

Molecular investigation of Indian White Shrimp (*P. indicus*) Populations from the Persian Gulf and Oman Sea using Microsatellite Markers

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Abstract

This study focuses on molecular investigation of *P. indicus* populations in order to find and introduce the genetic differentiations and also probable genotypes for monitoring and managing the genetic resources of populations in two major catch areas in the Oman Sea. Only four out of the eight primers produced good amplified PCR products with fixed annealing temperature. The rest of the primers were either not easily amplified or produced nonspecific bands. Six alleles were found to be unique to each of two populations of *P. indicus*. Occurrences of heterozygosity deficiency were found at most loci. These heterozygosity deficiencies in observed heterozygosity in compare to expected heterozygosity may be due to inbreeding, genetic drift and consequences of illegal overharvesting of *P. indicus* in the studied areas as well. Deviation from HWE was significant in most microsatellite loci ($P < 0.001$). We observed deviation from HWE in most loci with heterozygosity deficits. Results showed that the pairwise F_{st} values were significant between populations in both species. We observed high gene flow between Guatr and Jask populations for *P. indicus*. It seems that the changes in immigration patterns of populations between Jask and Guatr areas are depend on the influence of the mangrove forests and also life cycle of this species. All alleles among obtained studied species in this study were polymorphic. The highest number of alleles observed in this species belongs to the Jask area. A total of 6 unique alleles were found in the studied population of *P. indicus*. These alleles can be used in programs of breeding and hybridization.

Keywords: Microsatellite markers, *P. indicus*, PCR, Persian Gulf, Oman Sea.