

UNIVERSITI PUTRA MALAYSIA

DEVELOPMENT AND ISOLATION OF DNA MICROSATELLITE MARKERS FOR THE CHARACTERISATION AND IDENTIFICATION OF MYSTUS NEMURUS (C & V)

CHAN SOON CHOY

FSAS 2003 36

DEVELOPMENT AND ISOLATION OF DNA MICROSATELLITE MARKERS FOR THE CHARACTERISATION AND IDENTIFICATION OF MYSTUS NEMURUS (C & V)

By

CHAN SOON CHOY

Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia, Requirements for the Degree of Master of Science

October 2003



Abstract of thesis presented to the Senate of Universiti Putra Malaysia in fulfilment of the requirement for the degree of Master of Science

DEVELOPMENT AND ISOLATION OF DNA MICROSATELLITE MARKERS FOR THE CHARACTERISATION AND IDENTIFICATION OF Mystus nemurus (C & V)

By

CHAN SOON CHOY

October 2003

Chairman : Professor Tan Soon Guan, Ph.D.

Faculty : Science and Environmental Studies

Mystus nemurus or better known as 'ikan Baung' is an indigenous species in Malaysia. The popularity of this freshwater fish among the locals had made it an economically important aquaculture candidate. Of the so many DNA marker systems available, microsatellites are particularly useful for population studies and have been proven to be the most efficient due to their codominant modes of inheritance.

Two methods were used to isolate microsatellites in *M. nemurus*, namely Random Amplified Hybridisation Microsatellites (RAHMs) and Random Amplified Microsatellites (RAMs). A total of 88 microsatellite sequences and 18 cryptic simple regions were produced. The majority (90%) of these microsatellites were detected by the RAMs method while the RAHMs method required further optimisation and modification. The isolation of microsatellites resulted in 33 primer pairs being designed.



Of these, a total of 15 microsatellite loci were employed in a genetic variation study of *M. nemurus* from seven different locations in Malaysia. The populations involved in this study included Perak, Kedah, Terengganu, UPM, Sarawak, Johor (Layanglayang) and Johor (Kahang River). The number of alleles per locus ranged from 4 to 13 with an average of 8.5. The highest value of observed heterozygosity was 0.3914 (UPM) and the lowest value was 0.2356 (Terengganu). The F_{ts} values indicated heterozygote deficiencies in all the populations studied. Besides, the chi-square goodness of fit test and the G log-likelihood ratio test showed that the majority of loci deviated significantly from Hardy-Weinberg Equilibrium (HWE). The results obtained indicated that the small sample sizes caused the deviations from HWE and the deficiencies of heterozygotes. The presence of null alleles was another reason for such results since their occurrence was high (23.5%). The cluster analysis showed that the Perak and Terengganu populations were the closest and that the majority of the clusterings was in accordance with the geographical regions from which the populations were obtained.

Cross-species amplification studies of *M. nemurus* primers were conducted on *Pangasius micronemus* and *Clarias batrachus*. The successful cross-species amplifications indicated that microsatellite loci were conserved among catfish species in other family taxa. This conservation of microsatellites in other catfish species will save time and valuable resources since the development of microsatellite markers for each catfish species is not necessary. A cluster analysis was also performed to investigate the genetic relationships among the three catfish species. The results showed that *M. nemurus* was closer to *P. micronemus* based on the calculated genetic distance values.

Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai keperluan ijazah Master Sains

PEMBANGUNAN DAN PEMENCILAN BAGI PENANDA MIKROSATELIT DNA UNTUK PENCIRIAN DAN PENGENALPASTIAN BAGI Mystus nemurus (C & V)

Oleh

CHAN SOON CHOY

Oktober 2003

Pengerusi : Professor Tan Soon Guan, Ph.D.

Fakulti : Sains dan Pengajian Alam Sekitar

Mystus nemurus atau lebih dikenali sebagai "ikan Baung" merupakan spesies asli di Malaysia. Populariti ikan air tawar ini di antara penduduk tempatan menjadikannya calon akuakultur yang penting dari segi ekonomi. Bagi kebanyakan sistem penanda DNA yang tersedia, mikrosatelit sangat berguna untuk kajian populasi dan ia terbukti adalah paling efisien disebabkan oleh sifat perwarisan kodominannya.

Dua kaedah telah digunakan untuk memencil mikrosatelit dalam *M. nemurus*, iaitu "Random Amplified Hybrisation Microsatellites (RAHMs)" dan "Random Amplified microsatellites (RAMs)". Sejumlah 88 jujukan mikrosatelit dan 18 "cryptic simple regions" telah dihasilkan. Majoriti (90%) mikrosatelit telah dikesan dengan kaedah RAMs manakala kaedah RAHMs perlu dioptimumkan dan diubahsuaikan selanjutnya. Pemencilan mikrosatelit ini mengakibatkan 33 pasangan primer direka.



Daripada jumlah tersebut, sejumlah 15 lokus mikrosatelit digunakan dalam kajian variasi genetik bagi *M. nemurus* dari tujuh lokasi yang berlainan di Malaysia. Populasi-populasi yang terlibat dalam kajian ini merangkumi Perak, Kedah, Terengganu, UPM, Sarawak, Johor (Layang-layang) dan Johor (Sungai Kahang). Bilangan alel per lokus berjulat daripada 4 hingga 13 dengan purata 8.5. Nilai tertinggi bagi keheterozigotan yang dicerap ialah 0.3914 (UPM) dan nilai terendah ialah 0.2356 (Terengganu). Nilai F_{is} menunjukkan kekurangan heterozigot dalam semua populasi yang dikaji. Selain itu, ujian "chi-square goodness of fit" dan "G log-likelihood ratio" menunjukkan majoriti lokus menyimpang dengan signifikan daripada keseimbangan Hardy-Weinberg (HWE). Keputusan yang diperolehi ini menunjukkan bahawa saiz sampel menyebabkan penyimpangan dari HWE dan kekurangan heterozigot. Kehadiran "null alelles" adalah sebab lain bagi keputusan seumpama ini kerana kewujudannya adalah tinggi (23.5%). Analisis kelompok menunjukkan bahawa populasi Perak dan Terengganu adalah terdekat dan majoriti kekelompokan adalah selaras dengan kawasan geografi.

Kajian amplifikasi merentasi-spesies dengan primer *M. nemurus* dilakukan ke atas *Pangasius micronemus* dan *Clarias batrachus*. Kejayaan amplifikasi merentasispesies menunjukkan bahawa lokus mikrosatelit dipelihara di antara spesies ikan deduri dalam takson famili yang lain. Pemeliharaan mikrosatelit ini akan menjimatkan masa dan sumber bernilai kerana perkembangan penanda mikrosatelit bagi setiap spesies ikan deduri adalah tidak perlu. Analisis kelompok juga dilakukan untuk menyelidik hubungan genetik di antara ketiga-tiga spesies ikan deduri. Keputusan ini menunjukkan bahawa *M. nemurus* adalah terdekat dengan *P. micronemus* berdasarkan kepada nilai jarak genetik yang dikira.

ACKNOWLEDGEMENTS

I would like to express my deepest appreciation and thanks to my supervisors Prof. Dr. Tan Soon Guan, Associate Prof. Dr. Siti Shapor Siraj and Prof. Datin Dr. Khatijah Yusoff for their guidance, continuous support and interest in my research. Without their supervision and valuable comments, I would not have managed to come so far to complete this work.

I would like to gratefully acknowledge the financial support from the Intensification of Research in Priority Areas (IRPA) project grant no. 01-02-04-0074 headed by Prof. Dr. Tan Soon Guan and the Intensification of Research in Priority Areas (IRPA) project grant no. 09-02-04-0207 headed by Associate Prof. Dr. Siti Shapor Siraj. My research work would not have run smoothly without the support of these two IRPA project grants.

I would also like to thank Associate Prof. Dr. Siti Khalijah Daud for providing me access to her lab for the use of the gel documentation system, which is important for my work.

My thanks also go to my undergraduate student, Miss Chin Fee Wai who has helped me with the catfish project and also made teaching an exciting experience for me. With her company, I felt the work to be more enjoyable.



I sincerely thank my seniors in the genetics lab Dr. Sahar Usmani and Dr. Vijay Kumar for their friendship and their advice in the practical lab work and explanations on microsatellites when I first started this project.

I would like to thank my friends Hoh Boon Peng, Hisyam and especially Lee Kok Kuan for helping me with the fish breeding part of my project. I will always cherish their friendship. Without them, life in the lab would be boring, uneventful and uninteresting.

I am grateful and thankful to my parents and brother for their support and advice in my studies for so many years. I am really indebted for their love and faith in me.

Finally, I would like to acknowledge everyone who had helped me in one way or another in this project.



TABLE OF CONTENTS

AF	STRACT	Page ii	
	STRAK	iv	
	ACKNOWLEDGEMENTS		
AP	APPROVAL		
DE	CLARATION	х	
	ST OF TABLES	xiii	
	ST OF FIGURES	xv	
LIS	ST OF ABBREVIATIONS	xvii	
CF	IAPTER		
1	INTRODUCTION	1	
2	LITERATURE REVIEW	5	
	2.1 Taxonomy in suborder Siluroidei	5	
	2.1.1 Mystus nemurus (Cuvier and Valenciennes)	5	
	2.1.2 Pangasius micronemus (Bleeker)	8	
	2.1.3 Clarias batrachus (Linnaeus)	11	
	2.2 Importance of catfishes in the aquaculture industry	13	
	2.3 Genetic studies of the catfish family	16	
	2.4 Microsatellites	19	
	2.5 Random Amplified Microsatellites (RAMs) 2.6 Random Amplified Hybridisation Microsatellites (RAHMs)	21 23	
	2.0 Random Amplified Hybridisation Microsatemics (RATIVIS)	25	
3	MATERIALS AND METHODS	25	
	3.1 Collection of samples	25	
	3.1.1 Collection of samples for population study	25	
	3.1.2 Collection of samples for Mendelian inheritance study	27	
	3.1.3 Collection of samples for cross-species amplification study	28	
	3.2 Preparation of genomic DNA	28	
	3.2.1 Genomic DNA isolation	28	
	3.2.2 Genomic DNA quantification	29	
	3.2.3 Genomic DNA concentration standardisation	30	
	3.3 Isolation of Microsatellites	30	
	3.3.1 Random Amplified Hybridisation Microsatellites (RAHMs)	30 39	
	3.3.2 Random Amplified Microsatellites (RAMs) 3.3.3 Submission of DNA sequences to GenBank	39 41	
	3.3.4 Primer design for microsatellite markers	41	
	3.4 Application of microsatellite markers	42	
	3.4.1 Population study of <i>Mystus nemurus</i>	42	
	3.4.2 Cross-species amplification study	45	
	3.4.3 Gel electrophoresis	47	
	3.5 Statistical analysis	49	
	-		
4	RESULTS	51	
	4.1 Isolation and identification of Microsatellite loci	51	



4.1.1 Isolation of Microsatellites by RAHMs	51
4.1.2 Isolation of Microsatellites by RAMs	56
4.2 Microsatellite primer pairs designed	69
4.3 Population study of Mystus nemurus	72
4.3.1 Screening of Microsatellite primer pairs	72
4.3.2 Microsatellite banding profiles	75
4.3.3 Level of heterozygosity	82
4.3.4 Hardy-Weinberg Equilibrium (HWE)	83
4.3.5 Genetic distance and cluster analysis	99
4.3.6 Linkage Disequilibrium (LD)	104
4.3.7 Analysis of population subdivisions	104
4.3.8 Mendelian inheritance and family study of Microsatellite markers	105
4.4 Cross species amplification study	108
4.4.1 Microsatellite markers banding profiles	108
4.4.2 Genetic distance and cluster analysis	111
5 DISCUSSION	113
5.1 Isolation of Microsatellites	113
5.1.1 Isolation of Microsatellites by RAHMs	114
5.1.2 Isolation of Microsatellites by RAMs	115
5.1.3 Cryptic simple regions	116
5.2 Population study	117
5.2.1 Mendelian inheritance study of Microsatellite markers	117
5.2.2 Level of heterozygosity	118
5.2.3 Hardy-Weinberg Equilibrium (HWE)	119
5.2.4 Linkage Disequilibrium (LD)	120
5.2.5 Genetic distance and cluster analysis of Mystus nemurus	120
5.2.6 Cryptic species and hybrids	123
5.3 Cross-species amplification of Mystus nemurus microsatellite loci	126
5.3.1 Relationship of Mystus nemurus and other catfish species	127
5.3.2 Importance of cross-species amplification study	128
5.4 Application of Microsatellite markers in the aquaculture industry	129
5.5 Future studies	132
6 CONCLUSION	135
REFERENCES	137
APPENDICES	148
A.1 Microsatellite sequences of <i>M. nemurus</i>	148
B.1 Microsatellite primer pair sequences screened for the use in populations studies	154
C.1 Microsatellite allele frequencies at 15 polymorphic loci across seven populations of <i>M. nemurus</i>	159
 C.2 Linkage disequilibrium between pairs of microsatellite loci for each population calculated using Burrow's composite measure of linkage disequilibrium 	162

BIODATA OF THE AUTHOR

164

LIST OF TABLES

Table		Page
3.1	Sample size (N) of each population from different geographical locations	25
3.2	RAMs primers that were designed	40
3.3	Microsatellite markers used for the population and family segregation studies	44
3.4	List of microsatellite primer pairs and the annealing temperatures used in the cross-species amplification study	46
4.1	List of microsatellite probes and their GC contents	53
4.2	List of microsatellites isolated from <i>M. nemurus</i> using the RAMs and RAHMs methods	60
4.3	Types of microsatellites isolated by the RAMs and RAHMs methods	69
4.4	Microsatellites in <i>M. nemurus</i> , primer pair sequences and the expected PCR amplification product sizes	70
4.5	Microsatellite variation in seven populations of M. nemurus	84
4.6	Number of observed and expected alleles and the values of F_{is} statistics for all the loci	91
4.7	Chi-square and likelihood ratio tests for Hardy-Weinberg Equilibrium in all the populations	92
4.8	Nei's (1978) unbiased genetic distances (below diagonal) and identity based (above diagonal) on 15 microsatellite markers in seven populations of <i>M. nemurus</i>	101
4.9	Nei's (1978) unbiased genetic distances (below diagonal) and identity (above diagonal) based on 15 microsatellite markers in six populations of <i>M. nemurus</i>	102
4.10	Nei's (1978) unbiased genetic distances (below diagonal) and identity (above diagonal) based on 35 microsatellite markers in six populations of <i>M. nemurus</i>	103
4.11	Comparison of the observed and expected Mendelian ratios among the F_1 progenies for 15 microsatellite loci	107



Table

4.12	List of microsatellite markers used in the cross-species amplification study and the characteristic of the markers	109
4.13	Nei's (1978) unbiased genetic distance (below diagonal) and identity (above diagonal) based on five microsatellite markers for three different species of catfish	112



LIST OF FIGURES

Figure		Page
2.1	(A) Lateral view of <i>M. nemurus</i> and (B) shows a dorsal view of <i>M. nemurus</i>	7
2.2	A lateral view of P. micronemus	9
2.3	A lateral view of C. batrachus	12
3.1	Map of Malaysia indicating the sampling locations of <i>M. nemurus</i>	26
3.2	Southern blot – Capillary transfer of DNA from agarose gels	33
3.3	A vertical polyacrylamide gel electrophoresis apparatus	48
4.1	Comparison of bands produced by three RAPD primers before and after hybridisation	52
4.2	Colony hybridisation for both the RAHMs and RAMs methods	54
4.3	Microsatellite sequences produced by the ABI PRISM 377 DNA Sequencer	55
4.4	Electrophoresis of PCR product from the amplification of <i>M</i> . <i>nemurus</i> DNA using RAMs primer on a 2% agarose gel	57
4.5	Plasmid DNA of RAMs clones	57
4.6	Microsatellite sequences obtained from manual sequencing of LR2 positive clone	58
4.7	Cryptic simple sequence in clone LR2-1-21(ii)	59
4.8	Comparison of microsatellite banding profiles produced by primer pair MnRmD10-1	75
4.9	Diagram showing the position of a heteroduplex band in a gel	76
4.10	Microsatellite banding profile of <i>M. nemurus</i> samples from UPM using primer pair MnLR2-1-21A	78
4.11	Microsatellite banding profile of <i>M. nemurus</i> samples from Johor (Layang-layang) using primer pair MnLR2-1-19A	78
4.12	Microsatellite banding profile of <i>M. nemurus</i> samples from UPM using primer pair MnLR2-1-24C	79



Figure

4.13	Microsatellite banding profile of <i>M. nemurus</i> samples from Perak using primer pair MnSC4-1A	79
4.14	Microsatellite banding profile of <i>M. nemurus</i> samples from Johor (Layang-layang) using primer pair MnRmR2-1	80
4.15	Microsatellite banding profile of <i>M. nemurus</i> samples from Terengganu using primer pair MnRm9-1	80
4.16	Comparison of microsatellite banding profiles of samples from Johor (Kahang river) with UPM and Sarawak for primer MnSC4-1A	81
4.17	A dendrogram based on Nei's (1978) genetic distances clustered by UPGMA for seven populations of <i>M. nemurus</i> (based on 15 microsatellite loci)	101
4.18	A dendrogram based on Nei's (1978) genetic distances clustered by UPGMA for six populations of <i>M. nemurus</i> (based on 15 microsatellite loci)	102
4.19	A dendrogram based on Nei's (1978) genetic distances clustered by UPGMA for six populations of <i>M. nemurus</i> (based on 35 microsatellite loci)	103
4.20	Microsatellite banding profile of cross-species amplification samples from <i>P. micronemus</i> using primer pair MnRmB11-1.	110
4.21	Microsatellite banding profile of cross-species amplification samples from <i>C. batrachus</i> using primer pair MnRmC5-1	110
4.22	A dendrogram based on Nei's (1978) genetic distances clustered by UPGMA for three different species of catfish (based on five microsatellite loci)	112



LIST OF ABBREVIATIONS

α	alpha
γ	gamma
μg	microgram
μl	microlitre
ρmol	picomole
10X	ten times
1X	one time
A	adenosine
bp	base pair
C	cytosine
cM	centi Morgan
dATP	deoxyadenosine triphosphate
dCTP	deoxycytosine triphosphate
ddH₂O	double distilled water
dGTP	deoxyguanine triphosphate
DNA	deoxyribonucleic acid
dNTPs	deoxynucleotide triphosphate
dTTP	deoxythymine triphosphate
EDTA	ethylenediamine tetraacetic acid
g	gram
G	guanosine
h	hour
kb	kilobase
kg	kilogram
LB	Luria-Bertani
Μ	molar
mCi	milli curie
mg	milligram
mg/ml	milligram per millilitre
MgCl ₂	magnesium chloride
min	minute
mL	millilitre
mM	millimolar
mm	millimetre
ng	nanogram
nm %G	nanometre
°C	degree celsius
OD PCR	optical density
RNA	polymerase chain reaction ribonucleic acid
	relative centrifugal force
x g s	second
s SDS	sodium dodecyl sulphate
T	thymine
TBE	tris-borate-EDTA
U	unit
0	unit



UV	ultraviolet
V	volt
v/v	volume per volume
W	watt



CHAPTER 1

INTRODUCTION

The total population of the world at present exceeds six billion and the figure is expected to increase year by year. Because of this, food is one of the main agenda discussed globally. Due to the high demand for food security and the shortage of meat protein supply, attention is now being focussed more on aquaculture as a source of food.

Mystus nemurus is an indigenous freshwater fish that is found in the rivers and lakes of the Southeast Asian region. In Malaysia, *M. nemurus* is a favourite food among the locals for its good quality meat and taste. According to Kamarudin *et al.* (1987), the fish has high crude protein content and it is low in crude fat compared to chicken, beef and pork. Salmon and tuna fish are imported to Malaysia as alternative sources of food which are healthier due to their polyunsaturated fatty acid contents. Problems arise when the prices in the wet market are unaffordable for low income consumers. Thus, *M. nemurus* is an economical solution to the problem at hand. Since *M. nemurus* has gained popularity among the locals, it has the potential to be commercially produced to sustain the high demand of food from aquaculture. Therefore, introducing this fish to the aquaculture industry is an essential step towards commercial production of this fish.

At present most of the fish in the markets are caught from the wild. Extensive fishing at the commercial level will result in a decline of the natural fish population. Thus, it adds up to the importance of *M. nemurus* as an aquaculture species. As it is with



most terrestrial animal and plant breeding programmes, the ultimate goal of aquaculture particularly fish breeding is to improve commercially important quantitative traits such as colour, protein content, body mass and disease resistance through a predetermined direction. However, modern breeding programmes have led to the erosion of the genetic base for future breeding which poses a threat to the survival of aquacultured species (Kincaid, 1983). Besides, inbreeding depression arising from poor breeding practices often result in loss of heterozygosity of the breeding population, eventually causing constrictions in the gene pool.

Genetic variation of the natural population that had been introduced in the aquaculture industry needs to be assessed and managed. Variation is an important component of biodiversity and should be conserved for its intrinsic value (Ferguson *et al.*, 1995). The concept of the centre of diversity was introduced by the Russian geneticist, Nicolai I. Vavilov (Fairbanks and Andersen, 1999). This had led to the realisation of the importance of conserving genetic resources. The concept describes that a region of maximum variation, usually having a number of endemic forms and characteristics, can usually be considered as the centre of type-formation in the world. Indigenous fish species like *M. nemurus* has the most genetic diversity in Southeast Asia and needs to be conserved.

Conservation of natural populations of *M. nemurus* is essential to prevent the loss of genetic variation of the fish. Natural populations act as gene banks in nature. The genetic base of broodstock populations for the aquaculture industry must not be over exploited. By preserving the genetic diversity of natural populations, breeders will



always have the choice to select new broodstock populations that has superior quality for future selection and breeding programmes.

In fisheries, the use of DNA level markers for conservation and effective breeding programmes has gained considerable importance over the past decades. Polymorphisms reflect genetic variations and are detected at higher levels in the DNA when compared to other levels of markers such as isozymes and morphological markers. Of all the different DNA markers, microsatellites exhibit attributes that make them suitable for applications in aquaculture and fisheries research (O'Reilly and Wright, 1995). In some countries, genetic markers such as microsatellites have been widely used in fisheries management (Martin *et al.*, 1992; Ferguson *et al.*, 1995) to achieve efficient resource utilisation. This leads to the importance of identification and characterisation of population units by using genetic markers.

Broodstock management with the use of DNA level markers had not been widely realised and practised particularly in the Malaysian aquaculture industry. Most local farms still use the traditional approaches in breeding. In Malaysia, studies of local fish species through molecular markers are limited. For example, only limited studies on *M. nemurus* had been done at the DNA level (Chong *et al.*, 2000; Usmani, 2002). The studies that had been done were mainly at the protein level (Daud *et al.*, 1989; Patimah *et al.*, 1989; Siraj *et al.*, 1998). More studies on the fish population structure are therefore needed to give a better understanding of the species in order to encourage and establish more farms. Thus, it is essential to develop microsatellite markers for *M. nemurus* for more successful and effective breeding programmes.



Besides, microsatellite markers are applicable for careful monitoring of natural populations so as to ensure that the natural gene pool is conserved.

In this study, the objectives were:

- 1. to develop microsatellite markers for *M. nemurus*,
- 2. to characterise and evaluate the inheritance of these microsatellite markers from parents to offspring,
- 3. to employ these microsatellite markers for population study, and
- 4. to investigate the conservation of these microsatellites in closely related catfish species.



CHAPTER 2

LITERATURE REVIEW

2.1 Taxonomy in suborder Siluroidei

2.1.1 Mystus nemurus (Cuvier and Valenciennes)

2.1.1.1 Taxonomy

The classification of "ikan Baung" is shown as below (Mohsin and Ambak, 1983):

Kingdom	: Animalia
Phylum	: Chordata
Superclass	: Pisces
Class	: Osteichthyes
Subclass	: Teleostomi
Superorder	: Ostariophysi
Order	: Cypriniformes
Suborder	: Siluroidei
Superfamily	: Bagroidae
Family	: Bagridae
Genus	: Mystus
Species	: Mystus nemurus

The catfishes possessed many generic names. It was first given the name *Mystus* by Gronow in 1763 and this was later validated by Scopoli in 1977. In the year 1856, Dumerill replaced *Mystus* with *Macrones*, which is still used in most books, and it is preoccupied in entomology. Several other names used before as synonyms for this fish are *Aoria*, *Hemibagrus*, *Hypselobagrus* and *Aspidobagrus* (Mohsin and Ambak, 1983).



Mystus nemurus, better known to the locals as "ikan baung", is one of the popular freshwater fish in Malaysia which belongs to the catfish group. This species gained its popularity due to the high nutritional value and good taste. "Ikan baung" or river catfish resembles the cat with four pairs of whiskers like barbels around the mouth (Figure 2.1). The barbels are divided into a pair of nasal barbels, which reached the eyes; a pair of maxillary barbels reaching to the far end of the anal fin; a pair of mandibulary barbels reaching the base of the pectorals and a pair of mental barbels which are shorter.

Its head morphologically looks broader than high with upper jaw slightly longer than lower jaw. It has a long or moderate adipose fin and a dorsal fin with a pungent spine that is serrated in its hind border. The pectoral fins also have pungent spine serrated behind. The caudal fin is deeply forked with the upper lobe more or less produced and pointed.

Mystus species is scaleless with size and colour variation occurs depending on the habitat of origin. The catfish found in Thailand are generally yellowish in colour and the ones that are found in Malaysia are grey or black. The body size is much larger in Thailand compared to Malaysia. These wide variations could be attributed to several factors such as environmental as well as genetic variation (Chong *et al.*, 2000).

