



Development of microsatellite markers for a hard-shelled mussel, *Mytilus coruscus*, and cross-species transfer

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ABSTRACT. The Korean mussel *Mytilus coruscus*, an endemic marine bivalve mollusk, is economically important. Its population is currently decreasing due to overexploitation and invasion of a more competitive species, *Mytilus galloprovincialis*. In this study, microsatellite markers for *M. coruscus* were developed using a cost-effective pyrosequencing technique. Among the 33,859 dinucleotide microsatellite sequences identified, 176 loci that contained more than 8 CA, CT, or AT repeats were selected for primer synthesis. Sixty-four (36.4%) primer sets were produced from the 100- to 200-bp polymerase chain reaction products obtained from 2 *M. coruscus* individuals. Twenty of these were chosen to amplify DNA from 82 *M. coruscus* individuals, and 18 polymorphic loci and 2 monomorphic loci were selected as microsatellite markers. The number of alleles and the allele richness of the polymorphic loci ranged from 2 to 22 and from 2.0 to 19.7 with means of 10.8 and 10.1,

respectively. Null alleles were detected for all but three loci, which resulted in an observed heterozygosity lower than the expected heterozygosity and therefore an excess of homozygotes. In a cross-species transfer analysis of these markers using 7 Mytilidae species, the locus Mc65 was amplified from all species tested and was found to be polymorphic in all of them. Among the species, *M. galloprovincialis*, *Lithophaga curta*, and *Hormomya mutabilis* showed the same transferability of 25%, but the five amplified loci were polymorphic only in *M. galloprovincialis* and *H. mutabilis*. These microsatellite markers may be useful for future resource management and artificial production of juveniles for aquaculture.

Key words: *Mytilus coruscus*; Microsatellite; Cross-species transfer; Pyrosequencing