

## GENETIC EFFECTS OF HATCHERY RELEASES ON MARINE FINFISH POPULATIONS: CASE STUDIES FROM JAPAN

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In the late 1980s, concerns about hatchery programs were raised against the background of salmonid supplementation and aquaculture. One of the major concerns has been deleterious genetic effects of hatchery fish on wild populations. Both theoretical and empirical studies have focused on this issue. Several studies have tried to detect the genetic effects of hatchery releases for Japanese flounder and red sea bream in Japan. Although differences in allelic frequencies between hatchery and naturally produced individuals have been demonstrated, the genetic effects of marine stock enhancement on wild populations are unclear. To address this problem, we investigated the genetic population structure of several marine finfish species having stocking programs. This paper evaluates the genetic effects of hatchery releases on wild populations by a comparative analysis of Pacific herring, *Clupea pallasii*, and red sea bream, *Pagrus major*.

Three samples of Pacific herring were taken from spawning areas in Yudonuma (YD) and Funka Bay in Hokkaido and Obuchinuma in Honshu, where no stocking has occurred. Samples were also taken from three release areas: Lake Akkeshi (AK), where 4 million hatchery-produced juveniles were released; and Miyako Bay and Matsushima Bay, where 17.6 million juveniles were released between 1985 and 2004. Hatchery fish were distinguished from naturally produced fish based on otoliths marked by alizarin complexon. A total of 2,055 individuals were genotyped at five microsatellite loci. For red sea bream, 410 individuals caught in Kagoshima Bay (KB) and its vicinity were genotyped at three microsatellite loci. Hatchery fish were distinguished by a deformity of the inter-nostril epidermis. A total of 20.8 million red sea bream juveniles were released in KB between 1974 and 2002.

Although genetic differentiation over the herring samples was small with an  $F_{ST}$  of 0.017, local populations with a Hardy–Weinberg equilibrium were found. Genetic differentiation between wild and hatchery fish was very small and not significant. This was considered to be due to gametes from about 200 natural fish having been used for juvenile production every year. Genetic diversity was very high, especially in Hokkaido, but the diversity of AK was slightly smaller than YD, whose population size is supposed to be smaller than that of AK. The posterior mean of the effective population size in AK was estimated at 98 with a 95% credible interval of [9, 367], and that of the inbreeding coefficient was estimated at 0.021 [0.0095, 0.0547]. For red sea bream, genetic diversity was very high, even in the inner part of KB, where extensive releases have been done, but the number of alleles was smaller than for the other areas. The posterior mean of the effective population size in the inner part of KB was estimated at 1,391 [909, 2,213], based on an estimated temporal change in allele frequencies from the year before initiation of the releases. The inbreeding coefficient was estimated at 0.00038 [0.00023, 0.00056]. Genetic effects of hatchery releases on marine finfish populations are slow because of metapopulation structure, and are dependent on the effective population size and release intensity for targeted populations. Our results suggest the need for a cautious approach to stock enhancement programs, and the importance of genetic monitoring of wild and stocked populations.