

## Isozyme polymorphisms at the sublevel of Korean salmonid species

Jung-Youn PARK, Woo-Jin KIM\*, Jeong-Ho LEE\* and Kwang-Sik  
MIN\*\*

*Ulljin Marine Hatchery, National Fisheries Research & Development Institute*  
*\*Biotechnology Division, National Fisheries Research & Development Institute*  
*\*\*Aquaculture Division, National Fisheries Research & Development Institute*

### Introduction

The isozymic polymorphism among the *Oncorhynchus masou* subspecies (*O. m. masou* and *O. m. ishikawai*) and the genetic variation in the *O. mykiss* species (rainbow trout and its albino mutant) were examined in present study. The biochemical marker might be identified at the sublevel of species.

The aims of this study is to examine such feasibility of using the isozyme polymorphisms of the fish management and characterization between subspecies or morphomutants such as albinism.

### Materials and Methods

Horizontal starch gel electrophoresis was used according to standard procedures(Aebersold *et al.*, 1987). Extracts of liver and skeletal muscle were taken from individuals of rainbow trout and the *Oncorhynchus masou* species. In order to illustrate overall genetic differences between samples at the sublevel of same species, genetic distance was calculated for each pair of samples, applied to values of Nei's (1972).

### Results and Summary

Isozymic polymorphisms were screend according to starch gel electrophoresis procedure. Five enzymes coded by seven loci were resolved in *O. masou masou* and *O. masou ishikawai*, variant alleles at *Pgm-2* were significantly

different between the subspecies. The average heterozygosities were estimated in *O. m. masou* and *O. m. ishikawai* with 0.066 and 0.055, respectively.

On the other hand, isozyme variation was determined for four enzyme systems representing six loci in the *O. mykiss* species. There were significantly different between rainbow trout and its albino mutant at *Ldh-1*, *Pgm-1*, and *Sod*. The average heterozygosity was estimated in rainbow trout with 0.305, the value in the albino rainbow trout was 0.196, the Nei' distance was calculated with 0.014616 between two rainbow trout. Monomorphism in *Ldh-1* locus is peculiar to albino rainbow trout, and these data were useful for fishery management.

## References

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