



## Genetic characterization of *Mytilus coruscus* and *M. galloprovincialis* using microsatellite markers

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**ABSTRACT.** Korean (hard-shelled) mussels (*Mytilus coruscus*) are an economically important endemic marine bivalve mollusk of Korea; yet, the population has rapidly declined because of overharvesting and habitat competition from the invasive *Mytilus galloprovincialis* species. The population structures of *M. coruscus* and *M. galloprovincialis* were analyzed by next-generation sequencing using 5 microsatellite markers specifically developed for *M. coruscus*. *M. galloprovincialis* had an average of 5.4 alleles per locus (range = 2-10), with an average allelic richness of 4.9 per locus (range = 2.0-9.3). *M. coruscus* had an average of 5.7 alleles per locus (range = 2-13), with an average allelic richness of 5.2 per locus (range = 2.0-11.9). Excessive homozygosity was observed at 3 loci, which was assumed to be due to the presence of null alleles at these loci. Pairwise multilocus  $F_{ST}$  estimates showed that the *M. coruscus* and *M. galloprovincialis* populations were clearly separated. Six populations of *M. galloprovincialis* from the western, eastern, and southern coast of Korea formed 2 separate clusters, indicating that more than 2 populations of *M. galloprovincialis* have been introduced to the Korean Peninsula. Hybrids between *M. coruscus*

and *M. galloprovincialis* were not identified, probably because of genetic differences or different habitat preferences. Further genetic information is required to perform selective breeding, population management, and restoration of *M. coruscus*.

**Key words:** *Mytilus coruscus*; *Mytilus galloprovincialis*; Microsatellite; Populations