics and breeding sciences are introduced.

## Identification and Conservation of Genetic Diversity in Fish Populations

### *1) Genetic identification and conservation of Mekong giant catfish*

The Mekong giant catfish, *Pangasianodon gigas*, is endemic to the Mekong River and is a critical endangered species. We detected the genotypes of the msDNA and the mtDNA markers (right domain of the control region) to evaluate the present status of genetic divergence of this species from the Mekong River in Thailand and Cambodia. The observed heterozygosity (HO) and expected heterozygosity (HE) values of the Mekong giant catfish in Thailand and Cambodia were relatively low in comparison with those of other non-endangered freshwater fish species. These two populations from Thailand and Cambodia showed similar levels of genetic diversity, as evaluated by the 384 nucleotides of the mtDNA control region with 13 haplotypes. The pairwise $F_{ST}$ value between the two populations based on the genotype frequencies of msDNA and mtDNA markers suggested a close genetic relationship between the Thailand and Cambodia populations. The results of this study support the conclusion that the Mekong giant catfish is critically endangered. Care should be taken to sustain the genetic diversity of this species, as the level of genetic variability has already decreased in the wild population and this species is a target species for an ongoing stock enhancement program in the Mekong River in Thailand. We propose that these markers be applied for the proper broodstock management, such as for minimal kinship selective breeding in the hatchery (1).

### *2) Evaluation of Minimal Kinship Selective Breeding to Maintain Genetic Diversity in Masu Salmon, Based on Computer Simulation*

Hatchery-produced Masu salmon (*Oncorhynchus masou masou*) are released in to rivers to increase the stock of fish. However, there is a growing concern about the loss of genetic variation in wild populations due to the fact that only a small number of the adult broodfish used to produce Masu salmon seedling for stocking actually home to their native rivers. Therefore, because in some cases only a limited number of adult fish are available as hatchery broodfish, it is necessary to develop an efficient breeding method to minimize the loss of genetic variation of hatchery-produced fish. In this study, we used a computer simulation to address the effectiveness of the minimal kinship (MK) selective breeding method for genetic conservation of small populations. Two breeding methods were simulated based on the MK-selection concept. One selects parental fish based on the average *PSA* (population of shared alleles between individuals), and the other selects parental couples with the lowest *PSA* values. We found that both models were effective at maintaining, genetic variation in small populations (effective population size, $Ne<50$), except when the populations were extremely small ($Ne<20$) (2).

## Application of Quantitative Genetics to the Fish Breeding

### *1) Genetic Control of Growth in the Guppy*

In the guppy (*Poecilia reticulata*), differences of body size were observed among the strains maintained as a closed colony in our laboratory. To describe the genetic control of growth, the heritabilities of body length as a marker of growth were estimated by sib analysis. Furthermore, a cross between S and F strains estimated the number of loci influencing strain differences in body length. The S strain is small in size, and F strain is large. The estimated heritabilities from maternal and paternal half-sibs were different between females and males. The heritabilities from maternal half-sibs indicated a constant high value, however, those from paternal half-sibs indicated low values in females. On the other hand, in males more than 120 days old, the heritabilities from the paternal half had a high value. The estimated number of loci influencing strain differences was 4.0 in female and 1.7 in male at 180 days old offspring from the cross between females of S and males of F strain. However, these values were 1.8 in female and a negative value in male from reciprocal mating. The negative value was caused by a lower variance in the F2 generation than the F1 generation. These results suggest that a small number of genes were controlling the growth of the guppy, and some of them were located on the sex chromosome. In paticular, the gene(s) which detects the small size of the S strain may be located on Y chromosome (3).

### *2) Estimation of the mode of inheritance on thermal tolerance in the guppy*

High water temperature influences the survival, growth, and maturation of fish. Genetically characterizing thermal tolerance is therefore a very important subject in fish culture. To genetically characterize of thermal tolerance, the thermal tolerance was compared among strains and among parents and their offspring in the guppy (*Poecilia reticulata*). In the strain comparison, significant differences in survival rate were observed among the five strains examined, and between females and males. The females indicated a stronger thermal tolerance than the males in each strain. In a comparison between parents and their offspring, a stronger influence of the female parent than of the male was observed. The offspring obtained from surviving females indicated a stronger tolerance than those obtaines from dead females. This tendency was typically observed in male offspring. The survival rate in male offspring obtained from dead female parents was lower than that of those obtained from surviving females. The high temperature tolerance of male parents does not influence this characteristic in offspring as strongly as that of female parents. These results suggest that the major gene or genes, which have a dominant resistant allele and a recessive sensitive allele, are probably sex-linked inheritance, which locates on the X chromosome (4).

### 3) *Estimation of heritability and genetic correlation of the number of abdominal and caudal vertebrae in masu salmon*

We produced 10 sibship masu salmon, *Oncorhynchus masou masou*, families to estimate the heritability of the number of abdominal vertebrae (AV) and caudal vertebrae (CV), and we calculated the genetic correlation between the 2 traits. The AV and CV of both the parents and their offspring were counted separately, and the heritability was estimated by performing parent-offspring regression analysis. The mean vertebral number of the offspring differed among families, although they were reared under identical water temperature conditions and had the same parental vertebral number type in the crossbreeding. The heritabilities were estimated as 0.43–0.65 for AV and 0.84–1.02 for CV, and for all the families, the estimated values were higher for CV than for AV. The genetic correlation between the number of AV and CV was calculated as −1.0034. These results suggest that AV and CV are governed by different genetic components even when the fish are reared under identical environmental conditions, and the total vertebral number is expected to converge within a certain range.

It is necessary to separately analyze the variations in the number of AV and CV when investigating the vertebral number in masu salmon (5).

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