UNIVERSITI PUTRA MALAYSIA

MORPHOLOGICAL AND GENETIC RELATIONSHIPS AMONG SNAKEHEAD CHANNA STRIATA (BLOCH, 1793) POPULATIONS IN PENINSULAR MALAYSIA

MOHAMMAD HAFIZ BIN ABDUL RAHIM

FPSK(M) 2012 47

MORPHOLOGICAL AND GENETIC RELATIONSHIPS AMONG SNAKEHEAD *CHANNA STRIATA* (BLOCH, 1793) POPULATIONS IN PENINSULAR MALAYSIA

By

MOHAMMAD HAFIZ BIN ABDUL RAHIM

Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia,
in Fulfilment of the Requirement for the degree of Master of Science

January 2012

DEDICATED to

My father, Abdul Rahim Bin Ismail...
who believe in the richness of learning,
his love and support has enabled me to achieve my goals
and finish what I have started

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

MORPHOLOGICAL AND GENETIC RELATIONSHIPS AMONG SNAKEHEAD *CHANNA STRIATA* (BLOCH, 1793) POPULATIONS IN PENINSULAR MALAYSIA

By

MOHAMMAD HAFIZ BIN ABDUL RAHIM

January 2012

Chairman: Professor Abdul Manan Bin Mat Jais, PhD

Faculty: Medicine and Health Sciences

Haruan, the local name for the snakehead *Channa striata*, is a tropical freshwater fish from the Channidae family that is valuable in terms of importance in economics, i.e. as food, and in medicine. Thus, this study was undertaken to determine morphological and genetic relationships among 6 populations of *C. striata* in Peninsular Malaysia.

The morphological and genetic variation of *C. striata* was studied based on polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) of the mitochondrial DNA cytochrome *b* gene (mtDNA cyt *b*) and morphometric and meristic analysis of samples collected from 6 *C. striata* locations around Peninsular Malaysia, namely Johor, Kedah, Kelantan, Pahang, Perak, and Terengganu. A total 120 specimens were used, with standard lengths ranging 17.50–37.50 cm, total lengths ranging 20.60–44.10 cm, and weights ranging 76.70–675.00 g.

Five meristic counts and 23 morphometric measurements were used for the morphological analysis. The quantitative data were analysed by univariate analysis of variance (ANOVA) and multivariate analysis of discriminant function analysis (DFA). The morphometric characteristics were more adequate than the meristic characters for good separation of the populations. In DFA, the results indicated that *C. striata* from different populations can be distinguished using several morphometric characters, namely the ratios of dorsal fin height to standard length (DFH/SL) and caudal peduncle height to standard length (CPH/SL). The findings for the morphological analysis refute an earlier hypothesis of there being no morphological variation between populations of *C. striata*.

For *C. striata* population genetics, 5 restriction endonucleases yielded enzyme-specific restriction morphs in a total of 29 composite mitochondrial DNA (mtDNA) haplotypes. The pairwise Φ_{ST} statistics (-0.01861 to 0.60629) and analysis of molecular variance (AMOVA) (37.57%), results indicated consistency, with sufficient information existing to construct a rational explanation of the snakeheads' genetic heterogeneity. This support for the findings showed that the *C. striata* populations were separated into 2 major clusters, namely clade I (containing the Johor population) and clade II (a mixture of the Kedah, Kelantan, Pahang, Perak, and Terengganu populations), based on unweighted pair group method with arithmetic mean (UPGMA) cluster analysis and the haplotype network of mtDNA cyt *b*. The patterns of high levels of haplotype diversity (h = 0.6789–0.8737) and moderate nucleotide diversity (π = 0.008–0.0181), the observed star or dumbbell-shaped structure of the haplotype network, neutrality tests (D = -0.76304 to 0.53277, $P >$ 0.05 and Fs = -6.16223 to -2.97325, $P < 0.05$), and mismatch distribution (bimodal or unimodal) tests demonstrated that whole populations of *C. striata* saw a recent population demographic expansion. The estimated population expansion in the mtDNA cyt *b* of *C. striata* populations occurred 1.41–1.69 million years ago. However, based on the net Tamura and Nei genetic distance, the divergence among regional populations occurred 0.72–2.6 million years ago.

These findings suggest that morphological and genetic studies provide the information required for increasing the efficiency of *C. striata* management in Peninsular Malaysia, which will be helpful in fisheries, and to biologists, and taxonomists studying these fascinating fishes.

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

HUBUNGAN MORFOLOGI DAN GENETIK ANTARA POPULASI HARUAN *CHANNA STRIATA* (BLOCH, 1793) DI SEMENANJUNG MALAYSIA

Oleh

MOHAMMAD HAFIZ BIN ABDUL RAHIM

Januari 2012

Pengerusi: Profesor Abdul Manan Bin Mat Jais, PhD

Fakulti: Perubatan dan Sains Kesihatan

Haruan, nama tempatan untuk *Channa striata*, merupakan ikan air tawar tropika dari keluarga Channidae yang bernilai dari segi ekonomi, iaitu sebagai makanan, dan dari segi perubatan. Oleh itu, kajian ini dijalankan untuk menentukan hubungan morfologi dan genetik antara 6 populasi *C. striata* di Semenanjung Malaysia.

Variasi morfologi dan genetik *C. striata* dikaji berdasarkan tindak balas rantaian polimerase-polimorfisme panjang cebisan pemotongan (PCR-RFLP) gen sitokrom *b* mitokondria (mtDNA cyt *b*) dan analisis morfometrik dan meristik ke atas sampel yang di perolehi dari 6 lokasi *C. striata* di Semenanjung Malaysia, iaitu Johor, Kedah, Kelantan, Pahang, Perak dan Terengganu. Sejumlah 120 spesimen telah digunakan, dengan panjang piawai antara 17.50–37.50 sm, jumlah panjang antara 20.60–44.10 sm dan berat badan adalah 76.70–675.00 g.

Lima ciri meristik dan 23 ukuran morfometrik telah digunakan untuk analisis morfologi. Data kuantitatif dianalisa dengan analisis univariat varians (ANOVA) dan analisa multivariat analisis fungsi diskriminan (DFA). Ciri morfometrik adalah lebih mencukupi berbanding dengan ciri-ciri meristik untuk tujuan pemisahan terbaik di antara populasi yang dikaji. Keputusan DFA menunjukkan bahawa *C. striata* dari populasi yang berlainan boleh dibezakan dengan menggunakan beberapa ciri-ciri morfometrik, iaitu nisbah tinggi sirip dorsal ke panjang piawai (DFH/SL) dan tinggi kaudal pedunkel ke panjang piawai (CPH/SL). Hasil analisa morfologi telah menolak hipotesis awal yang menyatakan variasi tidak wujud di antara populasi *C. striata*.

Mengenai genetik populasi *C. striata*, 5 endonuklease pemotongan telah menghasilkan “morphs” pemotongan enzim-spesifik dalam jumlah 29 komposit haplotip mtDNA. Statistik Φ_{ST} berpasangan (-0.01861 ke 0.60629) dan analisis varians molekul (AMOVA) (37.57%) berpadan dengan maklumat yang ada, dan mencukupi untuk menghasilkan penjelasan yang rasional menegenai kepelbagaian genetik haruan. Oleh itu, keputusan yang diperolehi menyokong tanggapan bahawa populasi *C. striata* telah dipisahkan kepada 2 kelompok utama, iaitu klad I (yang mengandungi populasi Johor) dan klad II (yang merangkumi populasi Kedah, Kelantan, Pahang, Perak, dan Terengganu) berdasarkan analisis kelompok kaedah kumpulan pasangan tanpa penimbang dengan keertian aritmetik (UPGMA) dan rangkaian haplotip mtDNA sitokrom *b*. Corak paras kepelbagaian haplotip yang tinggi (h = 0.6789–0.8737) dan kepelbagaian nukleotida sederhana (π = 0.008–0.0181), struktur bentuk “star“ atau “dumbbell” rangkaian haplotip, ujian neutraliti (D = -0.76304 ke 0.53277, $P > 0.05$ dan Fs = -6.16223 ke -2.97325, $P < 0.05$), dan ujian pengagihan tidak sepadan (berbentuk bimodal atau unimodal) menunjukkan bahawa populasi keseluruhan *C. striata* mengalami pengembangan populasi demografi. Pengembangan populasi yang dianggarkan dalam mtDNA cyt *b* berlaku 1.41–1.69 juta tahun lalu. Walau bagaimanapun, berdasarkan net Tamura dan jarak genetik Nei, kecapahan pengembangan di populasi serantau berlaku 0.72–2.6 juta tahun lalu.

Keputusan yang diperolehi menunjukkan bahawa kajian morfologi dan genetik membekalkan maklumat yang diperlukan untuk meningkatkan kecekapan pengurusan *C. striata* di Semenanjung Malaysia, yang dan berkemungkinan dapat membantu dalam bidang perikanan serta ahli biologi dan taksonomi yang mengkaji spesis menarik ini.

ACKNOWLEDGEMENTS

First and foremost, I would like to express my thanks and syukur Alhamdullilah to Allah S.W.T for all His blessings and help in making sure the completion of this research study.

Without my supervisor, this research study can never complete the way it intended. I would like to express my gratitude and appreciation to my supervisor Professor Dr. Abdul Manan Mat Jais for his ideas, patience, priceless advices and support in guiding me throughout the whole process in completion of this research study. The special thanks goes to my helpful co-supervisors, Prof. Dr. Patimah Ismail, Madam Rozila Alias and Dr. Norwati Muhammad, who had ever taught me from the moment I step there to continue my master degree and for sharing their knowledge with me. It is only Allah that can repay all your kindness.

I also owe my loving thanks to my wife, Hidayah for her constant love and support all these years and for her standing beside me during the completion of this research and my sweet child Yusuf Fansuri, for always making me smile and for encouragement. Very special thanks go to my father Dr. Abdul Rahim Hj. Ismail who shared with me his knowledge and experience to finish this research study. He has been my inspiration and motivation for continuing to improve my knowledge. Thank you to my loving and supporting family especially my mum Norhayatti Razak who cares and understanding, who making sure I do my best in completing this research study.

My grateful thanks also go to my group and colleagues, Che Ku Dahlan, Sadegh Abedi, Muhamad Faris for providing me great ideas. To Dr. Millor Fernandes Rosario from University of São Paulo and Dr. Siti Azizah Mohd Nor from Universiti Sains Malaysia, who giving me an advices and guidance.

Special thanks to Universiti Putra Malaysia for providing partial financial support through Graduate Research Fellowship (GRF) during the study period and to UPEN Pahang (BSP©/BTK/006; Tabung Amanah-6362300-14001) for trusting and supporting grant of this research project. Great deals appreciated go to the contribution of Universiti Selangor (UNISEL), Forest Research Institute Malaysia (FRIM) and to the entire person who involved directly or indirectly in making this experiment a possible success for me. Million Thank and May Allah bless you all.

I certify that a Thesis Examination Committee has met on 17 January 2012 to conduct the final examination of Mohammad Hafiz Abdul Rahim on his thesis entitled "**Morphological and genetic relationships among snakehead *Channa striata* (Bloch, 1793) populations in Peninsular Malaysia**" in accordance with Universities and University Colleges Act 1971 and the Constitution of the Universiti Putra Malaysia [P.U.(A) 106] 15 March 1998. The Committee recommends that the student be awarded the Master of Science.

Members of the Thesis Examination Committee were follows:

Sabrina Sukardi, PhD
Associate Professor
Faculty of Medicine and Health Sciences
University Putra Malaysia
(Chairman)

Aziz Arshad, PhD
Professor
Faculty of Agriculture
University Putra Malaysia
(Internal examiner)

Siti Khalijah Daud, PhD
Associate Professor
Faculty of Science
University Putra Malaysia
(Internal examiner)

Vijay Kumar, PhD
Associate Professor
Biotechnology Research Institute
University Malaysia Sabah
(External examiner)

SEOW HENG FONG, PhD
Professor and Deputy Dean
School of Graduate Studies
Universiti Putra Malaysia

Date:

This thesis was submitted to the Senate of Universiti Putra Malaysia and has been accepted as fulfilment of the requirement for the degree of Master of Science. The members of the Supervisory Committee were as follows:

Abdul Manan Mat Jais, PhD
Professor
Faculty of Medicine and Health Sciences
University Putra Malaysia
(Chairman)

Patimah Ismail, PhD
Professor
Faculty of Medicine and Health Sciences
University Putra Malaysia
(Member)

Norwati Muhamad, PhD
Forestry Biotechnology Division,
Forest Research Institute Malaysia
(Member)

BUJANG BIN KIM HUAT, PhD
Professor and Deputy Dean
School of Graduate Studies
Universiti Putra Malaysia

Date:

DECLARATION

I declare that the thesis is my original work except for quotations and citations which have been duly acknowledged. I also declare that it has not been previously, and submitted for any other degree at Universiti Putra Malaysia or any other institution.

MOHAMMAD HAFIZ ABDUL RAHIM

Date: 16 January 2012

TABLE OF CONTENTS

CHAPTER

LIST OF TABLES

LIST OF FIGURES

LIST OF ABBREVIATIONS

AA	Arachidonic acid
AFLP	Amplified Fragment Length Polymorphism
AMOVA	Analysis of molecular variance
ANOVA	Analysis of variance
CV	Canonical Variance
Cyt *b*	Cytochrome *b*
DFA	Discriminant Function Analysis
DNA	Deoxyribonucleic acid
DO	Dissolved oxygen
EPA	Eicosapentaenoic acid
FRIM	Forest Research Institute Malaysia
GAP	Good Agriculture Product
GMP	Good Manufacture Practices
HSD	Honestly Significant Difference
IBD	Isolation by distance
LWR	Length Weight Relationship
mtDNA	Mitochondrial DNA
Nm	Gene flow
NTU	Nephelometric Turbidity Units
PCR	Polymerase Chain Reaction
PIC	Polymorphic Information Content
ppt	Parts per thousand
RAPD	Random Amplified Polymorphic DNA

REAP	Restriction Enzyme Analysis Package
RFLP	Restriction Fragment Length Polymorphism
SNPs	Single Nucleotides Polymorphisms
SSRs	Simple Sequence Repeats
STS	Sequence Tagged Sites
UNISEL	Universiti Selangor
UPGMA	Unweighted Pair Group Method with Aritmetic Mean
UPM	Universiti Putra Malaysia

CHAPTER 1

INTRODUCTION

1.1 General Introduction

Haruan, the local name for snakehead *Channa striata*, is an obligate freshwater fish from the Channidae family that possesses a 42 pair diploid (2n) chromosome karyotype. The fish possesses important economic value as a food fish, pharmacological properties, as well as medicinal value. In Malaysia, there is a demand for freshwater fish, *C. striata* in particular, as it has a very good composition of amino acids and fatty acids; a fatty acid compositional study of *C. striata* flesh revealed high levels of arachidonic acid, which is beneficial in the healing of internal and external wounds, an absence of eicosapentaenoic acids, as well as low cholesterol content and a high amount of good-quality protein (Yaakob and Ali, 1992; Mat Jais *et al*., 1998, 2002, 2007b; Gam *et al*., 2006; Zuraini, 2006; Supiwong *et al*., 2009).

Morphologically, *C. striata* is a unique group of freshwater fish. Compared to other species, the fish has distinctively small pelvic fins, while a few others lack them completely. The fish can be distinguished from Channidae family members by their elongated cylindrical body; flattened head; long, entirely soft-rayed dorsal and anal fins; large mouth with well-developed teeth on both upper and lower jaws; tube like anterior nostrils; round to somewhat truncated caudal fins; cycloid or ctenoid body scales; and shield-like scales on the head, where the shape of the head resembles that of a snake (Musikasinthorn, 2003). Moreover, *C. striata* can be distinguished based on coloration, meristics and morphometrics, as well as the distribution of scales on the underside of the lower jaw, shape of the head, morphology of the suprabranchial organs, and a sharp-pointed ridge at the mid-ventral part of the isthmus (Vishwanath and Geetakymari, 2009).

The wild species can be found in small rivers, lakes, pools, and shallow water bodies where agrochemicals are applied. In their natural habitats, *C. striata* are able to survive in harsh environments with low dissolved oxygen and high ammonia levels (Marimuthu and Haniffa, 2007; Cong *et al*., 2008; Jamaluddin *et al*., 2011).

Morphometrics (quantitative) and meristics (qualitative) are 2 types of morphologic characters that have been most commonly used to delineate fish stock. Morphometric characters are continuous characters describing aspects of the body shape. Meristic characters are the number of discrete, serially repeated, countable structures that are unchanged in embryos or larvae (Turan, 2004a). Morphometrics and meristics analysis is considered more appropriate than the use of single morphological characters to investigate and determine the relationship between populations or closely related species. Differences in morphometric and meristic characters among populations of a species are based on the consideration that morphometric characters are usually more related to genetic causes, while meristic characters are much more dependent on environmental differences (Costa *et al*. 2003; Remerie *et al*., 2005).

Cytochrome *b* is one the most important proteins encoding genes on a heavy strand of mtDNA molecules which has been widely used as a molecular marker technique for many applications to access intra- and interspecies genetic diversity, genetic variation, phylogeography, species and hybrid identification, phylogeny in numerous species and genera, population genetic structure, conservation and demographic history (Hsu *et al*., 2009; Li *et al*., 2009; Ma *et al*., 2010; Thangaraj and Lipton, 2010).

In recent years, preliminary analysis of *C. striata* populations has been carried out based on different molecular markers, such as analysis of mitochondrial DNA (mtDNA) (Abol-Munafi *et al*., 2007; Lakra *et al*., 2010; Jamaluddin *et al*., 2011), randomly amplified polymorphic DNA (RAPD; Ambak *et al*., 2006), microsatellite DNA markers (Jamsari *et al*., 2011), and allozyme markers (Hara *et al*., 1998). Restriction fragment length polymorphism (RFLP) combined with polymerase chain reaction (PCR) has been proven to be a successful method for studying the population genetic structure and differentiation of many fishes, such as skipjack tuna (Menezes *et al*., 2006), scad mackerel (Arnaud *et al.*, 1999), tilapia (Espinosa-Lemus *et al*., 2009), arctic grayling (Redenbach and Taylor, 1999), and salmon (King *et al*., 2000).

Due to the potential of *C. striata*, studies have analysed its genetics at the morphological, biological, dietary, physiological, biochemical composition, ecological, and chromosomal level for breeding programs, and medical and pharmaceutical activities for its anti-microbial, anti-inflammatory, cell proliferation, induction of platelet aggregation, and anti-nociceptive properties (Mat Jais, 2007a; Supiwong *et al*., 2009; Dahlan-Daud *et al*., 2010; Jamaluddin *et al*., 2011).

These findings would have potential implications for stock management, conservation, and identification as important resources for the fisheries industry. Such information on this species will be useful in the management of different populations of *C. striata* for Good Agriculture Practices (GAP) in farming technology, as well as provide the basis for Good Manufacturing Practices (GMP).

1.2 Justification of the Study

C. striata is a commercially important freshwater fish in Malaysia which has come to play an important economic role as a food resource, and possesses potential medical values and pharmacological properties. To ensure a constant supply of fresh *C. striata* in accordance with strict biochemical quality requirements and mineral, protein, and lipid composition specifications for biomedical and pharmaceutical products, researchers need to i) provide a preliminary assessment of the unit stock of *C. striata* in Peninsular Malaysia, and ii) investigate which population is of superior genetic quality in order to maintain a high percentage of genetic variability. The present study has potential application in fish stock estimation and proposes measures for sustainable management. If the extent of gene flow were low enough for the stocks to be managed as a single panmictic population, it would be advisable to manage them as a single unit.

1.3 Objective of the Study

The general objective of this thesis was to provide biological information on morphological, stock identification, genetic structure, relationship, and demographic histories on different geographical scales from major regions of the natural distribution areas of the species in Peninsular Malaysia. The specific objectives were:

1) To determine the morphometric and fin rays variations among 6 populations of *C. striata* in Peninsular Malaysia.

2) To determine the length weight relationship of *C. striata*.

3) To determine the level of genetic diversity between and within *C. striata* populations.

4) To estimate the degree of genetic differentiation between *C. striata* populations

REFERENCES

Abol-Munafi, A.B., Ambok, M.A., Ismail, P. and MinhTam, B. 2007. Molecular data from the cytochrome *b* for the phylogeny of Channidae (*Channa* sp) in Malaysia. *Biotechnology* 6 (1): 22–27.

Adam, D.C., Rohlf, F.J. and Slice, D.E. 2004. Geometric morphometrics: Ten years of progress following the 'Revolution'. *Ital. J. Zool.* 71: 5-16.

Adam, D.S. 2003. In: *Lab Math: A Handbook of measurements, calculations, and other quantitative skills for use the bench*, pp: 127. Cold Spring Horbor Laboratory Press.

Adamson, E.A.S., Hurwood, D.A. and Mather, P.B. 2010. A reappraisal of the evolution of Asian snakehead fishes (Pisces, Channidae) using molecular data from multiple genes and fossil calibration. *Molecular Phylogenetics and Evolution*, 56: 707-717.

Ahmed, E.O., Ali, M.E. and Aziz, A.A. 2011. Length-weight relationship and condition factor of six fish species in Atbara river and Khashm El-Girba reservoir, Sudan. *International Journal of Agriculture Sciences,* 3(1): 65-70.

Ali, A.B. 1990. Some ecological aspects of fish populations in tropical ricefields. *J. Hydrobiologia*, 190: 215-222.

Allendorf, F.W. and Leary, R.F. 1988. Conservation and distribution of genetic variation in a polytypic species, the cutthroat trout. *Conserv, Biol.* 2: 170-184.

Ambak, M.A., Bolong, A.A-M., Ismail, P. and MinhTam, B. 2006. Genetic variation of Snakehead fish (*Channa striata*) populations using random amplified polymorphic DNA. *Biotechnology* 5 (1): 104-110.

Angaji, S.A. 2009. Single nucleotide polymorphism genotyping and its application on mapping and marker-assisted plant breeding. *African journal of biotechnology* 8(6): 980-914.

Arnaud, S., Bonhomme, F. and Borsa, P. 1999. Mirochondrial DNA analysis of the genetic relationships among populations of scad mackerel (*Decapterus macarellus*, *D. macrosoma*, *D. russelli*) in South-East Asia. *Marine Biology* 135: 699-707.

Arshad, A., Nurul-Amin, S.M. Yu, G.T. Oh, S.Y., Bujang, J.S. and Ghaffar, M.A. 2008. Population characteristics, length-weight and length-length relationships of *Acetes vulgaris* (Decapoda: Sergestidae) in the Coastal Waters of pontian, Johor, Peninsular Malaysia. *Journal of Biological Sciences* 8(8): 1298-1303.

Arshad, A., Nurul-Amin, S.M., Siraj, S.S. and Japar, S.B. 2007. New distribution records of sergestid shrimp, *Acetes intermedius* (Decapoda: Sergestide) from Peninsular Malaysia with Notes on its Populations Characteristics. *Journal of Biological Sciences* 7(8): 1305-1313.

Avise, J.C. 1993. Molecular markers, natural history and evolution, 1st Edtiton. Chapman and Hall, New York.

Avsar, D.1994. A stock differentiation study of the sprat (*Sprattussprattus phalericus Risso*) off the southern coast of the Black Sea. *Fisheries Research* 19: 363 -78.

Bailey, K.M. Quinn T.J. II., Bentzen, P. and Grant, W.S. (1999). Population structure and dynamics of walleye Pollock, *Theragra chalcogramma. Adv. Mar. Biol.* 37:179-255.

Barriga-Sosa, D.L.A., Jimenez-Bandillo, M.D.L., Ibanez, A.L. and Arredondo-Figueroa, J.L. 2004. Variability of tilapias (*Oreochromis* spp.) introduced in Mexico: morphometric, meristic and genetic characters. *Ichthyology* 20: 7 -14.

Bartlett, S.E. and Davidson, W.S. 1991. Identification of *Thunnus* tuna species by the polymerase chain reaction and direct sequences analysis of their mitochondrial cytochrome *b* genes. *J. fish Aquat Sci.* 48: 309-317.

Beaumont, A.R. and Hoare, K. 2003. *Biotechnology and Genetics in Fisheries and Aquaculture*, pp. 29-31. Oxford: Blackwell Science Ltd.

Beek, J.G.V.D., Folkertsma, R., Zijistra, C., Koert, P.H.G.V., Poleij, L.M. and Bakker, J. 1998. Genetic variation among parthenogenetic *Meloigyne* species revealed by AFLPs and 2D-protein electrophoresis contrasted to morphology. *Fundam. Appl. Nematol.* 21(4):401-411.

Begg, G.A. and Waldman, J.R. 1999. An holistic approach to fish stock identification. *Fish. Res.*37: 269-280.

Bektas, Y. and Belduz, A.O. 2009. Morphological variation among atlantic horse mackerel *Trachurus trachurus* populations from Turkish coastal waters. *Journal of Animal and Veterinary Advances* 8(3):511-517.

Beyene, Y., Botha, A-M. and Myburg, A.A. 2005. A comperatice study of molecular and morphological methods describing genetic relationships in traditional Ethiopian highland maize. *African Journal of Biotechnology* 4(7): 586-595.

Blessing, J.J., Marshall, J.C. and Balcombe, S.R. 2010. Humane killing of fishes for scientific research: a comparison of two methods. *Journal of Fish Biology* 76(10):2571-2577.

Bobori, D.C., Moutopoulos, D.K., Bekri, M., Salvarina, I. and Monuz, A.I.P. 2010. Length-weight relationship of freshwater fish species caught in three Greek lakes. *Journal of Biological Research-Thessaloniki* 14: 219-224.

Boore, J.L. 1999. Animal mitochondrial genomes. *Nucleics Acids Research* 27 (8): 1767-1780.

Botstein, D., White, R.L., Skonick, M. and Davis, R.W. 1980. Construction of a genetic linkage map in man using restriction fragment length polymorphisms. *Am. J. Hum. Genet.* 32: 314-331.

Bowmaker, M., Yang, M.Y., Yasukawa, T., Reyes, A., Jacobs, H.T., Huberman, J.A. and Holt, I.J. 2003. Mammalian mitochondrial DNA replicates bidirectionally from an initiation zone. *Journal of Biological Chemistry* 278 (15): 50961-50969.

Branicki, W., Kupiec, T. and Pawlowski, R. 2003. Validation of cytochrome *b* sequence analysis as a method of species identification. *J. Forensic Sci.* 48: 83-87.

Brock, T.D. and Freeze, H. 1969. Thermus aquaticus gene, n and sp n, and non sporulating extreme thermophile. *J. Bacteriol,* 98: 289-297.

Bronwen, M. H. and Soundy, P. 2008. Southern Blotting as a Diagnostic Method. In *Molecular Niomethods Handbook*, 2nd Edition, ed. J. Walker and R. Rapley, pp. 55-64. Totowa, NJ: Humana Press.

Brown T.A. 1998. Gene cloning: an introduction, 3rd edition. Pp 60 – 249. *Stanley Thornes Ltd*.

Buj, I., Podnar, M., Mrakovcic, M., Caleta, M., Mustafic, P., Zanella, D. and Marcic, Z. 2008. Morphological and genetic diversity of *Sabanjeiwa balcninca* in Croatia. *Folia Zool.* 57(1-2): 100-100.

Cadrin, S.X. 1995. Discrimination of American lobster stocks off southern New England based on secondary sex character allometry. *Canadian Journal of Fisheries and Aquatic Science* 52(12): 2712-2723.

Cadrin, S.X. 2000. Advances in morphometric identification of fishery stocks. *Rev. Fish Biol. Fish.* 10: 91-112.

Canapa, A., Brucca, M., Marinelli, A. and Olmol, E. 2000. Molecular data from the 16s rRNA gene for the phylogeny of Pectinidae (Mollusca: Bivalvia). *Journal of Molecular Evolution* 50(1): 93-97.

Castro, J.A., Picornell, A. and Ramon, M. 1998. Mitochondrial DNAL a tool for populational genetics studies. *Internatl. Microbiol.* 1: 327-332.

Chang, C-H., Lin, W-W., Shao, Y-T., Arai, R., Ishinabe, T.I., Ueda, T., Matsuda, M., Kubota, H., Wang, F-Y., Jang-Liaw, N-H. and Kao, H-W. 2009. Molecular phylogeny and genetic differentiation of the *Tanakia himantegus* Complex (Teleostei: Cyprinidae) in Taiwan and China. *Zoological Studies* 48(6): 823 834.

Collard, B.C.Y., Jahufer M.Z.Z., Brouwer, J.B. and Pang E.C.K. 2005. An introduction to markers, quatitatve trait loci (QTL) mapping and marker assisted selection for crop improvement: The basic concepts. *Euphytica* 142:169-196.

Collin, H. and Fumagalli, L. 2011. Evidence for morphological and adaptive genetic divergence between lake and stream habitats in European minnows (*Phoxinus phoxinus*,Cyprinidae). *Molecular Biology* 20(21): 4490-4502.

Cong, N.V., Phuong, N.T. and Bayley, M. 2008. Brain cholinesterase response in the snakehead fish (*Channa striata*) after field exposure to diazinon. *Ecotoxicology and Environmental Safety* 71: 314-318.

Costa, J.L., Almeida, P.R.D. and Costa, M.J. 2003. A morphometric and meristic investigation of Lusitanian toadfish *Halobatrachus didactylus* (Bloch and Schneider, 1801: evidence of population fragmentation of Portuguese coast. *Sci. Mar*. 67(2): 291-231.

Crozier, R.H. and Crozier, Y.C., 1993. The cytochome *b* and ATPase genes of honeybee mitochondria DNA. *Mol. Biol. Evol.* 10(2): 474-482.

Dahlan-Daud, C.K, Mat Jais, A.M., Ahmad, Z., Akim, A.M. and Adam A., 2010. Amino and fatty acid compositions in Haruan traditional extract (THE). *Bio. Latinoam. Caribe Plant. Med. Aromaticas (BLACPMA)* 9(5): 414-429.

Dambisya, Y.M., Lee, T.L., Sathivulu, V. and Mat Jais, A.M. 1999. The influence of temperature, pH and naloxone on the antinociceptive activity of *Channa stratus* (Haruan) extracts in mice. *J. Ethnopharmacol*. 66: 181-186.

Darlina, M.N., Masazurah, A.R. Jayasamkar, P., Jamsari, A.F.J. and Siti, A.M.N. 2011. Morphometric and molecular analysis of mackerel (*Rastrelliger* spp) from the west coast of Peninsular Malaysia.*Genet. Mol. Res.* 10(3): 2078 2092.

Diaz-Matallana, M., Schuler-Garcia, I., Ruiz-Garcia, M. and Jaramillo, E.H. 2009. Analysis of diversity among six populations of Colombian mango (*Mangifera indica L. cvar*. Hilacha) using RAPDs markers. *Electronic Journal of Biotechnology* 12(3): 1-8.

Dibattista, J.D., Wilcox, C., Craig, M.T., Rocha, L.A. and Bowen, B.W. 2011. Phylogeography of the Pacific Blueline surgeonfish, *Acanthurus nigroris*, reveals high genetic connectivity and a cryptic endemic species in the Hawaiian Archipelago. *Journal of Marine Biology* 839134: 1- 17.

DiMauro, S. and Schon, E.A. 2003. Mitochondrial respitatory-chain diseases. *New Engl. J. Med.* 348: 2656-2668.

Dodgson, J.B., Cheng, H.H. and Okimoto, R. 1997. DNA Marker Technology: A Revolution in Animal Genetics. *Poultry sci*. 75: 1108-1114.

Dodson, J.J., Colombani, F. and Ng, P.K.L. 1995. Phylogeographic structure in mitochondrial DNA of a South-east Asian freshwater fish, *Hemibagrus nemurus* (Siluroidei; Bagridae) and Pleistocene sea-level changes on the Sunda Shelf. *Molecular Ecology* 4: 331-346.

Douglas, M.R., Brunner, P.C. and Douglas, M.E. 2003. Drought in an evolutionary context: molecular variability in Flannelmouth Sucker (*Catostomus latipinnis*) from the Colorado River Basin of western North America. *Freshwater biology* 48: 1254-1273.

Du, X., Chen, Z., Deng, Y. and Zeng, Q. 2009. Comparative analysis of genetic diversity and population structure of *Sipunclus nudus* as revealed by mitochondrial COI sequences. *Biochem. Genet*. 47: 884-891

.

Elliott, N.G., Haskard, K. and Koslow, J.A. 1995. Morphometric analysis of orange roughy *Hoplostethus atlanticus* off the continental slope of Southern Australia. *J. Fish Biol*. 46: 202-220.

Espinosa-Lemus, V., Arredondo-Figueroa, J.L. and Barriga-Sosa, I.D.L.A. 2009. Morphometric and genetic characterization of tilapia (Cichlidae: Tilapiini) stock for effective fisheries management into two Mexican reservoirs. *Hidrobiológica* 19 (2): 95-107.

Espoti, M.D., De Vries, S., Crimi, M., Ghelli, A., Patarnello, T. and Meyer, A. 1993. Mitochondrial cytochrome *b*: evolution and structure of the protein. *Biocimica et Biophysica Acta* 1143: 243-271.

Excoffier, L. and Lischer, H.E.L. 2010. Arlequin suite ver 3.5: a new series of program to perform population genetic analysis under Linux and Window. *Mol. Ecol. Resour*. 10: 564-567.

Excoffier, L. and Smouse, P.E. 1994. Using allele frequency and geographic subdivision to reconstruct gene trees within a species: molecular variance parsimony. *Genetics* 136(1): 343-359.

Fay, J.C. and Wu, C.I. 1999. A human population bottleneck can account for the discordance between patterns of mitochondrial versus nuclear DNA variation. *Mol. Biol. Evol*. 16(7): 1003-1005.

Felsenstein, J. 2005. *PHYLIP (Phylogeny Inference Package) version 3.6.* Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.

Fikiru, E., Tesfaye, K. and Bekele, E. 2007. Genetic diversity and population structure of Ethiopian lentil (*Lensculinaris Medikus*) landraces as revealed by ISSR marker. *African Journal of Biotechnology* 6(12): 1460-1468.

Florence, W.K., Hulley, P.R., Stewart, B.A. and Gibbons, M.J. 2002. Genetic and morphological variation of the lanternfish *Lampanyctodes hectoris* (Myctophiformes:Mytophidae) of southern Africa. *African Journal of Marine Science* 24(1): 193-203.

Froese, R. 2006. Cube law, condition factor and weight-length relationship: history, meta-analysis and recommendations. *J. Appl. Ichthyol* 2: 241-253.

Froese, R. and Pauly, D. 2012. *Channa striata* in Malaysia [Electronic version]. *Fishbase*, pp. 431.

Fry, A.J. and Zink, R.M. 1998. Geographic analysis of nucleotide diversity and song sparrow (Aves: Emberizidae) population history. *Molecular Ecology* 7: 1303 1313.

Fu, Y.X. 1997. Statistical test of neutrality of mutations against population growth, hitchhiking and background selection. *Genetics* 147: 915-925.

Fu, Y.X. and Li, W.H. 1993. Statistical tests of neutrality of mutations. *Genetics* 133(1): 693-709.

Gam, L.H., Leow, C.Y. and Baie, S. 2006. Proteomic analysis of shakehead fish (*Channa striatus*) musle tissue. *Malaysia Journal of Biochemistry and Molecular Biology* 14: 25-32.

Garcia, A.A.F., Benchimol, L.L., Barbosa, A.M.M., Geraldi, I.O., Souza Jr, C.L. and De Souza, A.P., 2004. Comparison of RAPD, RFLP, AFLP and SSR markers for diversity studies in tropical maize inbred lines. *Genetics and molecular biology* 27 (4): 578-588.

Garesse, R. and Vallejo, C.G. 2001. Animal mitochondrial biogenesis and function: a regulatory cross-talk between two genomes. *Gene* 263: 1-16.

Geetakumari, K. and Vishwanath, W. 2010. *Channa melanostigma*, a new species of freshwater shakehead from north-east India (Teleostei: Channidae). *Journal of the Bombay Natural History Society* 107(3): 231-235.

Ghorashi, S.A., Fatemi, S.M., Amini, F., Haushmand, M., Salehi Tabar, R. and Hazaie, K. 2008. Phylogenetic analysis of anemone fishes of the Persian Gulf using mtDNA sequences. *Afr. J. Biotechnol.* 7 (12): 2074-2080.

Goodarzi, F., Darvishzadeh, R., Hassani, A. and Hassanzaeh, A. 2011. Study on genetic variantion in Iranian castor bean (*Ricinus communis* L.) accessions using multivariate statistical techniques. *Journal of Medical Plants Research* 5(21): 5254-5261.

Gourene, G. and Teugals, G.G.1993. Morphological differences between some strains of the tilapias *Oreochromis niloticus et O. aureus* (Teleostei: Ciclidae) used in fishculture. *Cybium* 17: 343-355.

Govindaraju, R.D. 1989. Variation in gene flow levels among predominantly self-pollinated plants. *Journal of Evolutionary Biology* 2: 173-181.

Grant, W.A.S and Bowen, B.W. 1998. Shallow population histories in deep evolutionary lineages of marine fishes: insights from sardines and anchovies and lesion for conservation. *J. Hered.* 89(5): 415-426.

Gross, R., Kohlmann, K. and Kersten, P. 2002. PCR-RFLP analysis of the mitochondrial *ND-3/4* and *ND-5/6* gene polymorphisms in the European and East Asian subspecies of common carp (*Cyprins carpio* L.). *Aquaculture* 204: 504-516.

Guisande, C., Manjarres-Hernandez, A., Pelayo-Villamil, P., Granado-Lorencio, C., Riveriro, I., Acuna, A., Prieto-Piraquive, E., Janeiro, E., Matias, J.M., Patti, C., Patti, B., Mazzola, S., Jimenez, S., Duque, V. and Salmeron, F. 2010. IPez: An expert system for the taxonomic identification of fishes based on machine learning techniques. *Fisheries Research* 102: 240-427.

Gunawickrama, K.B.S. 2007. Morphological heterogeneity in some estuarine populations of the catfish *Arius jella* (Ariidae) in Sri Langka. *Cey. J. Sci.* (*Bio. Sci.*) 36(2): 100-107.

Habib, M., Lakra, W.S., Mohindra, V., Khare, P., Barman, A.S., Singh, A., Lal, K.K., Punia, P. and Khan, A.A. 2010. Evolution of cytochrome *b* mtDNA sequences in genetic diversity studies of *Channa marulius* (Channidae: Perciformes). *Mol. Biol. Rep.* 38(2): 841-846.

Hair, R., Anderson, J.F., Tatham, R. and Black, W. 1996. *Multivariate Data: Analysis with reading*, pp. 449. Prentice Hall Inc., New Jersey.

Halward, T., Stalker, T., Larue, E. and Kochert, G. 1992. Use of single primer DNA amplifications in genetics studies of peanut (*Arachis hypogaea* L.) *Plant Molecular Biology* 18: 315-325.

Han, Z.Q., Lin, S.L., Shui, B.N. and Goa, T.X. 2009. Genetic diversity of small yellow croaker *Larimichthys polyactics* revealed by AFLP markers. *African Journal of Agricultural Research* 4(7): 605-610.

Haniffa, M.A., Nagarajan, M. and Gopalakrishnan, A. 2006. Length-weight relationships of *Channa punctate* (Bloch, 1793) from Western Ghats river of Tamil Nadu. *J. Appl. Ichthyol.* 22: 308-309.

Hara, M., Sekino, M. and Na-Nakom, U. 1998. Genetic differentiation of natural populations of the snake-head, *Channa striatus* in Thailand. *Fisheries Science* 64(4): 526-530.

Harlid, A., Janke, A. and Árnason, Ú. 1997. The mtDNA sequence of the ostrich and the divergence between paleognathous and neognathous birds. *Mol. Biol. Evol.* 14: 754-761.

Harpending, H.C. 1994. Signature of Ancient population growth in a low-resolution mitochondrial DNA mismatch distribution. *Hum. Biol.* 66(4): 591-600.

Haynes, P.S., Allen, B.M., Brophy, D. and McGrath, D. 2008. Fin-ray count variation in 0-group flatfish: Plaice (*Pleuronectes platessa* (L.))and flounder (*Plastessa flesus* L.) on the west of Ireland. *Biology and Environment proceedings of the Royal Irish Academy* 108b(2): 61-67.

Haynes, P.S., McGrath. And Brophy, D. 2010. Variation in fin ray count of o-group turbot (*Psetta maxima*) and brill (*Scophyhalmus rhombus*) on the west coast of Ireland: 2006-2009. *Marine Biodiversity Records* 3: 1-6.

He, A., Luo, Y., Yang, H., Liu, L., Li, S. and Wang, C. 2010. Complete mitochondrial DNA sequences of the Nile tilapia (*Oreochromis niloticus*) and Blue Tilapia (*Oreochromis aureus*): genome characterization and phylogeny applications. *Mol. Biol. Rep.* 38(3): 2015-2021.

Helfman, G.S., Collette, B.B. and Facey, D.E. 1997. *The Diversity of Fishes*, pp.13. Malden, MA: Blackwell Science Press.

Hermida, M., Fernandez, J.C., Amaro, R. and Miguel, E.S. 2005. Morphometric and meristic variation in Galician threespine stickleback populations, northwest Spain. *Enviromental Biology of Fishes* 73:189-200.

Heydranejad, M.S. 2009. Length-weight relationships for six freshwater fish species in Iran. *Chinese J. Oceanol. Limnol.* 27: 61-62.

Hofmann, S. and Bauer, M.F. 2006. Mitochondrial disorders. In *Encyclopedia of Life Sciences (ELS)*. Chichester, UK: John Wiley & Sons, Ltd.

Hongbao, M. 2005. Development Application of Polymerase Chain Reaction (PCR). *The Journal of American Science* 1 (3): 1- 47.

Hossain, M.A.R. Nahiduzzaman, M., Saha, D., Khanam, U.H. and Alam.M.S. 2010a. Landmark-based morphometric and meristic variations of the endangered carp, kalibaus *Labeo calbasu*, from stocks of two isolated rivers, the Jamuna and Halda, and a Hatchery. *Zoological Studies* 49(4): 556-563.

Hossain, M.Y. 2010b. Morphometric Relation of Length-weight and length-length of four cyprinid small indigenous fish species from the Padma River (NW Bangladesh). *Turkish journal of fisheries and aquatic sciences* 10: 131-134.

Hoy, M.A. 2003. *Insect molecular genetics: An introduction to principles and applications*, 2nd Ed. pp. 412. San Diego, CA: Academic Press.

Hsu, F-H., Lin, F-J. and Lin, Y-S. 2001. Phylogeographic structure of the Formosan wood mouse, *Apodemus semotus* Thomas. *Zoological Studies* 40(2): 91-102.

Hsu, K-C, Shih, N-T., Ni, I-H. and Shao, K-T. 2009. Speciation and population structure of three *Trichiurus* species based on mitochondrial DNA. *Zoological studies* 48(6): 835-849.

Hu, Y., Mu, X., Wang, X., Liu, C., Wang, P. and Luo, J. 2009. Preliminary study on mitochondria DNA cytochrome *b* sequence and genetic relationship of three Asian Arowana *Scleropages Formosus*. *International Journal of Biology* 1 (2): 28-32.

Hühne, J., Pfeiffer, H., Waterkamp, K. and Brinkmann, B. 1999. Mitochondrial DNA in human hair shafts – existence of intra-individual differences?. *Int. J. Leg. Med.* 112 (3): 172-175.

Ibanez-Aguirre, A.L., Cabral-Solis, E., Gallardo-Cabello, M. and Espino-Barr, E. 2006. Comparative morphometrics of two populations of *Mugil curema* (Pisces: Mugilidae) on the Atlantic and Mexican Pacific coasts. *Scientia Marina* 70(1): 139–45.

Ihssen, P.E, Booke, H.E., Casselman, J.M., Glade, J.M.M., Payne, N.R. and Utter, F.M. 1981. Stock identification:Materials and Methods. *Can. J. Fish Aquat. Sci.* 38:1838-1855.

Innan, H. and Stephen, W. 2000. The coalescent in an exponentially growing metapopulation and its application to *Arabidopsis thaliana*. *Genetics* 155: 2015-2019.

Irwin, D.M., Kocher, T.D. and Wilson, C. 1991. Evolution of the cytochrome *b* gene in mammals. *Journal of Molecular Evolution* 32: 128-144.

Jamaluddin, J.A.F., Ahmad, A.T., Basir, S., Rahim, M.A. and Nor, S.A.M. 2010. *Restrelliger* systematics interred from mitochondrial cytochrome *b* sequences. *African Journal of Biotechnology* 9(21): 3063-3067.

Jamaluddin, J.A.F., Pau, T.M and Siti-Azizah, M.N. 2011. Genetic structure of the snakehead murrel, *Channa striata* (channidae) based on the cytochrome c oxidase subunit I gene: Influence of historical and geomorphological factors. *Genetics and Molecular Biology*, 34(1):152-160.

Jamsari, A.F.J., Min-Pau, T. and Siti-Azizah, M.N. 2011. Isolation and multiplex genotyping of polymorphic microsatellite DNA markers in the snakehead murrel, *Channa strita*. *Genetics and Molecular Biology* 34(2): 345-347.

Jamsari, A.F.J., Muchlin, Z.A., Musri, M. and Siti Azizah, M.N., 2010. Remarkably low genetic variation but high population differentiation in the climbing perch, *Anabas testudineus* (Anabantidae), based on the mtDNA control region. *Genetics and Molecular Research* 9(3): 1836-1843.

Janke, A, and Arnason, U. 1997. The complete mitochondrial genome of Alligator mississippiensis and the separation between recent archosauria (birds and crocodiles). *Mol. Biol. Evol.* 14: 1266-1272.

Jayasankar, P., Thomas, P.C., Paulton, M.P. and Mathew, J. 2004. Morphometric and genetic analyses of Indian Mackerel (*Rastrelliger kanangurta*) from Peninsular India. *Asian Fisheries Science* 17: 201-215.

Jensen, J.K., Bohonak, A.J. and Kelley, S.T. 2005. Isolation by distance, webservice. *B.M.C. Genetics* 6: 13.

Jones, N., Ougham, H. and Thomas, H. 1997. Markers and mapping: we are all geneticists now. *New Phytol*. 137: 165-177.

Joshi, K., Chavan, P., Warude, D. and Patwardhan, B. 2004. Molecular markers in herbal drug technology. *Curr. Sci.* 87: 159-165.

Kamaruddin, I.S., Mustafa-Kamal, A.S., Christianus, A. Daud, S.K., Amin, S.M.N. and Yu-Abit, L. 2011. Length-weight relationship and condition factor of three dominant species from the Lake Tasik Kenyir, Terengganu, Malaysia. *Journal of Fisheries and Aquatic Science* 6(7): 825-856.

Kamaruddin, K.K and Esa, Y. 2009. Phylogeny and phylogeography of *Barbonymus schwanenfeldii* (Cryprinidae) from Malaysia inferred using partial cytochrome *b* mtDNA gene. *Journal of Tropical Biology and Conservation* 5: 1-13.

Kan, X.Z., Li, X.F., Lei, Z.P., Wang, M., Chen, L., Gao, H. and Yang, Z.Y. 2010. Complete mitochondrial genome of Cabot’s, *Tragonpan caboti* (Galliformes: Phasianidae). *Genetics and Molecular Research* 9 (2): 1204-1216.

Karaoglu, H. and Belduz, A.O. 2011. Multivariate discrimination among three *Trachurus* species from Turkey. *Journal of Animal and Veterinary Advances* 10(1): 121-127.

Karuri, H.W., Ateka, E.M., Amata, R., Nyende, A.B., Muigai, A.W.T., Mwasame, E. and Gichuki, S.T. 2010. Evaluating diversity among Kenyan sweet patato genotypes using morphological and SSR markers. *Int. J. Agric. Bioal.*, 12:33 38.

Ke, H-M., Lin, W-W. and Kao H-W. 2009. Genetic diversity and differentiation of gray mullet (*Mugil cephalus*) in the coastal waters of Taiwan. *Zoological Science* 26(6): 421-428.

Khan, M.M.R., Arai, K., Kuroda, K., Umino, T. and Nakagawa, H. 2005. Genetic variation of Japanese loach inferred from restriction fragment length polymorphism analysis of mitochondrial DNA. *African Journal of Biotechnology* 4: 318-325.

Khan, S., Khan, M.A., Miyan, K. and Mubark, M. 2011. Length weight relationship for nine freshwater teleosts collected from River Ganga, India. *International Journal of Zoological Research* 7(6): 401-405.

Kim, G.E., Lee, Y-H., Kang, G., Kim, C-G., Jung, W., Seong, K-B.,Seeb, J.E., Kim, S. and Kang, S. 2007. Genetic diversity and population structure of Chum Salmon in the North Pacific. *NPAFC Bulletin* 4:203-209.

Kimura, M. and Weiss, G.H. (1964). The stepping-stone model of population structure and the decrease of genetic correlation with distance. *Genetics*, 49: 561-576.

King, T.L., Spidle, A.P., Eackles, M.S., Lubinski., B.A. and Schill, W.B. 2000. Mitochondrial DNA diversity in North American and European Atlantic salmon with emphasis on the Downeast Rivers of Maine. *Journal of Fish Biology* 57: 614-630.

Kinoshita, I., Seikai, T., Tanaka, M. and Kuwamura, K. 2000. Geograhpic variations in dorsal and anal ray counts of juvenile Japanese flounder, *Paralichtys olivaceus*, in the Japan Sea. *Environmental Biology of Fishes* 57: 305-313.

Kirstein, F. and Gray, J.S. 1996. A molecular marker for the identification of the zoonotic reservoir of lyme borreliosis by analysis of the blood meal in it European vector *Ixodes ricinus*. *Applied Environmental Mircrobiology* 62: 4060- 4065.

Kocher, T.D., Thomas, W.K., Meyer, A., Edwards, S.V., Paabo, S., Villablanca, F.X. and Wilson, A.C. 1989. Dynamics of mitochondrial DNA evolution in animals: Amplification and sequencing with conserved primers. *PNAS* 86(16): 6196-6200.

Korzun, V. 2003. Molecular markers and their application in cereals breeding. In *MarkerAssisted Selection: A Fast track to increase genetic gain in plant and animal breeding?*, pp. 18-22. Turin, Italy: FAO international workshop, 17-18 October 2003.

Kottelat, M., Whitten, A.J., Kartikasari, S.N. and Wirjoatmodjo, S. 1993. *Freshwater Fishes of western Indonesia and Sulawesi*, pp. 344. Hong Kong: Perplus Editions.

Kovitvadhi, S., Kovitvadhi, U., Sawangwong P., Trisaranuwatana P., and Machado, J. 2009. Morphometric relationship of weight and size of cultured freshwater pearl mussel, *Hyriopsis (Limnoscapha) myersiana*, under laboratory conditions and earthen pond phases, *Aquaculture international* 17: 57-67.

Kumar, P., Gupta, V.K., Misra, A.K., Modi, D.R. and Pandey, K.B. 2009. Potential of Molecular Markers in Plant Biotechnology. *Plant Omics Journal* 2(4): 141-162.

Kurose, N., Abramov, A.V. and Masuda, R. 2000. Intrageneric diversity of the cytochrome *b* gene and phylogenu of Eurasion species of the genus *Mustela*. *Zoological Science* 17: 673-679.

Lakra, W.S., Goswami, M., Gopalakrishnan, A., Singh, D.P., Singh, A. and Nagpure, N.S. 2010. Genetic relatedness among fish species of Genus *Channa* using mitochondrial DNA genes. *Biochemical Systematics and Ecology* 38(6): 1212-1219.

Lansman, R.A., Shade, R.O., Shapira, J.F. and Avice, J.C. 1981. The use of restriction endonucleases to measure mitochondrial DNA sequence relatedness in natural populations. III. Techniques and potential applications. *Journal of Molecular Evolution* 17: 214-226.

Lawson, E.O. 2010. Morphometric measurements and meristic count in mudskipper (*Periophthalmus papilio*) from mangrove swamps of Lagos lagoon, Nigeria. *J. Appl. Biosci.* 34: 2166-2172.

Lee, P.G. and P.K.L. Ng, 1994. The systematics and ecology of snakeheads (Pisces: Channidae) in Penisular Malaysia and Singapore. *J. Hydrobiol*. 285: 59-74.

Li, X., Musikasinthorn, P. and Kumazawa, Y. 2006. Molecular phyogenetic analyses of snakeheads (Perciformes: Channidae) using mitochondrial DNA sequences. *Ichtyol. Res*. 53: 148 – 159.

Li, Y.L, Kong, X.Y., Yu, Z.N., Kong, J., Ma, S. and Chen, L.M. 2009. Genetic diversity and historical demography of Chinese shrimp *Feneropenaeus Chinensis* in Yellow Sea and Bohai Sea based on mitochondrial DNA analysis. African Journal of *Biotechnology* 8(7): 1193-1202.

Liao, C-H., Liu, T-Y. and Hung, C-Y. 2010. Morphometric variation between the swordtip (*Photololigo edulis*) and mitre (*P. chinensis*) squids in water off Taiwan. *Journal of Marine Science and Technology* 18(3): 405-412.

Lin, L.S., Ying, Y.P., Han, Z.Q., Xiao, Y.S. and Gao, T.X. 2009. AFLP analysis on genetic diversity and population structure of small yellow croaker *Larimichthys polyactis*. *African Journal of Biotechnology* 8(12): 2700-2706.

Lin, W.F., Shiau, C.Y. and Hwang, D.F. 2005. Identification of four *Thunnus* tuna species using mitochondrial cytochrome *b* gene sequence and PCR-RFLP analysis. *J. Food Drug. Anal.* 13: 382-387.

Liu, S.Y.V., Kokita, T. and Dai, C.F. 2008. Population genetic structure of the neon damselfish (*Pomacentrus coelestis*) in the northwestern Pacific Ocean. *Mar. Biol*. 154: 745-753.

Liu, Z.J. and Cordes, J.F. 2004. DNA marker technologies and their applications in aquaculture genetics. *Aquaculture* 238: 1-37.

Löhrke, S. and Friauf, E., 2002. Developmental distribution of the glutamate receptorsubunits KA2, GluR6/7, and δ1/2 in the rat medial nucleus of the trapezoid body a quantitative image analysis. *Cell and Tissue Research* 308(1): 19-33.

Lu, G., Li, S. and Bernatchez, L. 1997. Mitochondrial DNA diversity, population structure, and conservation genetics of four native carps within the Yangtze River, China. *Can. J. Fish. Aquat. Sci.* 54: 47-58.

Ma, Z., Zhnong, J., Han, J., Xu, J., Bai, W., Li, J., Cairang, D., Jin, X. and Zhang, J. 2010. Genetic diversity and demographic history of wild Yak (*Bos grunniens mutus*) inferred from mtDNA D-loop sequences. *African Journal of Biotechnology* 9(46): 7805-7810.

Mantel, N.A. 1967. The detection of disease clustering and a generalized regression approach. *Cancer Res*. 27: 209-220.

Marimuthu, K. and Haniffa, M.A. 2007. Embryonic and larval development of the striped shakehead *Channa striatus*. *Taiwania* 52: 84-92.

Marimuthu, K. Haniffa, M.A. and Rahman, M.A. 2009. Spawning performance of native threatened spotted snakehead fish, *Channa Puctatus* (ActinopterygII: Channidae: Perciformes), induced with ovatide. *Acta Ichthyologica Et Piscatoria* 39: 1-5.

Marin-Garcia, J. 2010. Thyroid hormone and myocardial mitochondrial biogenesis. *Vascular Pharmacology* 52: 120-130.

Marques, J.F., Teixeira, C.M. and Cabral, H.N. 2006. Differentiation of commercially important flatfish populations along the Portuguese coast: Evidence from morphology and parasitology. *Fisheries Research* 81(2-3): 293-305.

Martin, A.P. and Palumbi, S.R. 1993. Protein Evolution in different cellular enviroments: cytochrome *b* in sharks and mammals. *Mol. Biol. Evol.* 10(4): 873-891.

Mat Jais, A.M. 1991. Haruan, *Channa striatus*, Farming in Backyard. *Proc. 3rd Asian Conference of Technology for Rural Development* 91: 230-232.

Mat Jais, A.M. 1997a. Haruan *Channa striatus* as a component of health food. *Proceedings of the Seminar of the Asian Food Technology, (SAFT 97), Asia* 39-43.

Mat Jais, A.M. 2007a. Pharmacognosy and Pharmacology of Haruan *Channa striatus* a Medicinal Fish with Wound Healing Properties. *Bio. Latinoam. Caribe Plant. Med. Aromaticas (BLACPMA)* 6(3): 52-60.

Mat Jais, A.M. 2007b. Molecular size of the bio-active components from Haruan *Channa striatus* extract. *Journal of Applied Sciences* 7(15): 2198-2199.

Mat Jais, A.M. Hazliana, H., Kamalludin, M.H., Abdul Kader, S. and Rasedee, A. 2002. Effect of Haruan (*Channa striatus*) fillet extract on blood glucose and cholesterol concentration and differential white blood cells counts in rats and mice. *Proceedings of the Regional Symposium on Environment and Natural Resources* 1: 566-573.

Mat Jais, A.M., Dambisya, Y.M. and Lee, T.L. 1997b. Antinociceptive activity of *Channa striatus* (haruan) extracts in mice. *Journal of Ethopharmacology* 57: 125-130.

Mat Jais, A.M., Matori, M.F., Kittakop, P. and Sowanborirux, K. 1998. Fatty acid compositions in mucus and roe of Haruan, *Channa striatus*, for wound healing. *Gen. Pharmac.* 30 (4): 561-563.

Mat Jais, A.M., McCullock, R. and Croft, K. 1994. Fatty acid and amino acid composition in Haruan as a potential role in wound healing. *Gen. Pharmacol*., 25: 947-950.

Mayden, R.Y. and Wiley, E.O, 1992. Phylogenetic systematics In *Systematics, historical ecology and North American freshwater fishes*, ed. Mayden, pp. 137. Stanford, California: Stanford university press.

McElroy, D.M., Moran, P., Bermingham, E. and Kornfield, I. 1992. REAP: an integrated environment for the manipulation and phylogenetic analysis of restriction data. *Journal Heredity* 83: 157-158.

Menezes, M.R., Ikeda, M. and Taniguchi, N. 2006. Genetic variation in skipjack tuna *Katsuwonus pelamis* (L.) using PCR-RFLP analysis of the mitochondrial DNA D-loop region. *Journal of Fish Biology*, 68: 156-161.

Meyer, A., 1994. DNA technology and phylogeny of fish. In: *Genetics and evolution of aquatic organisms*, ed. A.R, Beaumont, pp. 219-24. London, New York: Chapman and Hall.

Mimura, M and Aitken, S.N. 2007. Adaptive gradients and isolation-by-distance with postglacial migration in *Picea sitchensis*. *Heredity* 99: 224-232.

Mobley, K.B., Lussetti, D., Johansson, F., Englund, G. and Bokma, F. 2011. Morphological and genetic divergence in Swedish postglasial stickleback (*Pungitius pungitius*) populations. *BMC Evolutionary Biology* 11(287): 1-18.

Mohsin, A.K.M. and Ambak, M.A. 1983. *Freshwater fishes of Peninsula Malaysia*, pp. 282-284. Kuala Lumpur, Malaysia: Dewan Bahasa and Pustaka (DBP).

Mostafa, M.G., Ahmed, A.S.I., Mustafa, M.G., Rabbane, M.G., Islam, M.N. and Rafiquzzaman, S.M. 2009. Genetic diversity of wild and farmed kaliaus (*Labeo calbasu*, Hamilton, 1822) by RAPD analysis of the genomic DNA. *Ribarstvo.* 67(2): 41-52.

Musikasinthorn, P. 1998. *Channa panaw*, a new channid fish from the Irrawaddy and Sittang River basins, Myanmar. *Ichthyol Res*. 45: 355–362.

Musikasinthorn, P. 2000. *Channa aurantimaculata*, a new channid fish from Assam (Brahmaputra River basin), India, with designation of a neotype for *C. amphieus* (Mc-Clelland, 1845). *Jchthyol. Res.* 47(1): 27-37.

Musikasinthorn, P. 2003. Channoidei. In *Grzimek's Animal Life Encyclopedia*, 2nd edition, Volume 4 and 5, Fishes I and II, ed. M. Hutchins, D. A. Thoney, P. V. Loiselle and N. Schlager), pp. 437-447. Farmington Hills: Gale Group.

Musikasinthorn, P. and Taki, Y. 2001. *Channa siamensis* (Gunther, 1861), a jounior synonsym of *Channa Lucius* (Cuvier *in* Cuvier and Valenciennes, 1831). *Ichthyol. Res.* 48: 319-324.

Mustac, B. and Sinovcic, G. 2007. Morphometric and meristic characteristics of the sardine, *Sardina pilchardus* (walb., 1792), in the middle eastern Adriatic sea. *Rapp. Comm. Int. Mer Médit*. 38.

Muto, N., Kai, Y. and Nakabo, T. 2011. Genetic and morphological differences between *Seastes vulpes* and *S. zonatus* (Teleostei: Scorpaeniformes: Scorpaenidae). *Fish. Bull.* 109: 429-439.

Nakamura, T. 2003. Meristic and morphometric variations in fluvial Japanese charr between river systems and among tributaries of a river system. *Environmental Biology of Fishes* 66: 133–41.

Namkoong, B.G. 1986. Genetics and forests of the future. *Unasylva* 152:2-18.

Nazia, A.K., Suzana, M., Azhar, H., NguyenThuy, T.T. and Siti Azizah, M.N. 2010. No genetic differentiation between geographically isolated populations of *Clarias macrocephalus* Günther in Malaysia revealed by sequences of mtDNA cytochrome *b* and D-loop gene regions. *J. Appl. Ichtyol.*, 26: 568-570.

Neale, D.B. and William, C.G. 1991. Restriction fragment length polymorphism mapping in conifers and application to forest genetics and tree improvement. *Can J. Fors. Res*. 21: 545-554.

Nebauer, S.G., Castillo-Agudo, L.D. and Segura, J. 1999. RAPD variation within and among natural populations of outcrossing willow-leaved foxglove (*Digitalis obscura* L.). *Theor. Appl. Genet.* 98: 985-994.

Neebling, T.E. and Quist, M.C. 2010. Relationships between fish assemblages and habitat characteristics in Iowa's non-wadeable rivers. *Fisheries Management and Ecology* 17: 369–385.

Nei, M. and Miller, J.C. 1990. A simple method for estimating average number of nucleotide substituttions within and between populations from restriction data. *Genetics* 125: 873-879.

Nei, M. and Tajima, F. 1981. DNA polymorphisms detected by restriction endonucleoases, *Genetics* 97: 145-163.

Nei, M. 1987. *Molecular evolutionary genetic*, pp: 512. Columbia University Press, New York.

Nei, M., and Li, W.H. 1979. Mathematical amodel for studing genetic variation in terms of restriction endonuclease. *Proc. Natl. Acad. Sci. USA* 76: 5269-5273.

Neigel, J.E. 1997. A comparison of alternative strategies for estimating gene flow from genetic markers. *Annual Review of Ecology and Systematics*, 28: 105 -128.

Olive, D. M. and Bean, P. 1999. Principles and Application of Methods for DNA based Typing of Microbial Organisms. *Journal of Clinical Microbiology* 37: 1661-1669.

Olson, M., Hood, L., Cantor, D. and Botstein, D. 1989. A common language for physical mapping of the human genome. *Science* 245: 1434-1435.

Palma, J. and Andrade, J.P. 2002. Morphological study of *Diplodus sargus*, *Diplodus puntazzo* and *Lithoghathus mormyrus* (Sparidae) in the Eastern Alantic and Mediateranean Sea. *Fisheries Research* 57: 1-8.

Parameswaran, S. and Murugesan, V. K. 1976. Observations on the hypophysation of murrels. *Hydrobiol. Sin.* 50(1): 81-87.

Percin, F. and Akyol, O. 2010. Some Morphometric Relationships in Fattened BluefinTuna, *Thunnus thynnus L*., from the Turkish Aegean Sea. *Journal of Animal and Veterinary Advances* 9(11): 1684-1688.

Perdices, A., Sayanda, D. and Coelho, M.M. 2005. Mitochondrial diversity of *Opsariichthys bidens* (Teleostei, Cyprinidae) in three Chinese drainages. *Molecular Phylogenetics and Evolution*, 37(3): 920 927.

Pierce, G.J, Santos, M.B., Bishop, A.J., Bellido, J.M., Rasero, M. and Portela, J.M. 2002. Morphometric and meristic variation in Argentine hake (*Merluccius hubbsi*) and southern hake (*Merlucius australis*) from the southwest Atlantic. *ICES Annual Science Conference Copenhagen* pp 20

Piercy, R., Sullivan, K.M., Benson, N. and Gill, P. 1993. The application of mitochondrial DNA typing to the stduy of white Caucasion genetic identication. *Int. J. Leg. Med*. 106: 85-90.

Pinheiro, A., Teixeira, C.M., Rego, A., Marques, J.F. and Cabral, H.N. 2005. Genetic and morphological variation of *Solea lascaris* (Risso, 1810) along the Portuguese coast. *Fisheries Research* 73(1-2): 67-78.

Power, D.J. 1985. Morphometric differences between golden redfish (*Sebastes marinus*) and beaked redfish (*S. mentella and s. fasciatus*). *J. Northw. Atl. Fish. Sci.* 6: 1-7.

Price, T.D., Qvarnstrom, A. and Irwin, D.E. 2003. The role of phenotypic plasticity in driving genetic evolution. *Proc. R. Soc. Lond. B. Biol. Sci.* 270:1433-1440.

Qin, J. and Fast, A.W. 1996. Size and feed dependent cannibalism with juvenile snakehead *Channa striatus*. *Aquaculture* 144: 313-320.

Quinn, J.T. and R.B. Deriso, 1999. *Quantitative Fish Dynamics*, pp. 542. New York: Oxford University Press.

Rapley, R. 2008. Polymerase Chain Reaction. In *Molecular Biomethods Handbook*, 2nd Ed. J. Walker and R. Rapley, pp. 305-325. Totowa, NJ: Humana Press.

Rathod, S.R., Shinde, S.E. and More, P.R. 2011. Length-weight relationship in *Salmostoma navacula* and *Channa* Godavari river at Kaigoan Toka, Dist. Aurangabad (M.S.) India. *Recent Research in Science and Technology* 3(3): 104-106.

Ravago-Gatanco, R.G. and Juinio-Menez, M.A. 2004. Population genetic structure of the milkfish, *Chanos chanosi*, based on PCR-RFLP anlaysis of the mitochondrial control region. *Marine Biology* 145: 789-801.

Redenbach, Z and Taylor, E.B.1999. Zoogeographical implications of variation in mitochondrial DNA of Arctic grayling (*Thymallus arcticus*). *Molecular Ecology* 8: 23-35.

Remerie, T., Bourgois, T. and Vanreusel, A. 2005. Morhological differentiation between geographically separated populations of *Neomysis interger* and *Mesopodosis slabberi* (Crustacea, Mysida). *Hydrobiologia* 549:239-250.

Rice, W.R. 1989. Analyzing table of statistical tests. *Evolution* 43: 223-225.

Ricker, W.E.1975. *Computation and Interpretation of Biological Statistics of Fish Populations*. 3rd Ed. pp. 323. Canada: Bulletin of Fisheries Research Board.

Rippe, R.M. and Gellissen, G. 1993. The genes for cytochrome *b*, ND 4L, ND6 and two tRNAs from mitochondrial genome of the locust, *Locusta migratoria*. *Curr. Genet.* 25: 135-141.

Roausset, F. 1997. Genetic differentiation and estimation of gene flow from F statistics under isolation by distance. *Genetics* 145: 1219-1228.

Rogers, A.R and Harpending, H. 1992. Population growth makes waves in the distribution of pairwise genetic differences. *Mol. Biol. Evol*. 9(3): 552-569.

Rohlf, F.J. 2000. *NTSYS-pc: Numerical Taxonomy and Multivariate Analysis System.* Version 2.1, New York: Exeter Software Inc.

Rohlf, F.J. and Marcus, L.F., 1993. A revolution in morphometrics. *Trends Ecol. Evol.* 8: 129–132.

Rohlf, F.J., Loy, A. and Corti, M. 1996. Morphometric analysis of old world *Talpidae* (Mammalia, Insectivora) using partial-warp scores. *Syst. Biol*. 45: 344–362.

Said, M.Z.M. and Mohsin, A.K.M. 1992. Discriminant analysis of morphometrics of *Nemipterus* species. *Pertanika* 15(2): 127-129.

Saiki, R.K., Scharf, S., Faloona, F., Mullis, K.B., Horn, G.T., Erlich, H.A. and Arnheim, N. 1985. Enzymatic amplication of beta-globin genomic sequences and restriction site analysis for diagnosis of sickle cell anemia. *Science* 230 (4732): 1350-1354.

Saini, A., Dua, A. and Mohindra, V. 2008. Comparative morphometrics of two populations of giant river catfish (*Mystus seenghala*) from the Indus river system. *Integrative Zool.* 3: 219-226.

Sambrook, J. and Russell, D.W. 2001. *Molecular cloning*: *A laboratory manual*. 3rd Edition, pp: 99. Cold Spring Harbor Laboratory Press, New York.

Sambrook, J., Fritsch, E.F. and Maniatis, T. 1989. *Molecular cloning: a laboratory manual*, 2nd Ed. New York, USA: Cold Spring Harbor Laboratory Press.

Sanger, F., Nicklen, S. and Caolson, A.R. 1977. DNA sequencing with chain terminating inhibitors. *Proc. Natl. Acad. Sci.* 74: 5463-5467.

Santo, P.J., Saleh, G.B., Saleh, N.M. and Napis, S. 2005. Phyogenetic relationship Among10 *Durio* species bases on PCR-RFLP analysis of two chloroplast genes. *Indonesian journal of Agriculture Science* 6(1): 20 -27.

Santos, S., Hrbek, T., Farias, I.P., Schneider, H. and Sampaio, I. 2006. Population genetic structuring of the king weakfish, *Macrodon ancylodon* (Sciaenidae), in Atlantic coastal waters of South America: deep genetic divergence without morphological change. *Molecular Ecology*, 15: 4361-4373.

Scherrer, B. 1984. Biostatisque, 1st Ed. pp. 850. Montreal, Paris: Gaëtan Morin.

Schluter, D., and Smith, J. 1986. Natural selection on beak and body size in the song sparrow. *Evolution* 40(2):221-231.

Schneider, S and Excoffier, L. 1999. Estimation of past demographic parameters from the distribution of pair-wise differences when the mutation rates vary among sites, Application to human mitochondrial DNA. *Genetics* 152: 1079-1089.

Silva, A. 2003. Morphometric variation aming sardine (*Sardina pilchardus*) populations from the northeastern Atlantic and the western Mediterranean. *ICES Journal of Marine Sciences* 60:1352-1360.

Silva, K.H.G.M. 1993. The fishery, growth rates and notes on reproduction of the snakehead *Channa striata* (Bloch) (Perciformes: Channidae) in some irrigation reservoirs of Sri Langka. *Fisheries Research* 19: 257-268.

Siti-Balkhis, A.B., Jamsari, A.F.J. Hwai, T.S., Yasin, Z. and Siti-Azizah, M.N. 2011.evidence of geographical structuring in the Malaysia snakehead, *Channa striata* based on partial segment of the CO1 gene. *Genetics and Molecular Biology* 34(3). 520-523.

Slatkin, M and Hudson, R.R. 1991. Pairwise comparisons of mitochondrial DNA sequences in stable and exponentially growing populations. *Genetics* 129: 555-562.

Slatkin, M. 1995. A measure of population subdivision based on microsatellite allele frequencies. *Genetics* 139: 457-462.

Slatkin, M. and Bortan, N.H. 1989. A comparison of three indirect methods of estimating average levels of gene flow. *Evolution* 43(7): 1349-1368.

So, M., Van Houdt, J.K.J. and Volckaert, F.A.M. 2006. Genetic diversity and population history of the migratory catfishes Pangasianodon hypohthalmus and *Pangasius bocourti* in the Combodian Mekong River. *Fisheries Science* 72(3): 469-476.

Sokal, R.R. and Rohlf, F.J. 1981. *Biometry: The principles and practice of statistics in biological research*, 2nd Edition pp: 344-354. W.H. Freeman Publication, New York.

Soltis, D.E. and Soltis, P.S. 1990. Isozymes in plant biology, 1st Edition, Chapman and Hall, London.

Soong, M. K. 1949. Fishes of the Malayan padi-fields. II. Aruan: Serpent-head fishes. *Malayan Nat. J.* 4(1): 29-31.

Spruyt, N., Delarbre, C., Gachelin, G. and Laudet, V. 1998. Complete sequence ofthe amphioxus (*Branchiostoma lanceolatum*) mitochondrial genome: relations to vertebrates. *Nucleic Acids Research* 26(13): 3279-3285.

Srivastava, S. and Mishra, N. 2009. Genetic Markers – A Cutting-Edge Technology in Herbal Drug Research. *Journal of Chemical and Pharmaceutical Research* 1(1): 1-18.

Steuber, S., Abdel-Rady, A. and Clausen, P.H. 2005. PCR-RFLP: a promising technique identification of blood meals from tsetse flies (Diptera: Glossinidae). *Parasitol. Res.* 97: 247-254.

Storz, J.F. 2002. Constrasting pattern of divergene in quantitative traits and neutral DNA markers. Analysis of clinical variation. *Molecular Ecology* 11:2537 2551.

Supiwong, W., Jearranaiprepame, P. and Tanomtong, A. 2009. A New Report of Karyotype in the Chevron Snakehead Fish, *Channa striata* (Channidae, Pisces) from Northeast Thailand. *Cytologia* 74: 317-322.

Szalanski, A.L., Bischof, R. and Mestl, G. 2000. Population genetic structure of Nebraska Paddle fish based on mitochondrial DNA variation. *Transactions of the American Fisheries Society* 129: 1060-1065.

Tajima, F. 1989. Statistical method for testing the neutral mutation hypothesis. *Genetics* 105: 437-460.

Tajima, F. 1993. Statistical analysis of DNA polymorphism. *Jpn. J. Genet*., 68: 567-595.

Tamura, K., J. Dudley, M. Nei and S. Kurmar, 2007. Mega4: Molecular evolutionary genetic analysis (MEGA) software version 4.0. *Molecular Biology and Evolution* 24:1596-1599.

Tang, P.Y., Sivananthan, J.Y., Pillay, S.O. and Muniandy, S. 2004. Genetic structure and biogeography of Asian Arowana (*Scleropages formosus*) determined by microsatellite and mitochondrial DNA analysis. *Asian Fisheries Science*, 17: 81-92.

Tanksley, S.D. 1993. Mapping polygenes. *Annu. Rev. Genet.* 27: 205-233.

Tautz, D. 1989. Hypervariable of simple sequences as a general source of polymorphic DNA markers. *Nucleic Acids Res*. 17: 6463-6471.

Teacher, A.G.F. and Griffiths, D.J. 2011. Hapstar: automated haplotype network layout and visualization. *Molecular Ecology Resources* 11(1): 151-153.

Thangaraj, M. and Lipton, A.P. 2010. Genetic identity of three Indian populations of three spotted seahorse, *Hippocampus trimaculatus*. *Advances in Biological Research* 4(1): 37-41.

Thompson, J.D., Gibson, T.J., Plewniak, F., Jeanmougin, F and Higgins, D.G. 1997. The Clustal_X windows interface: flezible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Research* 25(24): 4876-4882.

Tranah, G.J. and Allen, L.G. 1999. Morphologic and genetic variation among six populations of spotted sand bass, *Paralabrax maculatofasciatus*, from southern California to the upper sea of Cortez. *Bull. Southern California Acad. Sci.* 98(3): 103-118.

Tsutsui, H., Kinugawa, S. and Matsushima, S. 2009. Mitochonrial oxidative stress and dysfunction in myocardial remodeling. *Cardiovascular Research* 81: 449-456.

Tudela, S., Graca-Marn, J.L. and Pla, C. 1999. Genetic structure of the European anchovy, *Engraulis encrasicolus*, in the north-west Mediterranean. *J.Exp. Mar. Biol. Ecol.* 234: 95-109.

Turan, C. 1999. A note on examination of morphometric differentiation among fish populations: the truss system. *Tr. J. of Zoology* 23: 259-263.

Turan, C. 2004a. Stock identification of Mediterranean horse mackerel (*Trachurus mediterraneus*) using morphometric and meristic characters. *ICES Journal of Marine Science* 61: 774-781.

Turan, C. and Yaglioglu, D. 2010. Population identification of common cuttlefish (*Sepia officinalis*) inferred from genetic, morphometric and cuttlebone chemistry data in the NE Mediterranean Sea. *Scientia Marina* 74(1): 77-86.

Turan, C., Erguden, D., Turan, F. and Gurlek, M. 2004b. Genetic and morphologic structure of Liza abu (Heckel, 1843) populations from the rivers Orontes, Euphrates and Tigris. *Turk. J. Vet. Anim. Sci.* 28: 729-734.

Turan, C., Gurlek, M., Yaglioglu, D and Ozturk, B. 2009. Genetic differentiation of Mediterranean hose mackerel (*Trachurus Mediterraneus*) populations as revealed by mtDNA PCR-RFLP analysis. *Journal of Applied Ichthyology* 25(2): 142-147.

Turan, C., Oral, M., Oztruk, B. and Duzgunes, E. 2006. Morphometric and meristic variation between stocks of bluefish (Pomatomus saltatrix) in the Black, Marmara, Aegean and Northeastern Mediterranean seas. *Fish. Res.* 79: 139-147.

Turan, C., Yalcin, S., Turan, F., Okur, E. and Akyuri, I. 2005. Morphometric of African catfish, *Clarias gariepinus*, populations in Turkey. *Folia zool.* 54 (1 2): 165-172.

Turki-Missaoui, O., Helti, M.M., Kraiem, M.M and Chriki, A. 2011. Morphological differentiation of introduced pikeperch (*Sander lucioperca* L., 1758) populations in Tunisian freshwaters.*J.Appl. Ichthyol.* 27: 1181-1189.

Tzeng, T-D. 2004. Morphological variation between populations of spotted mackerel (*Scomber australasicus*) off Taiwan. *Fisheries Research*, 68: 45-55.

Tzeng, T-D., Chu, T-J., Wang, D., Haung, H-L and Yeh, S-Y. 2008. Population structure in the sword prawn (*Parapenaeopsis hardwickii*) from the East China Sea and Taiwan Strait inferred from intron sequences. *Journal of crustacean biology*, 28(2): 234-239.

Ursing, B.M. and Arnason, U. 1998a. The complete mitochondrial DNA sequence of the pig (*Sus scrofa*). *J Mol Evol* 47:302–306.

Ursing, B.M. and Arnason, U. 1998b. Analyses of mitochondrial genomes strongly support a hippopotamus-whale clade. *Proc R Soc Lond B Biol Sci* 265: 2251-2255.

Van Deerlin, V.D.M. 2004. Molecular diagnosis of dementia. In *The Neuropathology of* Dementia, 2nd Ed. Margaret M. Esiri, Virginia, M.Y.L. and John Q. Trojanowski, pp. 96. Cambridge, UK: Cambridge University Press.

Vieira, E., Carvalho, F., Bertan, I., Kopp, M., Zimmer, P., Benin, G., Silva, D.A, Hartwig, I., Malone, G. and Oliviera, A. 2007. Association between genetic distances in wheat (*Triticum aestivum* L.) as estimated by AFLP and morphological markers.*Gen.Mol. Bio.* 30:392-399.

Vincze, T., Posfai, J. and Roberts, R.J. 2003. NEBcutter: a program to cleave DNA with restriction enzymes. *Nucleic Acids Research* 31(13): 3688-3691.

Vishwanath,W. and Geetakymari, K.H. 2009. Diagnosis and interrelationships of fishes of the genus *Channa Scopoli* (Teleostei: Channidae) of Northeastern India. *Journal of Threatened Taxa* 1(2): 97-105.

Vitten, H., Reusch, M., Friauf, E. and Löhrke, S. 2004. Expression of functional kainate and AMPA receptors in developing lateral superior olive neurons of the rat. *Journal of Neurobiology* 59(3): 272-288.

Vivekanandan, E. and Pandian, T.J. 1997. Surfacing activity and food utilization in a tropical air-breathing fish exposed to different temperatures. *Hydrobiologia* 54: 145-160.

Wagle, S.K., Pradhan, N. and Rai, A.K. 2008. A morphometric study on mahseer (*Tor puitora*) from a Mid-Hill Lake and river of Nepal. *Asian Fisheries Science* 21: 113-125.

Wee, K.L. 1982. Snakeheads-their biology and culture. In *Recent Advances in Aquaculture*, ed. Muir and Roberts, pp 181-213. Boulder, CO: Westview Press.

Williams, J.G.K., Kubelik, A.R., Livak, K.J., Rafalski, J.A. and Tingey, S.V. 1990. DNA polymorphism amplified by arbitrary primers are useful as genetic markers. *Nucleic Acid Res.* 18: 6531-6535.

Wilson, A.C., Cann, R.L., Goerge, M., Gyllensten, U., Helm-Bychowski, K., Higuchi, R., Palumbi, S.R., Prager, E., Sage, R.D. and Stoneking, M. 1985. Mitochondrial DNA and two perspectives on evolutionary genetics. *Biol. J. Linn. Soc*. 26: 375-400.

Wimberger, P.H. 1992. Plasticity of fish body shape: the effect of diet, development, family and age in two species of *Geophagus* (Pisces: Cichlidae). *Biol. J. Linn. Soc. Lond.* 45: 197-218.

Wimberger, P.H. 2008. Plasticity of fish body shape, the effects of diet, development, family and age in two species of *Geophagus* (Pisces: Cichlidae). *Biological Journal of the Linnean Society* 45(3): 197-218.

Winter, P. and Kahl, G. 1995. Molecular marker technologies for plant improvement. *World Journal of Microbiology and Biotechnology* 11: 438–448.

Xiao, Y., Takahasni, M., Yanagimoto, T., Zhang, Y., Gao, T., Yabe, M. and Sakurai, Y. 2008. Genetic variation and population structure of willowy flounder *Tanakius kitaharai* collected from Aomori, Ibaraki and Niigata in Northern Japan. *Afr. J. Biotechnol.* 7(21): 3836-3844.

Yaakob, W.A.A.W. and Ali, A. 1992. Simple method for backyard production of snakehead (*Channa striata* Bloch) fry. Naga. *The Iclarm Quarterly* 15: 22-23.

Yoon, Y.G., Koob, M.D. and Yoo, Y.H. 2010. Re-engineering the mitochondrial genomes in mammalian cells. *Anat. Cell Biol.* 43: 97-109.

Yousefian, M. and Laloei, F. 2011. Genetic variation and structure of common carp (*Crprinus carpio*) populations by use of biochemical, mitochondrial and microsatellite markers. *Middle-East Journal of Scientific Research* 7(3): 339 345.

Yusof, M.F., Siraj, S.S. and Daud, S.K. 2011. Length-weight relationship of seven catfish species in Peninsular Malaysia. *Journal of Fisheries and Aquatic Science* 6(7): 828-833.

Zabeau, M. and Vos, P. 1993. Selective restriction amplification: a general method for DNA fingerprinting. In *European Patent Publication no. 92402629.7 (Publication No. EP0534858A1).*

Zainudin, R., Nor, S.M., Ahmad, N., Md-Zain, B.M. and Rahman, M.A. 2010. Genetic structure of *Hylarana erytheraea* (Amphibia: Anura: Ranidae) from Malaysia. *Zoological Studies*, 49(5): 688-702.

Zar, J.H., 1996. Biostatistical Analysis, 3rd Edition. New Jersey: Prentice Hall.

Zhang, C-C., Yuan, W-Y. and Zhang, Q-F. 2011. *RPL1*, a gene involved in Epigenetic processes regulates phenotypic plasticity in rice. *Molecular Plant* 1-12.

Zhang, C-G. Musikasinthorn, P. and Watanabe, K. 2002. *Channa nox*, a new channid fish lacking a pelvic fin from Guangxi, China. *Ichthyol. Res.* 49: 140-146.

Zhao, L., Zhang, J., Liu, Z., Funk, S.M., Wei, F., Xu, M. and Li, M. 2008. Complex population genetic and demographic history of Salangid, *Neosalanx taihuensis*, based on cytochrome b sequences. *B.M.C. Evol. Biol.* 8: 201.

Zhao, Y., Li, Q., Kong, L. and Mao, Y. 2009. Genetic and morphological variation in the venus clam *Cyclina sinensis* along the coast of China. *Hydrobiologia* 635:227-235.

Zhou, G., Yung, L., Li, C., Xu, W. and Chen, G. 2010. Genetic diversity in endangered *Notopterygium forbesii Boissiau* based on intraspesies sequence variation of chloroplast DNA and implications for conservation. *Biochemical systematics and Ecology* 38: 911-916.

Zuraini, A., Somchit, M.N., Solihah, M.H., Goh, Y.M., Arifah, A.K., Zakaria, M.S., Somchit, N., Rajion, M.A., Zakaria, Z.A. and Mat Jais, A.M. 2006. Fatty acid and amino acid composition of three local Malaysian *Channa* spp. Fish. *Food Chemistry* 97: 674-678.