

# Genetic change in the first and second generations of hatchery stock of black seabream

N. Taniguchi<sup>1</sup>, K. Sumantadinata<sup>2</sup> and S. Iyama<sup>3</sup>

<sup>1</sup>Department of Cultural Fisheries, Faculty of Agriculture, Kochi University, Nankoku, Kochi 783 Japan

<sup>2</sup>Department of Aquaculture, Faculty of Fisheries, Bogor Agricultural University, Jl. Raya Pajajaran, Bogor Indonesia

<sup>3</sup>Department of Applied Genetics, National Institute of Genetics, Mishima, Shizuoka 411 Japan

## Abstract

The genic variability of hatchery stocks of black seabream was examined using 42 loci of biochemical markers, such as ADH, CK, EST, GPD, IDH, MDH, PGD, SDH, SP and others. The genic variability of the hatchery stocks, indicated by the proportion of polymorphic loci, number of alleles per locus, and heterozygosity, was lower than that in the natural population. A divergence in allelic frequency was observed in a few intermediate alleles, as shown by the indicators,  $F_{st}$  and genetic distance. Based on the magnitudes of random genetic drift in marker loci, the numbers of contributing parents in two first generation populations were estimated to be as small as 16 and 26 although the number of parents held in a hatchery tank was 102. It is proposed to increase the number of contributing parents in the program to propagate black seabream in Japan to avoid the influence of inbreeding.