

FINAL REPORT

GENETIC ANALYSIS OF GREEN-LIPPED MUSSEL (*PERNA VIRIDIS*) IN COASTAL WATERS OFF SABAH AND ITS IMPLICATION TO BROODSTOCK SELECTION FOR CAPTIVE BREEDING PROGRAM

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Abstract

The extraordinary growth performance and simple culture method of green mussel (*Perna viridis*) make it a potentially profitable aquaculture species. However, green mussel aquaculture in Sabah still relatively undeveloped. As green mussel aquaculture in Sabah is completely rely on wild green mussel population for both spats and broodstock, it is imperative to understand various population parameters of green mussel including the population genetic information before green mussel aquaculture improvement initiatives can be carried out. In this study, 200 green mussel specimens were collected from five locations in Sabah which included Kota Kinabalu, Kota Marudu, Kuala Penyu, Tuaran and Tawau. The population genetic of green mussel in Sabah was examined using mitochondrial DNA (D-loop) and microsatellite loci. Fifteen microsatellite loci were examined using polyacrylamide gel electrophoresis whereas mitochondrial DNA (d-loop) was examined using DNA sequencing method. Green mussel population showed high haplotype diversity and low nucleotide diversity ($H_d=0.916$; $\pi=0.00915$) in mitochondrial D-loop region whereas the microsatellite genetic diversity of green mussel in Sabah ($A=3.08$; $H_e=0.43$) was lower than some regions such as Thailand. The low average allele number indicated the adaptability of the green mussel population to sudden change in environment and disease outbreak is weak. Introduction of green mussel individuals from Thailand would probably increase the genetic diversity of the green mussel population in Sabah and may manifest the genetic differences in commercially significant phenotypic traits. AMOVA and pairwise F-statistic for both microsatellite and D-loop showed low but significant population structuring. Nested clade analysis based on mitochondrial DNA was unable to identify the population structure clearly. However, STRUCTURE and UPGMA dendrogram based on microsatellite data showed that the individuals from Kota Marudu and Tawau constituted a cluster whereas individuals from Kota Kinabalu, Kuala Penyu and Tuaran formed another cluster. The population structure pattern was probably affected by the local sea current, larvae behaviour or even anthropogenic activities. From fisheries management perspective, it is desirable to manage the two groups separately. Significant genetic bottleneck signature was not detected albeit green mussel population in Sabah passed through a severe mass mortality which lasted for almost three years. In conclusion, this study resulted in a need for green mussel aquaculture improvement program in Sabah.

