

ESTIMATING GENETIC DIVERSITY OF SOME SNOUT OTTER CLAM (*Lutraria rhynchaena*) POPULATIONS IN VIETNAM USING SNP MARKERS

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Summary

Snout otter clam is a high economical value aquaculture species. In this study, 3 loci were developed from a highly diverse database of SNP to assess the genetic diversity of some snout otter clam populations in Quang Ninh, Hai Phong and Khanh Hoa provinces. Results showed that 3 loci were polymorphic. Thymine and cytosine mutations were detected in most populations, Adenine mutations were very low and no Guanine mutations were observed. Observed and expected heterozygosity were 0.31 and 0.337, respectively. In the wild populations, the Van Don populations in Quảng Ninh province had the highest heterozygote ($H_o = 0.422$). There were inbreeding occur in all most populations ($F_{IS} = 0.1$), especially culturing Cat Ba population in Hai Phong province. The relationships among populations tree showed that the populations were divided into two major groups. The first group consisted of wild and natural Van Don populations, the second group of combine populations in Hai Phong and Khanh Hoa and the Dong Xa in Quang Ninh province. Results of AMOVA analysis showed that natural and cultured populations did not significantly different ($P > 0.05$). The largest difference was found in comparison between individuals from other populations (89.962%). The results of this study are significant knowlegdes as a scientific basis for maintaining the quality of populations and improving the quality of the breed through selective breeding programs.

Keywords: *Genetic diverity, SNP, Snout otter clam.*