

PHYLOGEOGRAPHY OF THE ASIAN SNAKEHEAD
FISH (*CHANNA STRIATA* BLOCH) IN SABAH AS
REVEALED BY MICROSATELLITE MARKERS

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PERPUSTAKAAN
UNIVERSITI MALAYSIA SABAH

DISSERTATION SUBMITTED IN FULFILLMENT FOR
THE DEGREE OF MASTER OF MOLECULAR BIOLOGY

BIOTECHNOLOGY RESEARCH INSTITUTE

UNIVERSITY MALAYSIA SABAH

2013



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UNIVERSITI MALAYSIA SABAH

ABSTRACT

PHYLOGEOGRAPHY OF THE ASIAN SNAKEHEAD FISH (*CHANNA STRIATA* BLOCH) IN SABAH AS REVEALED BY MICROSATELLITE MARKERS.

Channa striata (Bloch, 1793), locally known as Haruan or Jalak in Sabah, is an important fish in the Malaysian domestic market due to its high economic value as a food fish with therapeutic properties. The increase in demand for the fish has led to overfishing in the wild and presumably this has led to population fragmentation and a loss of genetic diversity of the fish. A previous study had investigated the amount of genetic diversity among four wild populations in the West coast region of Sabah (Tuaran, Papar, Penampang and Kota Belud) via microsatellite markers. However, this study focuses on samples from the East coast regions of Sabah. The data will be compiled to obtain a comprehensive picture of the genetic diversity that is present in the Asian snakehead fish in Sabah. DNA from Tawau (30 samples), Sandakan (20 samples), Lahad Datu (30 samples), Kinabatangan (16 samples) and Beluran (30 samples) was amplified using nine microsatellite loci. The PCR products were then subjected to fragment analysis through capillary electrophoresis using the ABI3130 Genetic Analyzer. A total of 242 individuals from the West coast and East coast populations show the presence of allelic polymorphism with the number of alleles ranging from five to twelve alleles per locus across all nine loci. The effective number of allele ranged from 1.5864 to 5.0624. The mean observed heterozygosity and expected heterozygosity of the populations ranged from 0.4148 to 0.7722 and 0.4243 to 0.6802, respectively. The result shows Sandakan has the highest, whereas Lahad Datu has the lowest level of genetic diversity among the nine wild populations. UPGMA analysis shows two groups of cluster that separates the East coast and West coast populations. Tuaran and Penampang, and Papar and Kota Belud were clustered together, respectively, as the first cluster, while Tawau and Sandakan, and Lahad Datu, Kinabatangan and Beluran were clustered together, respectively in a second cluster. The overall result indicates subdivision between the East coast and West coast region of Sabah. Meanwhile there is no population subdivision in the East coast region and shows a possible gene flow within the division. The information revealed from this study will be useful for the future conservation and management of the fish.