

MONITORING OF STOCK ENHANCEMENT PROGRAM FOR BLACK SEA BREEM (*ACANTHOPAGRUS SCHLEGELI*) IN HIROSHIMA BAY, JAPAN

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Black sea bream (*Acanthopagrus schlegeli*) represents an important marine species for both sport and commercial fisheries in Japan. This species has been a traditional source of proteins for people in Hiroshima. Its harvest in Hiroshima Bay exceeded 300 tones until the 1960`s, but over-fishing caused a significant drop to 100 tones in the 1970`s.

To maintain this living resource, stock enhancement programs began in 1982 in Hiroshima Bay. Black sea bream represents the fourth marine fish species for stock enhancement in Japan, with around 6 million juveniles released annually. Twenty five percent of the fingerlings produced in the country were released in Hiroshima Bay and adjacent areas. Despite the effectiveness of these programs as evidenced by the catch recovery in 1990`s, the genetic effects of stocking were not considered.

The present paper represents the first long-term study monitoring the effectiveness of black sea bream's stock enhancement into natural populations using genetic markers. To achieve this objective, wild and hatchery stocks were separated through 6 microsatellites DNA markers. Genetic divergence between wild and hatchery population and its effect in future generations was also tested. Finally, we traced the pedigree of the offspring and estimated the inbreeding levels.

The same group of 51 black sea bream was maintained as broodstock at Hiroshima City Marine Products Promotion Association between 1999 and 2002, comprised of 29 dams and 22 sires. Eggs produced in one night were collected during the spawning peak in 2000, 2001 and 2002. Afterwards, hatched eggs were transferred to a rearing tank. Two months before the release day, 70 offspring in 2000 and 110 in 2001 were collected for the pedigree analysis. A total of 20000 larvae from the same groups were randomly selected for release each year at a small cove in Hiroshima Bay. Furthermore, 50 wild specimens were collected at the release site before hatchery fish were released, with 50 more individuals sampled 10 days after stocking in 2000. Almost 200 more individuals were sampled two months after release in 2001, and 90 and 117 individuals during the spawning peaks of 2003 and 2004, respectively.

Similar levels of heterozygosity were observed between wild and hatchery black sea bream. However, domesticated specimens scored fewer alleles per locus. The loss of alleles in hatchery origin individuals increased from 16.5% in 2000 to 28.9% in 2004.

The effectiveness and contribution of black sea bream's stock enhancement program in the cove was evidenced by the presence of over 59% of previously stocked individuals in 2001, maintaining at 34% and 39% in 2003 and 2004 samples, respectively.

The use of 7 polymorphic microsatellite DNA markers successfully reassigned 69.3% of the offspring to their true parents in the offspring selected for pedigree before release in 2000 and 2001. In addition, another 70% and 80% of the samples identified as hatchery origin matched to their true parents using 6 microsatellite loci in 2003 and 2004, respectively.

In spite of the important contribution of previously stocked individuals, the effective population size was established as 19.8, 8.9, 23, and 9 in 2000, 2001, 2003 and 2004, respectively. This small size represented 2.5, 5.5, 2.5 and 5.5% of inbreeding for the same period. The consanguinity levels observed in this study exceeds the 1% recommended by FAO, warning of the necessity of applying important procedures to maintain the genetic resources of this species and reduce the inbreeding problems observed. This experience might be very useful to preserve the genetic diversity wherever stocking programs are implemented.