

Section 2

Executive Summary of the Project:

Genetic variations of three *Penaeus monodon* populations in Sri Lanka were estimated using both mitochondrial and nuclear gene regions. At the initial stage, population genetic analyses were carried out using Single Stranded Conformation Polymorphism (SSCP) method using partially amplified DNA fragment (600 bp) of mitochondrial control (mtC) gene region. However, due to difficulties experienced, finally population genetic analyses were carried out using direct sequencing technique of the same gene region. Sixty three individuals that represent three populations (southern, eastern and western) were sequenced and subjected to analyses. Total of twenty five haplotypes were identified from three populations and only one haplotype was common between southern and eastern populations. Mean haplotype diversity (h) and nucleotide diversity (π) among three populations were ranged from 0.35 (Southern) to 0.92 (eastern) and from 0.5% (southern) to 2.5% (western) respectively. Analysis of molecular variance (AMOVA) indicated within population variation as 78.89% and among population variation as 21.11% indicating high intra-population diversity. The overall F_{st} value indicated significant genetic structure among three populations ($F_{st} = 0.2111$, $P = 0.00 < 0.05$). When compare results of the present study with published data, it indicates availability of genetically more structured populations in south Indian Ocean than Indo – Pacific region.

Phylogenetic status of the derived haplotypes from three populations was estimated using mitochondrial control gene region and nuclear elongation factor gene region. Phylogenetic tree derived from mtC gene region revealed that among the haplotypes recorded from other geographic locations, southern Sri Lankan haplotypes formed a genetically distinct clade, which was also confirmed by the results of partial amplification of elongation factor gene region. Results of both gene regions revealed that Sri Lankan populations are genetically more closely related with the western Pacific Ocean populations than western Indian Ocean populations. Utility of the findings of the current study in future scientific advancement, fisheries and conservation programs are discussed.