

Genetic diversity of wild and cultured populations of *Penaeus monodon* using microsatellite markers.

ABSTRACT

Information on the genetic diversity of *Penaeus monodon* throughout its natural range in Malaysia is still limited even though it is a highly exploited species, thus this study was undertaken to genetically characterize the prawn populations. The *P. monodon* samples were randomly collected from Malaysian waters and were characterized using thirty polymorphic primer pairs which showed high level of polymorphism. The total number of alleles per locus ranged from 3 to 36 with allele size ranging from 100 to 275 base pairs. The mean observed heterozygosity (0.5166) was less than the expected (0.5552), highly significant deficiencies in heterozygotes were detected in total inbreeding ($F_{IS} = 0.5500$) and pair-wise genetic differentiation ($F_{ST} = 0.6308$) among the populations. Both the (χ^2) chi-square and (G^2) likelihood ratio tests detected significant differences ($p < 0.05$) which showed a deviation from the Hardy-Weinberg equilibrium, indicating a probable inbreeding might have occurred in the populations. A Cluster analysis based on genetic distance revealed a fair genetic relationship among all the populations and the pattern was in accordance to the populations' geographical origins. The highest genetic distance (0.7588) was observed between Lawas and Bulau Sayak populations while the lowest genetic distance (0.1191) was recorded between the Endau Rompin and Sedili populations. Various levels of genetic diversity of the *P. monodon* reported in this study indicated their genetic status in Malaysian waters and suitability for breeding and culture purposes. This information provides a basis for improvement through selective breeding and in the design of suitable management guidelines for this genetic material.

Keyword: Genetic diversity; Wild; Cultured populations; *Penaeus monodon*; Microsatellite markers.