Abstract

Channa striata, locally known as haruan has long been regarded as a valuable edible fish and it is also consumed for its putative effects on wound healing. The main objective of the project was to develop microsatellite markers for use in the study of genetic diversity of the wild *Channa striata* populations in Malaysia.

In this study, seven new microsatellite loci were isolated from *Channa striata* using a Random Amplified Microsatellite (RAMs) based technique which was an efficient and reliable method. Ten primers were used in population genetic studies of *Channa striata*.

Sixty sets of microsatellite primer pairs were used in the initial screening. Ten primer pairs produced clear and reproducible amplification products in six populations of *Channa striata* and were used to determine and compare the genetic structures of these populations. Thirty individuals from five populations and twenty-six individuals from Selangor were used to determine and compare the genetic structures of these populations. One hundred and seventy six individuals have been analyzed.

The number of observed alleles per locus ranged from 2 to 8 with an average value of 4.2 across all loci. The highest value of the mean effective allele number was 1.659 in the Negeri Sembilan population and the lowest was 1.313 in the Terengganu population. The highest mean observed heterozygosity was found in the Negeri Sembilan population with a value of 0.45 while the Johor population had the lowest value of 0.26. The F_{IS} values indicated heterozygosity excess in three populations. The analysis of molecular variance (AMOVA) based on the eight polymorphic loci investigated showed that 35.27% of the variations were among populations and 64.73% of the variations were within populations.

Out of ten loci, four showed significant deviations from Hardy-Weinberg equilibrium. This might have resulted from mutation, migration, selection, and small population size. The presence of null alleles and homozygote excess also could be the reason. The cluster analysis based on F_{ST} value revealed that the Selangor and Terengganu populations have the highest genetic differentiation and this is in accordance with the geographical regions from which the populations were obtained.

Cross-species amplification studies of *Cyprinus carpio* were conducted on *Channa striata*. The successful amplification demonstrated that microsatellite loci were conserved between these two species. This conservation of microsatellite in different species may provide a valuable and cost-effective alternative to isolating microsatellite loci in every species of interest.