MORPHOMETRICS, MERISTICS AND MOLECULAR GENETICS OF SNAKEHEAD FISH IN MALAYSIA

BUT MINH TAM

DUCTOR OF PHILOSOFHY KOLEJ UNIVERSITI SAINS DAN TEKNOLOGI MALAYSIA 2006

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BUI MINH TAM

Thesis Submitted in Fulfilment of the Requirement of the Degree of Doctor of Philosophy in the Institute of Tropical Aquaculture Kolej Universiti Sains dan Teknologi Malaysia

September 2006

DEDICATION

To the loving and sacred memory of my father

BÙI VĂN ÚT

Who left me forever on 6th December, 2004

Abstract of thesis presented to the Senate of Kolej Universiti Sains dan Teknologi Malaysia in fulfilment of the requirements for the degree of Doctor of Philosophy

MORPHOMETRICS, MERISTICS AND MOLECULAR GENETICS OF SNAKEHEAD FISH IN MALAYSIA

BUI MINH TAM

September 2006

Chairperson	:	Associate Professor Abol Munafi Ambok Bolong, Ph.D.
Member	:	Professor Azmi Ambak, Ph.D. Associate Professor Patimah Ismail, Ph.D.
Institute	:	Institute of Tropical Aquaculture

Most of the Southeast Asian countries including Malaysia, 70% of the protein sources come from fish. Fish and aquatic organisms constitute a major portion of Malaysian diets. The snakehead fishes play an important role among the freshwater food fish species. There are six species of snakehead fish in Malaysia, namely *Channa marulioides, C. melasoma, C. lucius, C. gachua, C. micropeltes,* and *C. striatus.* Some aspects of morphology and molecular genetics of these species were conducted in this study. The main objectives of this study were (i) to taxonomy snakehead species of Malaysia based on morphology, (ii) to detect genetic variation among snakehead species in Peninsular Malaysia using RAPD, (iii) to definite the phylogeny of Channidae using mitochondria (iv) to design specific primer (Microsatellite method) for snakehead species.

RAPD technology is a useful tool for identifying DNA polymorphism, estimation of genetic diversity and differentiation of related species in fish. However, it is essential

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to optimize RAPD amplification condition and ascertain the reproducibility of RAPD markers for individual taxa prior to apply RAPD fingerprinting to any genetic analysis. In current study, the dendrogram showed that *Channa striatus*, *C. melasoma* and *C. gachua* were closer. The genetic similarity coefficient was 0.7563. It can be concluded that they were in the same group. Meanwhile *C. marulioides* and *C. micropeltes* were in the same cluster. However, *C lucius* was not the same group with other five species.

Mitochondria DNA was sequenced using cytochrome *b* gene. Genomic were extracted from 35 individuals of 6 snakehead species in Malaysia. Primers named cytochrome *b* (L14841: 5' -AAA AAG CTT CCA TCC AAC ATC TCA GCA TGA TCA AA- 3' and H15149: 5' -AAA CTG CAG CCC CTC AGA ATG ATA TTT GTC CTC A- 3') were used as gene amplification. Results indicated that the species belonged to two major clades. The first clade was *C. marulioides* and *C. micropelte*. The second clade comprised of species named *C. striata, C. gachua, C. lucius* and *C. melasoma*.

Microsatellite are widely used as genetic markers. The randomly amplified microsatellites (RAM) is one of new procedures to amplify repeat locus. The anchor primers (PCT4, PCTA, PCTB, PCTC) were succeeded the amplification. Transformation and ligation were done successfully with 4 anchor primers. Among the designed primers, Haruan 4-2 gave the good band. The result have developed a novel technique to produce a microsatellite rich PCR profile from genomic DNA which was cloned to yield a genomic library enriched for microsatellites. Sequence data and subsequence allele scoring within pedigrees revealed that these

microsatellites retained their original repeat length and segregated normally. This technique permits genomic amplification with only one specific primer. Together with enrichment, the savings in primer cost reduces the cost of microsatellite characterization considerably.

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