MOLECULAR GENETIC MARKERS AS A TOOL FOR CONSERVATION AND BROODSTOCK MANAGEMENT OF PENAEID SHRIMPS

SIRAWUT KLINBUNGA[1], BAVORNLUCK KHAMNAMTONG[1], ANCHALEE TASSANAKAJON[2], AND PIAMSAK MENASVETA[1,3]

[1]Marine Biotechnology Research Unit, National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA), 113 Paholyothin Rd., Klong 1, Klong Luang, Patthumthani 12120, Thailand

[2]Department of Biochemistry, [3]Department of Marine Science, Faculty of Science, Chulalongkorn University, Bangkok 10330, Thailand

The giant tiger shrimp (*Penaeus monodon*) is one of the world's most economically important cultured crustaceans. Farming of *P. monodon* relies entirely on ocean-caught females for seed supply. This open cycle and reliance on natural stocks of *P. monodon* results in heavy exploitation of female broodstock from wild populations. Several molecular genetic approaches were used for analysis of genetic diversity and population differentiation of the giant tiger shrimp (*Penaeus monodon*) in Thai waters. Based on mitochondrial DNA polymorphism, large genetic heterogeneity was observed between the Gulf of Thailand (east) and the Andaman Sea (west) samples ($P < 0.0001$) but not within each coastal region ($P < 0.05$). This indicated the existence of genetic population structure of *P. monodon* in Thailand. Nevertheless, contradictory results on patterns of differentiation were observed between *P. monodon* within the Gulf of Thailand when analysed by different DNA markers. Analysis of nuclear DNA polymorphism using microsatellite and RAPD analyses consistently indicated a significant difference between *P. monodon* from Chumphon and Trat located in the Gulf of Thailand genetically ($P < 0.0001$). Under a presumption of selective neutrality for genetic markers, biased female-mediated gene flow may exist between geographic samples within the Gulf of Thailand.

In addition, molecular markers used for identification of shrimps originating from the Andaman Sea and Trat (950 bp from UBC428 and 260 bp from UBC268, respectively) and families (*CUPmo18*, *Di25*, *Di27*, *CSCUPmo1* and *CSCUPmo2*) were developed and can be applied for selective breeding programmes of *P. monodon*. Highly polymorphic levels of microsatellites can also be applied for individuality and parentage analysis eliminating problems from traditional selective breeding programs in which offspring of different family lines need to be cultured separately.

Species-diagnostic markers in *P. monodon*, *P. semisulcatus*, *P. japonicus*, *P. vannamei* and *P. merguiensis* were identified based on restriction analysis of 16S rDNA with *Vsp* I, *Alu* I, *Mbo* I and *Ssp* I. Differentiation between *P. vannamei* (CCBB and BCBB) and *P. merguiensis* (BBAA) can be unambiguously carried out. Nevertheless, *P. monodon*, *P. semisulcatus* and *P. japonicus* could not completely differentiated because shared mitotypes between species (AACB and AAAA between *P. monodon* and *P. merguiensis* and BBAB between all three species) were observed. Using SSCP analysis of 16S rDNA, these species could be further differentiated accurately.