



Genetic differentiation between natural and hatchery populations of Manila clam (*Ruditapes philippinarum*) based on microsatellite markers

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ABSTRACT. Manila clam (*Ruditapes philippinarum*) is one of the major aquaculture species around the world and supports an important segment of the aquaculture industry in China. In this study, we used ten microsatellite markers to detect genetic diversity within six *R. philippinarum* populations and genetic differentiation between them. A total of 109 alleles were detected across all loci. Compared to wild populations ($N_A = 8.4-9.1$ alleles/locus, $H_E = 0.75-0.77$, $H_O = 0.67-0.73$), hatchery stocks showed less genetic variation as revealed in lower number of alleles and lower heterozygosity ($N_A = 7.4-7.5$ alleles/locus, $H_E = 0.72-0.75$, $H_O = 0.68-0.70$), indicating that a bottleneck effect has occurred in hatchery history. Significant genetic differentiation was observed between cultured stocks ($P < 0.05$), and between cultured and wild populations ($P < 0.05$). Phylogenetic analysis showed a clear separation of the northern three populations and the southern three populations, suggesting that

geographically separated populations of *R. philippinarum* could be genetically differentiated with limited genetic information exchanged between them. The information obtained in this study indicates that the northern and southern populations of *R. philippinarum* should be managed separately in hatchery practices for the preservation of genetic diversity in wild populations.

Key words: *Ruditapes philippinarum*; Microsatellite; Genetic diversity; Wild population; Hatchery stock; Genetic differentiation