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Abstract

The present study attempts to assess the population structure and phylogenetics of the commercially important local black scar oyster, *Crassostrea iredalei* (Faustino 1932) from wild and cultured populations. We analyzed the mitochondrial DNA (mtDNA) sequence variation in 581 base pairs (bp) of the cytochrome c oxidase I (COI) gene among 141 individuals from eight localities within Peninsular Malaysia. The population genetics data showed a low within population nucleotide diversity, π (0.001 \pm 0.003) and the total haplotype diversity, h was moderate (0.417 \pm 0.682). Minimum spanning network revealed a complex geographical distribution of the haplotypes. Phylogenetic relationships among the populations inferred by Neighbor-Joining and Maximum Parsimony algorithm failed to detect differentiation between these sites, indicating genetic homogeneity across the populations. The findings from this study will have important implications for aquaculture, management and monitoring of cultured populations as well as conservation of wild oyster species in Malaysia.

Keywords: COI, mtDNA, phylogenetics, population structure, *Crassostrea iredalei*