

Abstract

Spiny lobster *Panulirus homarus* is one of the commercially important, most abundant crustacean species in the southern coastal belt of Sri Lanka (SCSL). Their wild populations are declined due to over-exploitation and environmental changes however there is a potential to mariculture. Therefore, this study focused on three main objectives that are important in sustainable management of lobster fishery industry in Sri Lanka.

The first objective was to obtain DNA barcodes for five *Panulirus* spp. and to investigate the phylogenetic status of *P. homarus* along the SCSL using mitochondrial DNA (mtDNA) markers (16S rRNA and Cytochrome Oxidase I (COI)). Additional sequences were downloaded from the NCBI Genbank and phylogenetic trees were constructed according to the accepted methods. DNA barcode sequences for Sri Lankan lobster species were produced and submitted to NCBI GenBank and BOLDSYSTEM. Phylogenetic trees resulted from COI and 16S rRNA data analyses revealed three and two major clades respectively. The most closely related species of *P. homarus* were *P. ornatus* and *P. versicolor*. Sri Lankan *P. homarus* samples grouped with both sub species *P. h. homarus* and *P. h. megasculpta* indicating 2.6% nucleotide divergent level between them.

Second objective was to assess the pattern of genetic diversity and genetic structure of wild populations of *P. homarus* across the SCSL using mitochondrial DNA markers (partial sequence analysis of mtDNA COI, Cytochrome b (CytB) and control region (D-Loop) gene regions) and nuclear microsatellite markers (four loci). Four populations were selected along the SCSL: Hikkaduwa (HIK), Weligama (WEL), Godawaya (GOD) and Kirinda (KIR) to collect *P. homarus* samples. Analyses of mtDNA and microsatellite DNA revealed high genetic variation within population and low variation among populations. Two genetically distinct subpopulations could be recognized as southwest (HIK+WEL) and southeast (GOD+KIR) based on both molecular markers. Tests of neutral evolution and analysis of mismatch distribution suggested that potential in population expansion of *P. homarus* along the SCSL.

Third objective was to determine habitat characteristics of *P. homarus* along the SCSL using GIS technology. Four sites were selected from southeast (Kirinda, Godawaya) and from southwest (Weligama, Hikkaduwa) of the SCSL. Four physiochemical parameters of the bottom water and benthic substrate types of their habitats were analyzed using samples from a 25m X 25m area including 16 sub sampling points with locality information. With

the use of geographical information systems (GIS) tools, the spatially distribution maps of environmental parameters were produced. Results indicated that preferable habitats of *P. homarus* not only depend on one parameter however on several co-related factors, such as temperature, salinity, Dissolved Oxygen (DO) and the substrate. The muddy sand and rocks are the most common substrate types in all selected habitats. According to the results, Patanagalle site could be suggested as the most suitable area for future culturing and conservation programmes of *P. homarus*. In overall, this study suggests suitable approaches to follow and carry out when constructing management and conservation strategies to establish sustainable lobster fishery industry in Sri Lanka.