Microsatellite marker analysis reveals the distinction between the north and south groups of hard clam (*Meretrix meretrix*) in China

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ABSTRACT. *Meretrix meretrix* is one of the important commercial bivalves in China. A total of 198 individual clams were collected from 5 locations characteristic of the clam's 5 main natural habitats in China, that is, Shandong, Jiangsu, Fujian, Guangdong, and Guangxi. Ten polymorphic microsatellite markers were selected to examine the genetic diversity and identify genetic differences between the 5 populations. A total of 183 alleles across 10 loci were detected in the individual clams. The observed heterozygosity and expected heterozygosity ranged from 0.197 to 0.7026 and from 0.6264 to 0.9408, respectively. The genetic diversity within samples was high (8.6-11.2 alleles per locus, observed heterozygosity = 0.25-0.875 and expected heterozygosity = 0.6848-0.9259). Most of the genotype distributions significantly deviated from Hardy-Weinberg equilibrium. Genetic structure analysis showed that

the 5 populations could be divided into 2 groups, the north and south groups. Neighbor-joining analysis revealed a clear distinction between the north group (Shandong and Jiangsu) and the south group (Fujian, Guangdong, and Guangxi). Locus MM1031 was used to distinguish between groups. Our results can be used for population identification and crossbreeding of *M. meretrix*.