



# Population genetic structure of wild and hatchery black rockfish *Sebastes inermis* in Korea, assessed using cross-species microsatellite markers

H.S. An<sup>1</sup>, E.-M. Kim<sup>2</sup>, J.-H. Lee<sup>1</sup>, J.K. Noh<sup>1</sup>, C.M. An<sup>2</sup>, S.J. Yoon<sup>3</sup>,  
K.D. Park<sup>4</sup> and J.-I. Myeong<sup>1</sup>

<sup>1</sup>Genetics and Breeding Research Center,  
National Fisheries Research and Development Institute,  
Gyeongsangnamdo, Korea

<sup>2</sup>Biotechnology Research Institute,  
National Fisheries Research and Development Institute, Busan, Korea

<sup>3</sup>Fisheries Resources Enhancement Center,  
National Fisheries Research and Development Institute, Busan, Korea

<sup>4</sup>Fishery Resource Research Institute, Gyeongsangnamdo, Korea

Corresponding author: H.S. An  
E-mail: [hsan@nfrdi.go.kr](mailto:hsan@nfrdi.go.kr)

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**ABSTRACT.** The population structure of the black rockfish, *Sebastes inermis* (Sebastidae), was estimated using 10 microsatellite loci developed for *S. schlegeli* on samples of 174 individuals collected from three wild and three hatchery populations in Korea. Reduced genetic variation was detected in hatchery strains [overall number of alleles ( $N_A$ ) = 8.07; allelic richness ( $A_R$ ) = 7.37; observed heterozygosity ( $H_O$ ) = 0.641] compared with the wild samples (overall  $N_A$  = 8.43;  $A_R$  = 7.83;  $H_O$  = 0.670), but the difference was not significant. Genetic differentiation among the populations was significant (overall  $F_{ST}$  = 0.0237,  $P < 0.05$ ). Pairwise  $F_{ST}$  tests, neighbor-joining tree, and

principal component analyses showed significant genetic heterogeneity among the hatchery strains and between wild and hatchery strains, but not among the wild populations, indicating high levels of gene flow along the southern coast of Korea, even though the black rockfish is a benthic, non-migratory marine species. Genetic differentiation among the hatchery strains could reflect genetic drift due to intensive breeding practices. Thus, in the interests of optimal resource management, genetic variation should be monitored and inbreeding controlled within stocks in commercial breeding programs. Information on genetic population structure based on cross-species microsatellite markers can aid in the proper management of *S. inermis* populations.

**Key words:** Black rockfish; *Sebastes inermis*; Genetic structure; Hatchery strain; Microsatellite loci; Wild population