Genetic diversity evaluation of white shrimp populations (*Litopenaeus vannamei* Boone, 1931) using microsatellite DNA markers

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Abstract

In the present study, we evaluated the genetic diversity of white shrimp (*Litopenaeus vannamei* Boone, 1931) broodstock from 6 populations of DOF hatcheries and Private hatcheries in Thailand by using microsatellite DNA markers. A total of 488 individuals shrimp was investigated using seven microsatellite loci: CNM-MG339, CNM-MG479, Lvan0014, Lvan0016, Lvan0017, Lvan0022 and TUMXLv.9.93. The results from POPGENE version 1.32 presented the genetic diversity per populations per locus including average observed number of alleles (n_a) 2.5714 – 11.0000, average effective number of alleles (n_e) 2.4170 – 6.2857, observed heterozygosity (H_o) 0.5259 – 0.7757, expected heterozygosity (H_e) 0.5174 – 0.8454 and gene diversity (I) 0.8379 – 1.9983. Significant deviation from Hardy-Weinberg equilibrium were found in all populations ($P_{HWE}<0.05$). Genetic diversity among spatial populations was high (F_{st} = 0.0877 - 0.2549). The UPGMA dendrogram separated the populations into two groups. The first group consisted of DOF hatchery 1 (WH01) and the second group consisted of DOF hatchery 2, 3, 6 and Private hatchery 4, 5 (WH02, WH03, WH04, WH05 and WH06). The knowledge of genetic diversity in this study will be important for the initiation of white shrimp genetic improvement program, the optimal broodstock management and preservation of the white shrimp genetic diversity in the future.

Key words: Genetic diversity, White shrimp (*Litopenaeus vannamei* Boone, 1931),
Microsatellite DNA markers

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