

ABSTRACT

Channa striata (better known as Haruan in Malaysia), is a freshwater species that is well known as a protein source and also for its pharmaceutical value among wounded patients. Unfortunately stocks have declined over the past few years, thus an in-depth study is needed to rule out genetic irregularities that might be causing the slow extinction of the species.

This study was conducted for the purpose of studying the population diversity and genetic structure of *Channa striata* (striped snakehead) in seven different locations around the peninsular of Malaysia.

Microsatellite markers were isolated and identified using Random Amplified Microsatellite (RAM) primers. As a result, seven microsatellite primers were proven to be polymorphic and thereafter tested on 30 individuals from Johore, Kedah, Negeri Sembilan, Pahang, Penang, Selangor and Terengganu.

The primers chosen were not highly variable. As a matter of fact, most of the primers had 2-5 alleles, except for one that had 17. Observed heterozygosities ranged from 0.4341 to 0.7931. Expected heterozygosities however ranged from 0.4332 to 0.8635. There is no indication of inbreeding among individuals of each population, yet there is reasonable variation among the seven populations.

Clustering did not adhere to the geographical allocations, just as would have been expected initially. Negeri Sembilan branched off as an outgroup with not much similarities between the sampled individuals from other regions. Other unusual hybridizations and clusterings were observed; most probably due to human intervention and changes made to the water sources.