

Mitochondrial DNA variation and population genetic structure of white shrimp



The white shrimp (*Fenneropenaeus indicus*) is an ecologically and economically important penaeid species, widely distributed in the Indo-Pacific region. To obtain information on the genetic variation and population structure of *F. indicus*, sequencing analysis was conducted on a fragment of cytochrome oxidase subunit I (COI) of the mitochondrial DNA. Individuals ($n = 217$) from eight locations covering four main geographic regions along the coastal belt of Sri Lanka were analysed. The sequences, a 602-base pairs (bp) fragment in length, revealed high haplotype and nucleotide diversity that yielded 82 haplotypes. A mismatch analysis produced a unimodal distribution of pairwise differences between haplotypes, consistent with a historic rapid population expansion. Little or no genetic differentiation was observed between most samples, although genetic distances based on pairwise differences between haplotypes started to increase when geographic distances exceeded about 130 km. A population in Bundala (southeast) had lower diversity and was genetically differentiated from the others. This information could be important for the sustainable management and utilization of this resource.

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