

LOSS OF FAMILY VARIATION IN JAPANESE FLOUNDER DURING SEED PRODUCTION AND SHORTLY AFTER RELEASE

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Genetic divergence of hatchery reared Japanese flounder *Paralichthys olivaceus* decreases during fry production because of insufficient broodstock contributing to the next generation, artificial size-selection, and so on. Moreover, as the rapid reduction in CPUE of the released juveniles shortly after release was usually observed, it is expected that the loss of genetic variation occurs soon after release. However, there is no information available for assessing the change in genetic variation of released fish during this period. In the present study, the change in family composition of mass-produced juvenile was examined by means of microsatellite DNA polymorphism during fry production and 4 weeks after release.

A total of 48 (male:female=28:20) matured fish from the wild population were used as broodstock. Juvenile were sampled at the stage of settlement and release during fry production. Size-selection was conducted twice between settlement and release. Fifty-five thousands juveniles marked by ALC were released into Wakasa Bay (1 m depth) on 21 May 2001. The samples released were collected at 8 stations (surf zone to 7 m depth) on 0, 1, 2, 4, 5, 7, 10, 11, 14, 21, and 28 days after release. Three microsatellite loci (Takagi et al. 1999) were used to determine the parents of each juvenile. The genetic variation was assessed for broodstock, wild juveniles, and offspring populations as the number of alleles per locus and the expected heterozygosity. For analyzing the family diversity, we used the Simpson's index of diversity ($1/\lambda$). We also analyzed the effective population size (N_e) based on the formula described by Lande and Ballowclough (1987). The 95% confidence interval (95% CI) of family size, $1/\lambda$ and N_e was estimated by non-parametric bootstrap methods.

We successfully assigned 93.7% of the offspring back to a single parental couple. Thirteen females (65.0%) and 17 males (60.7%) contributed to the next generation. The most largest family, *Fam 1*, significantly increased in family compositions (%) between settlement (25.8%) and release (41.3%) while small families significantly decreased (41.6 to 21.7%). This change was due to the artificial size-selection of juveniles during seed production. H_e , $1/\lambda$ and N_e decreased during fry production and the lowest value of the three indices were observed in the sample collected from deeper areas on the 4th day after release. Our results suggest that the genetic diversity decreases shortly after release, when strong size or growth dependent mortality or both occurs in the release area.