

Genetic diversity of scalloped spiny lobster (*Panulirus homarus*) populations of southern coast of Sri Lanka

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Genetic variability of wild scalloped spiny lobster; *Panulirus homarus* populations of Southern Sri Lanka was evaluated using four microsatellite markers. A group of 120 individuals belonging to four wild populations; Kirinda (KIR), Godawaya (GOD), Weligama (WEL) and Hikkaduwa (HIK) were screened. The number of alleles per locus ranged from 3 to 4. The average observed and expected heterozygosity values ranged from 0-0.950 and from 0.435-0.926 respectively. Polymorphism information contents (PIC) were ranged between 0.489 and 0.679, and the averages values for each population were as 0.564 (GOD), 0.552 (HIK), 0.577 (KIR) and 0.596 (WEL).

The calculated genetic diversity parameters and PIC values indicated middle level polymorphism and genetic variations in the four populations. According to the results of the analysis of molecular variance (AMOVA), high genetic variation within population (72.38%) and low variation among populations (1.56%) were observed. The reduction of effective number of alleles was observed which may have been caused due to the overexploitation and environmental degradation. On the basis of the genetic relationships, analysis of Unweighted Pair Group Method with Arithmetic mean (UPGMA) dendrogram indicated that the four sampled geographic locations could be grouped into two broader distinct populations; South East (KIR and GOD) and South West (WEL and HIK). The results are significant as this is the first population genetic study conducted for *P. homarus* using microsatellite markers. This information provides basis for selective breeding programs and constructing suitable management guidelines for conservation of this species in Sri Lanka.

Keywords: Microsatellite, *Panulirus homarus*, Population genetic, Spiny lobster, Sri Lanka

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