



UNIVERSITI PUTRA MALAYSIA

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

SANGA LEESANGA

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By

SANGA LEESANGA

**Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia,
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Abstract of thesis presented to the senate of Universiti Putra Malaysia in fulfilment of the requirement for the degree of Doctor of Philosophy.

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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

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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 perwarna~~an~~an 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 Songkhal 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 (Chiangrai dan Sukhotai), kumpulan tengah (Kanchanaburi dan Chainat), kumpulan timur laut (Nongkhai dan Nakhon Phanom) dan kumpulan selatan (Suratthani, 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 ($P < 0.05$). Peratus lokus polimorfik berjangka 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 berjangka daripada 0.167 hingga 0.364, manakala nilai antara 2 spesies *Tachysurus* adalah 0.359. Jarak genetik antara *Mystus* dan *Tachysurus* berjangka 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

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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.

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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.

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Date : May 2, 2002

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