



UNIVERSITI PUTRA MALAYSIA

**GENETIC STUDIES AND GROWTH PERFORMANCE OF
THE YELLOW CATFISH, MYSTUS NEMURUS (CUV. & VAL.)
IN THAILAND**

SANGA LEESANGA

FSAS 2002 8

**GENETIC STUDIES AND GROWTH PERFORMANCE OF
THE YELLOW CATFISH, *MYSTUS NEMURUS* (CUV. & VAL.)
IN THAILAND**

SANGA LEESANGA

**DOCTOR OF PHILOSOPHY
UNIVERSITI PUTRA MALAYSIA**

2002



**GENETIC STUDIES AND GROWTH PERFORMANCE OF
THE YELLOW CATFISH, *MYSTUS NEMURUS* (CUV. & VAL.)
IN THAILAND**

By

SANGA LEESANGA

**Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia,
in Fulfilment of the Requirement for the Degree of Doctor of Philosophy**

April 2002



Abstract of thesis presented to the senate of Universiti Putra Malaysia in fulfilment of the requirement for the degree of Doctor of Philosophy.

**GENETIC STUDIES AND GROWTH PERFORMANCE OF
THE YELLOW CATFISH, *MYSTUS NEMURUS* (CUV. & VAL.)
IN THAILAND**

By

SANGA LEESANGA

April 2002

Chairman : Associate Professor Dr. Siti Shapor Siraj, Ph.D.

Faculty : Science and Environmental Studies

Yellow catfish, *Mystus nemurus*, was examined to determine levels of genetic sub-population differentiation among samples of this species obtained from different parts of its range, as well as to compare the genetics of wild and hatchery-bred fish. Horizontal starch gel electrophoresis and histochemical staining techniques were used to examine genetic variation within and among 8 wild and one hatchery populations of *M. nemurus* in Thailand. Individual specimens were analyzed at 23 protein-coding loci. Fifteen of the 23 loci examined (65.22 %) were polymorphic. Observed heterozygosities ranged from 0.041 to 0.111. Genetic distance estimates ranged from 0.005 to 0.164. The greatest genetic distance was found between the Chainat and Suratthani populations (0.164), which probably, a level indicative of subspecific differentiation in *M. nemurus* from within Thailand.

Eight wild populations collected from throughout Thailand and a hatchery stock of *M. nemurus* were also analyzed at the molecular (DNA) level using the technique of RAPD-PCR fingerprinting. Five arbitrary primers were chosen to amplify products which showed 28 polymorphic loci (60.87 %). The highest genetic distance (D) was found between the Chainat and Suratthani populations with a value of 0.289, whereas the lowest was found in the pair of Songkhla population and hatchery stock with a value of 0.087. The dendrogram depicts the genetic relationships among populations of *M. nemurus* which grouped into four clusters according to their regions of origin namely northern group (Chiengrai and Sukhothai), central group (Kanchanaburi and Chainat), north-eastern group (Nongkhai and Nakormpanom) and southern group (Suratthani, Songkhla and hatchery stock).

Horizontal starch gel electrophoresis was applied to differentiate between Mystid and Tachysurid species of catfish : *Mystus nemurus*, *M. cavasius*, *M. gulio*, *Tachysurus caelatus* and *T. truncatus*, collected from the Tapee River, Thailand. Individual fishes were analysed for 22 enzymatic loci. Eleven loci (50.00 %) were found to be polymorphic ($P < 0.95$). The percentage of polymorphic loci ranged from 14.3 % in *T. caelatus* to 38.1 % in *M. nemurus*. The highest mean heterozygosity was found in *T. truncatus* (0.121 ± 0.048) and the lowest in *M. cavasius* (0.026 ± 0.014). Genetic distance estimates among *Mystus* species ranged from 0.167 to 0.364 while genetic distance was 0.359 between the two species of *Tachysurus*. The genetic distance estimates between *Mystus* and *Tachysurus* populations ranged from 0.693 to 0.878.

Morphometric and meristic variation among two populations from Chainat and Suratthani, which showed the highest genetic distance based on both the isozyme and DNA data, were studied. From the 23 morphometric characters examined, 20 characters showed significant differences. Most characters from the Chainat population differed from the Suratthani population especially for eye diameter (ED) and the distance from the posterior end of the dorsal fin to the anterior end of the adipose fin (DDA), which seemed to be consistent diagnostic characters differentiating the two populations.

The relative growth performance of *M. nemurus* collected from northern (Uttaradith), central (Chainat), and southern Thailand (Suratthani) were investigated. Three populations of fish broodstocks were induced to spawn at the same time. The fish larvae were nursed in 0.5 x 2.0 x 0.2 m tanks for 8 weeks. After nursing the fingerlings were separated into 2 groups and cultured at a stocking density of 50 fish/cage in 1.0 x 1.0 x 1.5 m floating net cages, in which one group was placed in the north (Lumpang) and another group in the south of Thailand (Suratthani). Fish were fed to satiation with 30 % protein pellets for 48 weeks. At the end of the experiment, the growth performance of fish from both locations (north and south Thailand) were taken and analyzed. The highest growth was found in the population from the south, whereas the lowest growth was found in the central population. The results are in accordance with the values of genetic distances based on both isozyme and RAPD data.

Abstrak tesis ini adalah dipersembahkan kepada Senat Universiti Putra Malaysia untuk memenuhi keperluan untuk Ijazah Doktor Falsafah.

**GENETIK DAN KAJIAN PERTUMBUHAN IKAN BAUNG,
MYSTUS NEMURUS (CUV. & VAL.) DI THAILAND**

Oleh

SANGA LEESANGA

April 2002

Pengerusi : Prof. Madya Dr. Siti Shapor Siraj, Ph. D

Fakulti : Sains dan Pengajian Alam Sekitar

Perbandingan sub populasi ikan baung, *Mystus nemurus* yang diambil dari tempat yang berlainan dan juga perbandingan ikan liar dengan ikan hatcheri (ternakan) telah dijalankan. Elektroforesis gel kanji horizontal dan teknik perwarnaann histokimia telah dilakukan untuk mengenalpasti variasi genetik antara 8 populasi liar dengan 1 populasi hatcheri *Mystus nemurus* di Thailand. Dua puluh tiga lokus pengkodan protein telah dianalisis untuk setiap spesimen. Antara 23 lokus yang dikaji 15 lokus atau 65.22% adalah polimorfik. Diperhatikan bahawa heterozigositi berjulat daripada 0.005 hingga 0.164. Jarak genetik yang paling besar dijumpai antara populasi Chainat dan populasi Suratthani (0.164), ini menunjukkan terdapatnya perbezaan subspesifik dalam *M. nemurus* di Thailand.

Lapan populasi liar sekitar Thailand dan stok hatcheri *M. nemurus* juga telah diuji pada peringkat molekul (DNA) dengan menggunakan teknik cap jari RAPD-PCR.

Lima primer pengenalpastian telah dipilih dalam mengamplifikasikan produk-produk yang menunjukkan 28 lokus polimorfik (60.87%). Jarak genetik (D) yang tertinggi juga dijumpai antara populasi Chainat dan Suratthani dengan nilai 0.289. Manakala yang terendah telah dijumpai antara populasi Songkala dan stok hatcheri dengan nilai 0.087. Dendrogram menerangkan hubungan genetik antara populasi-populasi *M. nemurus* yang dapat dibahagikan kepada 4 kumpulan berdasarkan kawasan: iaitu kumpulan utara (Chianggrai dan Sukhotai), kumpulan tengah (Kanchanaburi dan Chainat), kumpulan timur laut (Nongkhai dan Nakornpanon) dan kumpulan selatan (Surathani, Songkhla dan stok hatcheri).

Elektroforesis gel kanji horizontal telah digunakan untuk membandingkan antara spesies Mystid dan Tachysurid : *Mystus nemurus*, *M. cavacius*, *M. golio* *Tachysurus caelatus* dan *T. truncatus* yang diambil dari sungai Tapee, Thailand. Setiap ekor ikan dianalisis pada 22 lokus enzim. Sebelas lokus (50.00 %) telah dikenalpasti sebagai polimorfik ($P < 0.95$). Peratus lokus polimorfik berjulat daripada 14.3% pada *T. caelatus* hingga 38.1% pada *M. nemurus*. Min heterozigositi yang tertinggi didapati pada spesies *T. truncatus* (0.121 ± 0.048), manakala yang terendah pada *M. cavacius* (0.026 ± 0.014). Jarak genetik antara spesies *Mystus* adalah berjulat daripada 0.167 hingga 0.364, manakala nilai antara 2 spesies *Tachysurus* adalah 0.359. Jarak genetik antara *Mystus* dan *Tachysurus* berjulat daripada 0.693 hingga 0.878.

Ciri-ciri morfometrik dan meristik juga dikaji untuk 2 populasi dari Chainat dan Suratthani yang menunjukkan jarak genetik tertinggi dari segi isozim dan paras DNA.

Daripada 23 ciri-ciri morfometrik yang diuji, 20 ciri menunjukkan perbezaan bererti pada 99% menggunakan ujian-T. Banyak ciri-ciri dari populasi Chainat yang berbeza dari populasi Suratthani, terutamanya pada diameter mata (ED) dan jarak antara hujung posterior sirip dorsal dengan hujung jarak anterior sirip adipos (DDA), ciri-ciri tersebut menunjukkan perbezaan yang ketara antara kedua-dua populasi.

Kadar pertumbuhan *M. nemurus* yang berasal dari bahagian utara (Uttaradith), bahagian tengah (Chainat) dan selatan Thailand (Suratthani) telah dikaji. Induk ikan dari 3 populasi tersebut telah dibiakkan pada masa yang sama. Larva dipelihara dalam tangki bersaiz 50 x 200 x 20 cm selama 8 minggu. Selepas tempoh ini anak-anak ikan dari setiap populasi dibahagikan kepada 2 kumpulan untuk dikultur di utara (Lumpang) dan selatan (Suratthani) Thailand. Anak-anak ikan tersebut dikulturkan dalam sangkar terapung yang bersaiz 1.0 x 1.0 x 1.5 m dengan ketumpatan 50 ekor/sangkar. Makanan rumusan yang mengandungi 30% protein diberikan selama 48 minggu. Pada akhir ujikaji ini, kadar pertumbuhan dari kedua-dua lokasi ini (utara dan selatan Thailand) diambil dan dianalisis. Populasi dari selatan Thailand (Suratthani) telah menunjukkan kadar pertumbuhan yang tertinggi, manakala populasi tengah Thailand (Chainat) telah menunjukkan kadar pertumbuhan yang terendah dengan paras perbezaan pada $P < 0.05$. Keputusan ini telah menunjukkan persamaan dengan nilai jarak genetik yang berdasarkan isozim dan teknik cap jari RAPD

ACKNOWLEDGEMENTS

First and foremost, I would like to express my utmost gratitude to my highly respected supervisors, Assoc. Prof. Dr. Siti Shapor Siraj, Assoc. Prof. Dr. Siti Khalijah Daud, Prof. Dr. Tan Soon Guan, and Assoc. Prof. Dr. Sharr Azni Harmin for their valuable advice, guidance and support throughout my project.

I wish to extend my sincere thanks to Dr. Plodprasop Surassawadi, Mr. Sanay Polprasith, Mr. Sompote Ukkataweewat, Mr. Suebpong Chatmalai and Dr. Cherdskak Veerapat, Fisheries Department of Thailand, Dr. Anake Topakngam, Khon Khen University, for giving me an opportunity to study and allowance.

I would like to thank Dr. Panom K. Sodsuk and Dr. Srirat Sodsuk (National Aquaculture Genetics Research Institute, Thailand), Dr. Pattana Srifa and Mr. Grisana Pintong (Kasetsart University), Mrs. Salimah Said, Miss Chong Lee Kim, Mr. Foo Thong Lim and Miss Carol Wong Yoke Pei (Universiti Putra Malaysia) for their kind information about the various techniques used in this project.

Special thanks are extended to Mrs. Annie Christianus, Mr. Lee Kok Kuan, Mr. Krisanuphan Komenpririn, Mr. Noppadol Jindhaphan, Mrs. Jareeporn Meesri, and Miss. Naiyana Teekha who have provided their kind assistance in this thesis.

I wish to thank the staff of the Department of Fisheries, Thailand for their assistance on tissue collection. I would also like to thank the Department of Biology, Faculty of Science and Environmental Studies, Universiti Putra Malaysia (UPM) for the facilities of laboratory and unfailing support.

Financial support from the SEAMEO Regional Center for Graduate Study and Research in Agriculture (SEARCA) and the Government of Malaysia through IRPA (Intensification of Research in Priority Areas) program of the Ministry of Science, Technology and the Environment are gratefully acknowledged.

Last but not least, my deepest appreciation to my parent, my wife (Mrs. Sermsiri Leesanga) and my children (Gunthira Leesanga and Leenapatra Leesanga) for their constant encouragement and understanding during the course of the study.



I certify that an Examination Committee met on 30th April 2002 to conduct the final examination of Mr. Sanga Leesanga on his Doctor of Philosophy thesis entitled "Genetic studies and growth performance of the yellow catfish, *Mystus nemurus* (Cuv. & Val.) in Thailand" in accordance with Universiti Petanian Malaysia (Higher Degree) Act 1980 and Universiti Petanian Malaysia (Higher Degree) Regulations 1981. The Committee recommended that the candidate be awarded the relevant degree. Members of the Examination Committee are as follows:

AZIZ ARSHAD, Ph.D.

Senior Lecturer,
Faculty of Science and Environmental Studies,
Universiti Putra Malaysia
(Chairman/Independent Examiner)

SITI SHAPOR SIRAJ, Ph.D.

Associate Professor,
Faculty of Science and Environmental Studies,
Universiti Putra Malaysia
(Member)

SITI KHALIJAH DAUD, Ph.D.

Associate Professor,
Faculty of Science and Environmental Studies,
Universiti Putra Malaysia
(Member)

TAN SOON GUAN, Ph.D.

Professor,
Faculty of Science and Environmental Studies,
Universiti Putra Malaysia
(Member)

SHARR AZNI HARMIN, Ph.D.

Associate Professor,
Faculty of Agriculture,
Universiti Putra Malaysia
(Member)

PETER B. MATHER, Ph.D.

Associate Professor,
School of Natural Resource and Science,
Queensland University of Technology
(Independent Examiner)



SHAMSHER MOHAMAD RAMADILI, Ph.D.,

Professor/Deputy Dean,
School of Graduate studies,
Universiti Putra Malaysia

Date: 06 MAY 2002



This thesis submitted to the Senate of Universiti Putra Malaysia has been accepted as fulfilment of the requirement for the degree of Doctor of Philosophy.

AINI IDERIS, Ph.D.
Professor/Dean,
School of Graduate Studies,
Universiti Putra Malaysia

Date:

DECLARATION

I hereby declare that the thesis is based on my original work except for quotations and citations which have been duly acknowledged. I also declare that it has not been previously or concurrently submitted for any other degree at UPM or other institutions.

Name: **SANGA LEESANGA**

Date : **May 2, 2002**

TABLE OF CONTENTS

		Page
	ABSTRACT	ii
	ABSTRAK	v
	ACKNOWLEDGEMENTS	viii
	APPROVAL SHEETS	x
	DECLARATION	xii
	LIST OF TABLES	xv
	LIST OF FIGURES	xviii
	LIST OF ABBREVIATIONS OF TERMS	xxiv
CHAPTER		
I	INTRODUCTION	1
II	LITERATURE REVIEW	6
	Taxonomic Classification	6
	<i>Mystus</i> spp.	6
	<i>Mystus nemurus</i> (Cuvier & Valenciennes)	7
	<i>Mystus cavasius</i> (Hamilton)	13
	<i>Mystus gulio</i> (Hamilton)	14
	<i>Tachysurus</i> spp.	15
	<i>Tachysurus caelatus</i> (Cuvier & Valenciennes)	16
	<i>Tachysurus truncatus</i> (Cuvier & Valenciennes)	16
	Biochemical Genetic Markers	16
	Molecular Genetic Markers	19
	Random Amplified Polymorphic DNA (RAPD)	20
	Polymerase Chain Reaction (PCR)	21
	Breeding of <i>M. nemurus</i>	22
	Growth Performance of <i>M. nemurus</i>	22
III	BIOCHEMICAL POLYMORPHISMS IN YELLOW CATFISH, <i>Mystus nemurus</i> (CUV. & VAL.), FROM THAILAND	27
	Introduction	27
	Materials and Methods	28
	Results	39
	Discussion	56
IV	INTRASPECIFIC POLYMORPHISMS IN <i>Mystus nemurus</i> (CUV. & VAL.) DETECTED BY RAPD-PCR FINGERPRINTING	58
	Introduction	58

CHAPTER	Page
Materials and Methods	59
Results	67
Discussion	82
V	
GENETIC DIVERGENCE AND RELATIONSHIPS AMONG FIVE SPECIES OF <i>Mystus</i> AND <i>Tachysurus</i> SPECIES	95
Introduction	95
Materials and Methods	96
Results	102
Discussion	119
VII	
MORPHOLOGICAL AND MERISTIC DIFFERENCES IN COMPARISON TO BIOCHEMICAL AND MOLECULAR DIFFERENCES BETWEEN TWO POPULATIONS OF YELLOW CATFISH, <i>Mystus nemurus</i> (CUV. & VAL.), IN THAILAND	121
Introduction	121
Materials and Methods	122
Results	127
Discussion	130
VIII	
GROWTH PERFORMANCE IN CAGE CULTURE AMONG THREE POPULATIONS OF YELLOW CATFISH, <i>Mystus nemurus</i> (CUV. & VAL.) REARED IN THAILAND	132
Introduction	132
Materials and Methods	133
Results	141
Discussion	164
IX	
DISCUSSION	166
X	
SUMMARY	171
BIBLIOGRAPHY	173
APPENDICES	182
BIODATA OF THE AUTHOR	220

LIST OF TABLES

Table		Page
1	Number of fish, total length (cm) and body weight (g) of yellow catfish, <i>M. nemurus</i> , from different localities in Thailand.	29
2	List of enzymes, sarcoplasmic protein and haemoglobin examined, loci identified and tissue specificity observed in <i>M. nemurus</i> .	40
3	List of monomorphic and polymorphic loci.	49
4	Allele frequencies of polymorphic isozyme and protein loci (at 0.95 level) in <i>M. nemurus</i> .	50
5	Genetic variability at 23 loci in all populations (standard error in parentheses) of <i>M. nemurus</i> in Thailand.	52
6	Genetic similarity among pairs of populations of <i>M. nemurus</i> from Thailand (Nei, 1978).	53
7	Nei's (1978) genetic distances among pairs of populations of <i>M. nemurus</i> from Thailand.	54
8	Sequence and OPERON codes of primers used to study polymorphisms of <i>Mystus nemurus</i> .	64
9	Sequence and OPERON codes of the random primers used to study polymorphisms of <i>Mystus nemurus</i> .	68
10	Number of amplified bands together with size range of amplified fragments (bp) in eight wild populations and a hatchery stock of <i>M. nemurus</i> revealed by RAPD fingerprinting.	74
11	Total number of bands, percentage of monomorphic and polymorphic bands found in 8 wild populations and a hatchery stock of <i>M. nemurus</i> from Thailand, which were generated by RAPD fingerprinting.	77
12	Estimated similarity index (<i>S</i>) within the eight wild populations and a hatchery stock of <i>M. nemurus</i> revealed by RAPD fingerprinting.	79

Table	Page
13 Similarity index of 8 wild populations and a hatchery stock based on Nei and Li's (1979) band sharing similarity indices from RAPD markers.	80
14 Genetic distances of 8 wild populations and a hatchery stock based on Nei and Li's (1979) band sharing similarity indices from RAPD markers.	81
15 Number of fishes, total length (cm) and body weight of <i>Mystus</i> spp and <i>Tachysurus</i> spp from the Tapee River, southern Thailand.	98
16 List of enzymes, sacroplasmic protein and haemoglobin examined, loci identified and tissue specificity observed in <i>Mystus</i> spp and <i>Tachysurus</i> spp.	101
17 Allelic variants of the five species : <i>Mystus cavasius</i> , <i>M. gulio</i> , <i>M. nemurus</i> , <i>Tachysurus caelatus</i> , <i>T. truncatus</i> , according to their mobilities.	111
18 Allele frequencies of polymorphic allozyme and protein loci (at P=0.05) in <i>Mystus</i> spp and <i>Tachysurus</i> spp.	112
19 Genetic variability at 22 loci in all species (standard error in parentheses) of <i>Mystus</i> spp. and <i>Tachysurus</i> spp. in Thailand.	115
20 Similarity index in each pair of five species of <i>Mystus</i> spp. and <i>Tachysurus</i> spp. (following Nei, 1978).	116
21 Genetic distance coefficients for each pair of <i>Mystus</i> spp and <i>Tachysurus</i> spp. (following Nei, 1978).	117
22 Detail information of yellow catfish, <i>Mystus nemurus</i> , which were used for morphological analysis.	125
23 Proportion of measured morphological characters in the two populations of yellow catfish, <i>Mystus nemurus</i> (Cuv. & Val.), collected from central (Chainat) and southern Thailand (Suratthani), and comparison between both populations by <i>t-test</i> .	128
24 Values of meristic characters of yellow catfish, <i>Mystus nemurus</i> , collected from the central (Chainat) and southern Thailand (Suratthani), and comparison between both populations by <i>t-test</i> .	129

Table		Page
25	Summary of data on induced spawning of <i>M. nemurus</i> using bucerelin acetate together with domperidone.	143
26	Growth performance of yellow catfish, <i>M. nemurus</i> populations from Uttaradith, Chainat and Suratthani cultured in cages in the north Thailand (Lumpang province).	146
27	Growth performance of yellow catfish, <i>M. nemurus</i> populations from Uttaradith, Chainat and Suratthani cultured in cages in the south Thailand (Suratthani province).	147
28	Growth, survival rate and production of yellow catfish, <i>M. nemurus</i> from Uttaradith, Chainat and Suratthani populations cultured in cage in the north (Lumpang) and south Thailand (Suratthani).	159
29	Range of air temperatures and water quality parameters in nursing tanks of yellow catfish, <i>M. nemurus</i> , fry produced by parents from the populations of the north (Uttaradith province), central (Chainat province), and south Thailand (Suratthani province).	162
30	Range of air temperature and water quality parameters in the experimental cages of yellow catfish, <i>M. nemurus</i> , cultured both in the north (Lumpang) and south Thailand (Suratthani).	163

LIST OF FIGURES

Figure		Page
1	Sampling locations of <i>Mystus nemurus</i> in Thailand.	30
2	Electrophoretic patterns of Aspartase amino transferase, <i>AAT-1*</i> from the liver of <i>M. nemurus</i> collected from Chiengrai (lane 1-3), Sukhothai (lane 4-6), Kanchanaburi (lane 7), Chainat (lane 8-10), Nongkhai (lane 11), Nakornpanom (lane 12), Suratthani (lane 13), Songkhla (lane 14), and hatchery of SIFDC (lane 15).	41
3	Electrophoretic patterns of Isocitrate dehydrogenase, <i>IDH-1*</i> from the liver of <i>M. nemurus</i> collected from Chiengrai (lane 1), Sukhothai (lane 2), Kanchanaburi (lane 3), Chainat (lane 4), Nongkhai (lane 5-7), Nakornpanom (lane 8-9), Suratthani (lane 10-12), Songkhla (lane 13-15), and hatchery of SIFDC (lane 16-18).	42
4	Electrophoretic patterns of Phosphoglucomutase, <i>PGM*</i> from the liver of <i>M. nemurus</i> collected from Chiengrai (lane 1), Sukhothai (lane 2-3), Kanchanaburi (lane 4-6), Chainat (lane 7-8), Nongkhai (lane 9-10), Nakornpanom (lane 11-13), Suratthani (lane 14-16), Songkhla (lane 17), and hatchery of SIFDC (lane 18-21).	43
5	Electrophoretic patterns and genotypes postulated for Aspartase amino transferase (<i>AAT-1*</i>) from the liver of yellow catfish, <i>Mystus nemurus</i> , collected from the Chiengrai (a), Sukhothai (b) and Chainat (c) populations.	44
6	Electrophoretic patterns and genotypes postulated for Glucose phosphate isomerase (<i>GPI*</i>) from the liver of yellow catfish, <i>Mystus nemurus</i> , collected from Suratthani population.	45
7	Electrophoretic patterns and genotypes postulated for Isocitrate dehydrogenase (<i>IDH*</i>) from kidney (a) and liver (b and c) of yellow catfish, <i>Mystus nemurus</i> , collected from Chiengrai (a), Songkhla (b) and hatchery stocks (c).	46
8	Electrophoretic patterns and genotypes postulated of Malate dehydrogenase (<i>MDH*</i>) from the liver of yellow catfish, <i>Mystus nemurus</i> , collected from Chiengrai population.	47

Figure	Page
9 Electrophoretic patterns and genotypes postulated for Phosphoglucomutase (<i>PGM*</i>) from the liver of yellow catfish, <i>Mystus nemurus</i> , collected from Sukhothai (a), Chainat (b) and Suratthani (c) populations.	48
10 UPGMA dendrogram constructed based on Nei's genetic distances among populations of <i>M. nemurus</i> in Thailand.	55
11 RAPD patterns obtained from <i>M. nemurus</i> genotypes using primer OPA-11.	69
12 RAPD patterns obtained from <i>M. nemurus</i> genotypes using primer OPA-14.	70
13 RAPD patterns obtained from <i>M. nemurus</i> genotypes using primer OPA-18.	71
14 RAPD patterns obtained from <i>M. nemurus</i> genotypes using primer OPA-19.	72
15 RAPD patterns obtained from <i>M. nemurus</i> genotypes using primer OPA-20.	73
16 UPGMA cluster analysis based on genetic similarity from RAPD-PCR markers for fourteen fish, <i>M. nemurus</i> , of Chiengrai population.	83
17 UPGMA cluster analysis based on genetic similarity from RAPD-PCR markers for fourteen fish, <i>M. nemurus</i> , of Sukhothai population.	84
18 UPGMA cluster analysis based on genetic similarity from RAPD-PCR markers for fourteen fish, <i>M. nemurus</i> , of Kanchanaburi population.	85
19 UPGMA cluster analysis based on genetic similarity from RAPD-PCR markers for fourteen fish, <i>M. nemurus</i> , of Chainat population.	86
20 UPGMA cluster analysis based on genetic similarity from RAPD-PCR markers for fourteen fish, <i>M. nemurus</i> , of Nakornpanom population.	87

Figure	Page
21 UPGMA cluster analysis based on genetic similarity from RAPD-PCR markers for fourteen fish, <i>M. nemurus</i> , of Nongkhai population.	88
22 UPGMA cluster analysis based on genetic similarity from RAPD-PCR markers for fourteen fish, <i>M. nemurus</i> , of Suratthani population.	89
23 UPGMA cluster analysis based on genetic similarity from RAPD-PCR markers for fourteen fish, <i>M. nemurus</i> , of Songkhla population.	90
24 UPGMA cluster analysis based on genetic similarity from RAPD-PCR markers for fourteen fish, <i>M. nemurus</i> , of hatchery population.	91
25 UPGMA dendrogram constructed based on RAPD-PCR genetic distances among populations of <i>M. nemurus</i> in Thailand.	92
26 Five species of catfish which were investigated using horizontal starch gel electrophoresis.	99
27 Map showed sampling site for all species of <i>Mystus</i> spp and <i>Tachysurus</i> spp.	100
28 Electrophoretic patterns of lactase dehydrogenase (<i>LDH*</i>) and relative mobility in different tissues : heart (H), liver (L), kidney (K), and muscle (M) shown by <i>Mystus caelatus</i> (lane 1, 6, 11, 16), <i>M. gulio</i> (lane 2, 7, 12, 17), <i>M. nemurus</i> (lane 3, 8, 13, 18), <i>Tachysurus caelatus</i> (lane 4, 9, 14, 19) and <i>T. truncatus</i> (lane 5, 10, 15, 20), collected from the Tapee River, Thailand.	104
29 Electrophoretic patterns of malate dehydrogenase (<i>MDH*</i>) and relative mobility in different tissues : heart (H), liver (L), kidney (K), and muscle (M) shown by <i>Mystus caelatus</i> (lane 1, 6, 11, 16), <i>M. gulio</i> (lane 2, 7, 12, 17), <i>M. nemurus</i> (lane 3, 8, 13, 18), <i>Tachysurus caelatus</i> (lane 4, 9, 14, 19) and <i>T. truncatus</i> (lane 5, 10, 15, 20), collected from the Tapee River, Thailand.	105
30 Electrophoretic patterns of haemoglobin (<i>HB*</i>) and sarcoplasmic protein (<i>SP*</i>) and relative mobility shown by <i>Mystus caelatus</i> (lane 1, 6), <i>M. gulio</i> (lane 2, 7), <i>M. nemurus</i> (lane 3, 8), <i>Tachysurus caelatus</i> (lane 4, 9) and <i>T. truncatus</i> (lane 5, 10), collected from the Tapee River, Thailand.	106

Figure	Page
31 Electrophoretic patterns and genotypes postulated of phosphoglucosmutase (<i>PGM*</i>) from the liver of <i>Tachysurus truncatus</i> collected from the Tapee River, Thailand.	107
32 Electrophoretic pattern of phosphoglucosmutase (<i>PGM*</i>) from the liver of <i>Mystus caelatus</i> (lane 1-3), <i>M. gulio</i> (lane 4-7), <i>M. nemurus</i> (lane 8-10), <i>Tachysurus caelatus</i> (lane 11-12) and <i>T. truncatus</i> (lane13-15) collected from the Tapee River, Thailand.	108
33 Electrophoretic patterns and genotypes postulated of glucose phosphate isomerase (<i>GPI-1*</i> and <i>GPI-2*</i>) from the liver of <i>Tachysurus truncatus</i> collected from the Tapee River, Thailand.	109
34 Electrophoretic pattern of glucose phosphate isomerase (<i>GPI-1*</i> and <i>GPI-2*</i>) from the liver of <i>Mystus caelatus</i> (lane 1), <i>M. gulio</i> (lane 2-3), <i>M. nemurus</i> (lane 4-5), <i>Tachysurus caelatus</i> (lane 6-7) and <i>T. truncatus</i> (lane9-13) collected from the Tapee River, Thailand.	110
35 UPGMA dendrogram constructed from Nei's genetic distances among species of <i>Mystus</i> spp and <i>Tachysurus</i> spp from Thailand.	118
36 Yellow catfish, <i>Mystus nemurus</i> , collected from Chainat (a) and Suratthani (b) provinces, Thailand.	124
37 Diagram of a catfish, <i>Mystus nemurus</i> (Cuv. & Val.), showing measurements taken for the morphometric analysis.	126
38 Collecting sites of broodstocks (Uttaradith, Chainat, and Suratthani), and culture places (Lumpang and Suratthani) of <i>Mystus nemurus</i> in Thailand.	140
39 Mean weight of yellow catfish, <i>M. nemurus</i> , fry which were produced by the parent populations from the north (Uttaradith), central (Chainat), and south Thailand (Suratthani).	144
40 Mean length of yellow catfish, <i>M. nemurus</i> , fry which were produced by the parent populations from the north (Uttaradith), central (Chainat), and south Thailand (Suratthani).	145
41 Mean weight of yellow catfish, <i>M. nemurus</i> , which were produced by the parent populations from the north (Uttaradith), central (Chainat), and south (Suratthani), cage cultured in the north of Thailand (Lumpang province).	148

Figure	Page
42 Mean weight of yellow catfish, <i>M. nemurus</i> , which were produced by the parent populations from the north (Uttaradith), central (Chainat), and south (Suratthani), cage cultured in the south of Thailand (Suratthani province).	149
43 Total length of yellow catfish, <i>M. nemurus</i> , which were produced by the parent populations from the north (Uttaradith), central (Chainat), and south (Suratthani), cage cultured in the north of Thailand (Lumpang province).	150
44 Total length of yellow catfish, <i>M. nemurus</i> , which were produced by the parent populations from the north (Uttaradith), central (Chainat), and south (Suratthani), cage cultured in the south of Thailand (Suratthani province).	151
45 Weight frequency of yellow catfish, <i>M. nemurus</i> , which were produced by the parent populations from the north (Uttaradith), central (Chainat), and south (Suratthani), cage cultured in the north of Thailand (Lumpang province).	152
46 Weight frequency of yellow catfish, <i>M. nemurus</i> , which were produced by the parent populations from the north (Uttaradith), central (Chainat), and south (Suratthani), cage cultured in the south of Thailand (Suratthani province).	153
47 Length frequency of yellow catfish, <i>M. nemurus</i> , which were produced by the parent populations from the north (Uttaradith), central (Chainat), and south (Suratthani), cage cultured in the north of Thailand (Lumpang province).	154
48 Length frequency of yellow catfish, <i>M. nemurus</i> , which were produced by the parent populations from the north (Uttaradith), central (Chainat), and south (Suratthani), cage cultured in the south of Thailand Suratthani province).	155
49 Percentage weight gain of yellow catfish, <i>M. nemurus</i> , which were produced by the parent populations from the north (Uttaradith), central (Chainat), and south (Suratthani), cage cultured in the north of Thailand (Lumpang province).	156
50 Percentage weight gain of yellow catfish, <i>M. nemurus</i> , which were produced by the parent populations from the north (Uttaradith), central (Chainat), and south (Suratthani), cage cultured in the south of Thailand (Suratthani province).	157

Figure		Page
51	Survival rate of yellow catfish, <i>M. nemurus</i> , which were produced by the parent populations from the north (Uttaradith), central (Chainat), and south (Suratthani), cage cultured in the north (Lumpang) and south of Thailand (Suratthani).	160
52	Production of yellow catfish, <i>M. nemurus</i> , which were produced by the parent populations from the north (Uttaradith), central (Chainat), and south (Suratthani), cage cultured in the north (Lumpang) and south of Thailand (Suratthani).	161