UNIVERSITI PUTRA MALAYSIA

FISH LARVAE SPECIES IDENTIFICATION AND POPULATION GENETIC STRUCTURE OF Boleophthalmus boddarti (Pallas, 1770) FROM SELECTED MANGROVE SITES IN PENINSULAR MALAYSIA

Izzati Adilah Azmir

FP 2018 21

FISH LARVAE SPECIES IDENTIFICATION AND POPULATION GENETIC STRUCTURE OF *Boleophthalmus boddarti* (Pallas, 1770) FROM SELECTED MANGROVE SITES IN PENINSULAR MALAYSIA

By

IZZATI ADILAH BINTI AZMIR

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

January 2018

DEDICATED

To

My Mother and Father

Who always think highly of me, grace me with never ending prayers and help me with what they think best for the moment.

My Husband

For working so hard to support me both spiritually and financially as to ensure I can give full attention to my studies. For being so patient and a loyal listener who at the same time thinks that I am the smartest, brightest person on earth.

My Children

Who has become the sunshine during my bad days, who have taught me to be more patient and wanted to be a better person each day.

My Friends

Especially to Kak Ida and Kak Aslizah who always reminded me that I can do it, to my lab mates Punes, Marshi, Ayu, Chai, Nima and Aisyah who have always been a phone call away and also to Azim who helped me a lot during sampling. Last but not least, to Dr. Roushon Ara who has been a wonderful mentor, thank you very much.

May Allah bless all of you with His kindness.

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

FISH LARVAE SPECIES IDENTIFICATION AND POPULATION GENETIC STRUCTURE OF *Boleophthalmus boddarti* (Pallas, 1770) FROM SELECTED MANGROVE SITES IN PENINSULAR MALAYSIA

By

IZZATI ADILAH BINTI AZMIR

January 2018

Chairman : Associate Professor Yuzine bin Esa, PhD
Faculty : Agriculture

A study on fish larvae species identification from mangrove areas of Pendas Johor, Matang Perak, Pekan Pahang and Setiu Terengganu and population genetic assessment of Blue-spotted mudskipper *Boleophthalmus boddarti,* from similar sampling areas except Setiu Terengganu has been done. The fish larvae collection occurred from April 2015 to September 2015 by using a bongo net, towed at a depth of about 0.5 m from the surface for 5 min against the tidal flow. The mudskipper was collected with casting nets, hand net and bare hands at night time and especially when the tide is low, in between the month of January 2016 and September 2016. This study aims to identify fish larvae to species level by adopting integrative method; a combination of comparative and molecular method. The composition, abundance, diversity and phylogenetic relationship among fish larvae samples were also investigated. The lack of species identification work on fish larvae in Peninsular Malaysia has warrant this study to be conducted. The status of genetic population of mudskipper *B. boddarti* is investigated using two markers, mitochondrial and microsatellite. Specific microsatellite loci for the *B.boddarti* are absent and information on population structure and phylogenetic relationship among *B. boddarti* populations are lacking. Therefore, this study was conducted to characterize the genetic structure of *B. boddarti* in Peninsular Malaysia through mitochondrial Cytochrome *c* Oxidase I (*COI*) gene and new set of microsatellite marker developed using Next Generation Sequencing (NGS) method.

A total of 354 individuals of fish larvae were collected and through morphological analyses they were identified morphologically into 21 families, 20 genus and 18 species. Among the 21 families, the top 3 families, namely, Gobiidae (39.26%), Engraulidae (14.97%), and Clupeidae (14.40%), occurred in all sampling areas except in Setiu. The highest diversity of fish larvae was recorded for Pendas, Johor with Shannon Wiener index *H* = 2.699, and the lowest was for Setiu Terengganu with *H* = 0.832. Setiu Terengganu recorded the lowest evenness value, indicating high single-species dominance. From the total of 354 fish larvae collected, a representative of 177 fish larvae were selected and sequenced using Cytochrome *c* Oxidase I (*COI*) gene where they corresponded to 18 families, 33 genus and 41 species of larval fish. Results from BLAST and BOLDSYSTEM search showed all sequences have high percentage identity index and similarity (90% to 100%). The identification of fish larvae was mostly successfully confirmed through phylogenetics analysis showing monophyletic status between query sequences with reference sequences obtained from GenBank. However the *Sillago vittata* and *Sillago sihama* sequences was found to be in separate clusters despite their similar genus. A few strong match of specimens from different genus was found with high bootstrap value (n>90%) through Neighbour-Joining (NJ) and Maximum-likelihood (ML) analysis. The *Paramugil parmatus* was matched with *Liza melinoptera* (NJ =100%, ML = 99%) and *Pseudogobius oligactis* was matched with *Eugnathogobius oligactis* (NJ = 92%, ML 94%).

A total of 11,957 short sequence repeats (SSR) motifs were identified via analysis of 6.87 Gb nucleotides conducted by using Illumina sequencing to produce a comprehensive transcript dataset for *B. boddarti* motif. The most abundant type of repeat motif was mono-nucleotide (63.66%), followed by tri-nucleotide (18.88%), di-nucleotide (15.54%), tetra-nucleotide (0.83%) and both penta- and hexanucleotide was found the least (0.11%). Experimental screening of 27 pairs of microsatellite primers detected 30% of microsatellite loci were polymorphic.

Both markers showed strong genetic differentiation between populations with result from mitochondrial *COI* analysis revealed haplotype sharing between Pekan Pahang and Pendas Johor populations (KY754661) and Pendas Johor and Matang Perak populations (MF572075). Zero connectivity between Matang Perak and Pekan Pahang populations (*Fst* = 0. 53086); *Nm* was 0.44186) due to huge biogeographical barrier. Microsatellite marker analysis detected minimal differentiations (*Fst)* among Pendas Johor and Matang Perak populations (*Fst*=0.26461) and between Pekan Pahang and Matang Perak populations (*Fst*=0.38423, *Nm*=0.80129) reflecting isolation between populations. However the species was found to be locally adapted where genetic variation was more likely to occur within populations rather than among populations (ratio of 6:3). The mtDNA marker further showed no evidence of recent population expansion through Tajima's *D,* Fu *Fs'* and Bayesian skyline plots but possible occurrence

in population expansion did occurred long before present years during Pleistocene era.

High haplotype diversity (0.680 to 0.819) and moderate nucleotide diversity (0.00657 to 0.05886) was found from *COI* analysis showing genetic variation was in moderation even though Pendas Johor possessed highest number of sample. Thus this reflect possibility of environmental degradation and further supported by microsatellite marker analysis where moderate genetic variation was also seen (mean *Ho* = 0.4337, mean *He* = 0.4535). Deviated Hardy-Weinberg equilibrium was mainly due to heterozygote deficiencies and possibility of inbreeding especially in Pekan Pahang with small sample size (Izz 4-6, *Ho* = 0.280, *He* = 0.497). The high *Ho* compared to expected heterozygosity *(He)* value documented in Pendas Johor population particularly, signal recently bottleneck event showed through Wilcoxon test with probability value less than 0.05 after applying three mutational model (IAM, SMM and TPM) and Mode-Shift indicator further confirmed the population was under shifted mode. The population structure of *B. boddarti* inferred based on the two types of markers was not showing significant differences. In conclusion, integrative identification provide better results to phenotypically ambiguous specimen like the fish larvae and application of mitochondrial and nuclear gene markers were able to characterize genetic structure and evolutionary kinship of *B. boddarti.*

Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai memenuhi keperiuan untuk ijazah Doktor Falsafah

IDENTIFIKASI SPESIES LARVA IKAN DAN STRUKTUR POPULASI GENETIK *Boleophthalmus boddarti* (Pallas, 1770) DARIPADA KAWASAN PAYA BAKAU TERPILIH DI SEMENANJUNG MALAYSIA

Oleh

IZZATI ADILAH BINTI AZMIR

Januari 2018

Pengerusi : Profesor Madya Yuzine bin Esa, PhD
Fakulti : Pertanian

Kajian ke atas identifikasi spesies larva ikan di kawasan paya bakau di Pendas Johor, Matang Perak, Pekan Pahang dan Setiu Terengganu serta semakan populasi genetik ikan belacak berbintik biru *Boleophthalmus boddarti,* dari kawasan kajian yang sama kecuali Setiu Terengganu telah dijalankan. Pengumpulan larva ikan telah dilakukan antara April 2015 sehingga September 2015 menggunakan jaring bongo, ditunda di kedalaman 0.5m dari permukaan air laut selama 5 minit secara melawan arus. Ikan belacak telah dikumpul menggunakan jala, penyauk tangan dan juga tangan pada waktu malam semasa air surut, di antara bulan Januari 2016 hingga September 2016. Kajian ini bertujuan untuk mengidentifikasi larva ikan hingga ke tahap spesies dengan menggunakan kaedah integratif; kombinasi kaedah perbandingan dan molekular. Komposisi, kelimpahan, kepelbagaian dan hubungan filogenetik antara larva ikan turut dikaji. Didapati terdapat kekurangan kajian identifikasi spesies larva ikan di Semenanjung Malaysia maka menjadikan kajian ini harus dijalankan. Status populasi genetik ikan belacak *B. boddarti* telah dikaji menggunakan dua penanda, mitokondria dan mikrosatelit. Penanda mikrosatelit khusus untuk *B. boddarti* masih tidak wujud dan informasi tentang populasi genetik serta hubungan filogenetik di antara populasi *B. boddarti* masih kurang. Maka dengan itu, kajian ini dijalankan adalah untuk mencirikan struktur genetik *B. boddarti* di Semenanjng Malaysia menggunakan gen *sitokrom c oksides I* dan penanda baru mikrosatelit yang dibina khas melalui kaedah 'Next Generation Sequencing' (NGS).

Sejumlah 354 larva ikan telah dikumpul dan dikenalpasti tergolong ke dalam 21 famili, 20 genus dan 18 spesies melalui analisis morfologi. Antara 21 famili yang dikenalpasti, 3 famili iaitu Gobiidae (39.26%), Engraulidae (14.97%) dan Clupeidae (14.40%), dijumpai di semua kawasan kajian kecuali di Setiu Terengganu. Kepelbagaian larva ikan paling tinggi dicatatkan di Pendas Johor melalui Indeks Shannon Wiener *H* = 2.699, manakala kepelbagaian paling rendah dicatatkan di Setiu Terengganu dengan *H* = 0.832. Setiu Terengganu juga mencatatkan nilai kesamaan paling rendah menunjukkan Setiu Terengganu di dominasi oleh satu jenis spesies. Daripada jumlah terkumpul sebanyak 354 larva ikan, sebanyak 177 individu dipilih sebagai wakil, di jujuk dan mendapati tergolong kepada 18 famili, 33 genus dan 41 spesies larva ikan. Keputusan dari pencarian BLAST dan BOLDSYSTEM menunjukkan semua jujukan DNA mempunyai peratusan identiti dan kesamaan yang tinggi (90% hingga 100%). Identifikasi larva ikan didapati berjaya dibuktikan melalui analisis filogenetik apabila status monofiletik terhasil diantara jujukan yang dikaji dengan jujukan rujukan yang diperoleh daripada GenBank. Bagaimanapun, jujukan *Sillago vittata* dan *Sillago sihama* didapati berada di kumpulan berlainan sedangkan tergolong di dalam kumpulan genus yang sama. Beberapa sampel berlainan genus menunjukkan padanan dengan nilai 'bootstrap' yang tinggi (n>90%) melalui analisis 'Neighbour-joining' (NJ) dan analisis 'Maximum-likelihood' (ML) termasuklah *Paramugil parmatus* berpadanan dengan *Liza melinoptera* (NJ =100%, ML = 99%) dan *Pseudogobius oligactis* berpadanan dengan *Eugnathogobius oligactis* (NJ = 92%, ML 94%).

Sebanyak 11, 957 jujukan pendek berulang dikenalpasti melalui analisis ke atas 6.87 Gb nukleotid yang dilakukan menggunakan jujukan Illumina yang mampu menghasilkan motif dataset transkrip meyeluruh untuk *B. boddarti.* Didapati jenis ulangan motif yang paling tinggi adalah mono-nukleotid (63.66%), diikuti oleh tri-nukleotid (18.88%), di-nukleotid (15.54%), tetra-nukleotid (0.83%) manakala penta- dan heksanukleotid didapati paling sedikit (0.11%). Sebanyak 30% lokus mikrosatelit menunjukkan polimorfik setelah ujian saringan dilakukan ke atas 27 penanda mikrosatelit.

Kedua-dua jenis penanda menunjukkan perbezaan genetik yang besar di antara populasi yang dikaji dengan hasil daripada penanda mitokondria menunjukkan haplotaip didapati dikongsi diantara populasi Pekan Pahang dan Pendas Johor (KY754661) dan di antara populasi Pendas Johor dan Matang Perak (MF572075). Tiada perkaitan didapati diantara populasi Matang Perak dan Pekan Pahang (*Fst* = 0. 53086); *Nm* = 0.44186) disebabkan perpisahan biogeografi. Penanda mikrosatelit menunjukkan perbezaan minimal nilai *Fst* di kalangan populasi Pendas Johor dan Matang Perak (*Fst*=0.26461) dan diantara populasi Pekan Pahang dan Matang Perak (*Fst*=0.38423, *Nm*=0.80129) mencerminkan pengasingan berlaku diantara populasi kajian. Walaubagaimanapun, spesies ikan belacak ini didapati lebih beradaptasi dengan kawasan asal mereka dimana variasi genetik dilihat berlaku dikalangan populasi tempatan berbanding dengan populasi yang berlainan kawasan

(nisbah 6:3). Penanda mikrosatelit turut menunjukkan tiada bukti berlakunya pengembangan populasi ikan belacak menerusi Tajima's *D,* Fu *Fs'* and 'Bayesian skyline plots' tetapi berkemungkinan telah berlaku pada Pleistocene era sebelum tahun masihi.

Kepelbagaian haplotaip didapati tinggi (0.680 hingga 0.819) manakala kepelbagaian nukleotid adalah sederhana (0.00657 hingga 0.05886) melalui analisis *sitokrom c oksides I* menandakan variasi genetik berada di tahap sederhana walaupun Pendas Johor mempunyai bilangan sampel yang paling banyak. Ini menyimpulkan kemungkinan berlakunya degradasi persekitaran kajian dan seterusnya disokong oleh analisis penanda mikrosatelit dimana variasi genetik turut berada dalam keserdahanaan (min *Ho* = 0.4337, min *He* = 0.4535). Keseimbangan Hardy-Weinberg menyimpang adalah disebabkan kekurangan heterozigositi dan kemungkinan berlakunya pembiakan dalam populasi yang sama terutama di Pekan Pahang yang mempunyai bilangan sampel kecil (Izz 4-6, Ho = 0.280, He = 0.497). Ketinggian nilai Ho berbanding nilai purata heterozoigositi terjangka (He) disaksikan di populasi Pendas Johor terutamanya, memberi isyarat telah berlakunya kesesakan genetik dan dibuktikan menerusi ujian Wilcoxon dengan nilai kemungkinan kurang dari 0.05 setelah mengaplikasi tiga model mutasi (IAM, SMM and TPM) dan penunjuk 'Mode-shift' juga menunjukkan keputusan yang sama. Kajian struktur populasi *B. boddarti* melalui dua jenis penanda menyimpulkan keputusan yang hampir sama. . Kesimpulannya identifikasi secara integratif memberi keputusan yang lebih baik kepada sampel kajian yang sifat fizikalnya meragukan seperti contoh larva ikan. Aplikasi penanda gen mitokondria dan nuklear terbukti mampu mencirikan struktur genetik dan hubungan kekeluargaan serta evolusi *B. boddarti.*

ACKNOWLEDGEMENTS

I would like to thank Allah S.W.T for granting my wish to pursue my studies at this level before turning 30 years old, for always listening to my prayers and permitted me to finish my studies smoothly.

A million thank you to my main supervisor Associate Professor Dr. Yuzine bin Esa who have given endless attention and guidance during my study period and to always tell me to take a breather whenever I was about to combust. My deepest appreciation goes to you for the opportunity and knowledge that you have given me. Without your patience and supervision this dissertation would not have been possible.

I would like to thank my committee members, Associate Professor Dr. S. M. Nurul Amin, Associate Professor Dr. Ina Salwany binti Md Yasin and Associate Professor Dr. Farida Zuraina binti Md Yusof for their advice and trust. Their cooperation was highly appreciated.

Finally, I would like to thank Southeast Asian Regional Center for Graduate Study and Research in Agriculture (SEARCA) for awarding me with scholarship which without it I won't be able to have the opportunity to pursue my studies at this level. Not to forget, thank you to Malaysia Genome Institute for allowing me to conduct my lab work at their Molecular Laboratory. It was such a valuable experience.

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

Yuzine bin Esa, PhD
Associate Professor
Faculty of Agriculture
Universiti Putra Malaysia
(Chairman)

S. M. Nurul Amin, PhD
Associate Professor
Faculty of Agriculture
Universiti Putra Malaysia
(Member)

Ina Salwany binti Md Yasin, PhD
Associate Professor
Faculty of Agriculture
Universiti Putra Malaysia
(Member)

Farida Zuraina binti Md Yusof, PhD
Associate Professor
Faculty of Applied Sciences
Universiti Teknologi MARA
(Member)

ROBIAH BINTI YUNUS, PhD
Professor and Dean
School of Graduate Studies
Universiti Putra Malaysia

Date:

Declaration by graduate student

I hereby confirm that:

- this thesis is my original work;
- quotations, illustrations and citations have been dully referenced;
- this thesis has not been submitted previously or concurrently for any other degree at any other institutions;
- intellectual property from the thesis and copyright of thesis are fully-owned by university Putra Malaysia, as according to the University Putra Malaysia (Research) Rules 2012
- written permission must be obtained from supervisor and the office of Deputy Vice Chancellor (Research and Innovation) before thesis is published (in the form of written, printed or in electronic form) including books, journals, modules, proceedings, popular writings, seminar papers, manuscripts, posters, reports, lecture notes, learning modules or any other materials as stated in the University Putra Malaysia (Research) Rules 2012;
- there is no plagiarism or data falsification/ fabrication in the thesis and scholarly integrity is upheld as according to the University Putra Malaysia (Graduate Studies) Rules 2003 (Revision 2012-2013) and University Putra Malaysia (Research) Rules 2012. The thesis has undergone plagiarism detection software.

Signature: _____ Date:_____

Name and Matric No: Izzati Adilah binti Azmir, GS40388

Declaration by Members of Supervisory Committee

This is to confirm that:

- the research conducted and the writing of this thesis was under our supervision;
- supervision responsibilities as stated in the Universiti Putra Malaysia (Graduate Studies) Rules 2003 (Revision 2012-2013) are adhered to.

Signature: _____
Name of Chairman of Supervisory Committee: Associate Professor Dr. Yuzine bin Esa

Signature: _____
Name of Member of Supervisory Committee: Associate Professor Dr. S. M. Nurul Amin

Signature: _____
Name of Member of Supervisory Committee: Associate Professor Dr.Ina Salwany binti Md Yasin

Signature: _____
Name of Member of Supervisory Committee: Associate Professor Dr. Farida Zuraina binti Md Yusof

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF ABBREVIATIONS

°	Degree
°C	Degree Celsius
&	And
%	Percentage
=	Equal
µm	Micrometer
-th	is a suffix which forming ordinal and fractional numbers
™	Trade mark
π	Nucleotide diversity
16S	rRNA(16S)
A	Ampere
AFLP	Amplified fragment length polymorphism
AMOVA	Molecular variance
ANOVA	One-way analysis of variance
Ar	Allele richness
bp	Base pair
BOLD	Barcode of Life Data System
BSP	Bayesian Skyline Plots
cytb	Cytochrome *b*
COI	Cytochrome *c* oxidase I gene
dbEST	Division of GenBank containing EST
DNA	Deoxyribnucleotide
dNTP	Deoxynucleotide
E	Evenness Index
et al.	And others
EPP	Extrapair paternity
EST	Expressed sequence tags
FIASCO	Fast isolation by AFLP of sequences containing repeats
F*is*	The inbreeding coefficient
Fs	F-statistic

F*st*	Fixation index
h	Haplotype diversity
H	Shannon–Wiener diversity index
He	Expected heterozygosity
HKY+G	Hasegawa-Kishino-Yano model
Ho	Observed heterozygosity
HWE	Hardy Weinberg equation
ISSR	Inter-simlpe Sequence Repeat
K2P	Kimura 2-Parameter
LD	Linkage disequilibrium
N/A	Not available
N/n	Total number of individuals caught
NCBI	National Center for Biotechnology Information
Ne	Effective population size
NGS	Next Generation Sequencing
NJ	Neighbour-joining
Nm	Gene flow
m	Meter
M	Molar
MCMC	Markov Chain Monte Carlo
ML	Maximum likelihood
mm	Milimiter
mM	Milimolar
MSN	Minimum Spanning Network
mtDNA	Mitochondrial DNA
P	Probability
PCR	Polymerase chain reaction
PIMA	PCR-based isolation of microsatellite arrays
RAMPO	Random-amplified microsatellite polymorphisms
RAMS	Randomly amplified microsatellites
RAPD	Random Amplified Polymorphic DNA
RFLP	Restriction Fragment Length Polymorphism

RNase	An enzyme to promote RNA breakdown
s	Second
SE	Standard error
SNP	Single nucleotide polymorphisms
SSR	Simple sequence repeat
Ta	Temperature of annealing
TrN	Tamura Nei model
UPGMA	Unweighted pair-group using arithmetic averages
V	Volt
VNTR	Variable number of tandem repeat
X	Times
xg	Earth gravitational force

CHAPTER 1

INTRODUCTION

1.1 Background of the study

Integrative identification of fish larvae

Mangrove forest is one of the vegetation in Malaysia which harbours variety kind of plants and animals. Throughout this study, focus on fish larvae identification and the population genetic studies of a mangrove resident fish the Blue-spotted mudskipper, *Boleophthalmus boddarti* will be the main highlights. The selection of specimen for this study was based on their importance in reflecting the current mangrove ecosystem status in general and on their own importance towards the ecosystem, in particular. Selection of mangrove ecosystem as sampling sites was based on the ample amount of mangrove forest available in Malaysia (505,382 ha) which automatically ranked as the second largest surface area covered with mangrove forest among Asian countries (Sandilyan and Kathiresan, 2014). About 99,180 ha of mangrove area was distributed in Peninsular Malaysia (Tan, 2007), and the rest of them were in Sabah and Sarawak. Mangrove is a productive area used by aquatic animals, especially fish.

Three hypotheses to explain on high abundance of fish in mangrove areas have been proposed (Laegdsgaard and Johnson, 2001; Wang *et al.,* 2009) with first hypothesis was on the predator refuge hypothesis, where the presence of mangrove pneumatophores and prop roots provide hiding place for the juvenile and fish larvae who migrated into vegetated mangrove areas especially at the areas where the trees was surrounded by water. The second hypothesis was on feeding where the aquatic organisms was more attracted to an area with ample amount of food available in the mangrove due to the presence of benthic fauna (Chong *et al.,* 1990; Laegdsgaard and Johnson, 2001); the third hypothesis was stressing on the huge spread of mangrove areas along the coastline offering wide space for the mangrove migrant to reside (Hajisamae *et al.,* 2006).

The newly hatched fish eggs and fish larvae tend to reside in a habitat that provide high food sources, low predation rate and stable ocean conditions for growth (Frietas and Muelbert, 2004). They also generally reside in shallow waters as larger predators will usually avoid such environments (Ara *et al.*, 2011a). With the notion of ample fish larvae in mangrove areas, it is important for the stakeholders to properly recognize the exact species acquiring the

habitat. This is to ensure the wellbeing of fish larvae is intact despite any anthropogenic activities around the habitat.

However the morphological identification of fish larvae can be a huge challenge with the minimal amount of taxonomic key available and the rapid development of larva to juvenile stage. Other than that, it also requires considerable skills and taxonomic expertise. Traditionally, larvae identification has always used morphological characters such as body shape, pigmentation, meristic count and measurements. Nevertheless, the presence of rare and cryptic species which are morphologically similar but genetically distinct has limited the ability for traditional method such as morphology in the identification process (Ko *et al.*, 2013). Furthermore, the different levels of expertise and capabilities among fish larvae taxonomist has make it as a dependent variable in fish larvae morphological identification process. Due to these concerns, adoption of molecular method in identification of fish larvae has been integrated in this study.

A molecular method called DNA barcoding has shed a new light in identification process of animal across many taxa. The utilization of the mitochondrial DNA especially the cytochrome *c* oxidase I (*COI*) gene as a marker in the identification process was found fitting as they are present in almost all eukaryotes and have higher evolution rates than nuclear genes hence confirms it is best to discriminate between closely related taxa (Hebert *et al.*, 2003). It was not only help in resolving animal classification but also plays an important role in identification of fish larvae as the early stage of fish are mostly unknown and the fish larvae of different fish are usually quite similar (Leis and Carson-Ewat, 2000) especially with the available records for public viewing are 135,627 fish barcode sequences, representing 10,757 fish species in the Barcode of Life Data System (BOLD). This platform provides an independent means of testing the validity of existing taxonomic systems, revealing cases of inappropriate synonymy or overlooked taxa (Krishna *et al.*, 2012). However, the introduction of DNA barcoding by Hebert *et al*. (2003) was with the intention to help solve species identification conflicts using mitochondrial genes without any means to undermine the work of taxonomist as claimed by Ebach and de Carvalho (2010).

The Blue-spotted mudskipper, *Boleophthalmus boddarti* as claimed earlier, a resident fish in mangrove ecosystem were also amphibious where they are well adapted to survive outside water. The ability of them to not only swim, but also walk and skip (Ravi, 2005) might offer interesting information regarding their genetic relationship in between population both at inter- and intrapopulation level. The relationship among and within population of marine organism was worth to be studied as they was found to have high dispersal potential due to the lack of barriers in the ocean hence enable the fish larvae to disperse long distance via ocean currents (Tenggardjaja *et al.*, 2016).

Both nuclear marker and mitochondrial marker were applied for this assessment as more information is expected to be seen from two kinds of markers. Both markers were actually functionally interdependent as most mitochondrial proteins are encoded by nuclear genes. However, due to maternal inheritance, the effective population size for mitochondrial genes is approximately one-quarter that for nuclear genes. Mitochondrial genes are expected to detect lower mutation rates and selection pressure meanwhile higher divergences will be seen between populations as compared to nuclear genes (Castro *et al.*, 1998).

1.2 Problem statement

The reduction in mangrove forest could have a significant impact on the levels of diversity of mangrove fish residents since the mangrove ecosystem act as an important nursery ground to many aquatic organism especially fish larvae. The acknowledgement of their existence will be better when they are identified to species level as proper conduct can be alerted to stakeholders. However, the lack of fish larvae identification keys and the possibility of changes in characteristics due to preservation such as pigmentation have limited the ability to identify the fish larvae to species level. Therefore, the limitation in morphological-based identification systems and the dwindling pool of taxonomist signal the need for a new approach to taxon recognition, for instance DNA-based identification. The mitochondrial gene of the cytochrome *c* oxidase subunit I (*COI*) which was maternally inherited and possessed by all livings in the world have made identification of fish larvae to species level possible. Through DNA barcoding system based on the sequence diversity and robust barcoding data available, it was found as an effective tool in differentiating animal taxa and especially in solving rare and cryptic species.

The population genetic study of a mudskipper fish is able to reflect population mixing and connectivity among locations. Thus by assessing the genetic diversity, genetic polymorphism and demographic history through mitochondrial and microsatellite markers will help uncover the evolutionary process of *Boleophthalmus boddarti* such as selection, local adaptation and genetic drift. The lack of specific microsatellite marker for *B. boddarti* justifies the selection of the species for new set of markers to be developed. At the same time the findings will also reflect on the health of their habitat as the Blue-spotted mudskipper is known as mangrove resident fish and ecosystem having high tolerance to pollutants made them suitable to act as bio-indicator to the mangrove.

1.3 Significant of the study

Applying the comparative method coupled with the molecular method in identifying fish larvae opens up a possibility to solve the unsolved cases of the unknown identity of an organism. The taxonomic keys helps determine the identity of a larva specimen based on its morphological features and with the utilization of the mitochondrial DNA especially the cytochrome *c* oxidase I (*COI*) gene allows scientists to further confirms the identity of not only a fully formed organism but also organisms at any stage of development including the egg, which was previously was inadequate in some cases, through the conventional method alone. At the same time, determining patterns and distribution of genetic variation within a species is a key step in understanding the evolutionary legacy. However, until the advent of molecular genetic markers, genetic structure was difficult, if not impossible, to be determined in natural populations. The discovery of fish larvae species in the mangrove areas and the characterization of genetic structure of a fish population provides key information useful in managing genetic stock; conservation efforts, estimation of sustainable harvest levels, proper management to avoid a population crash that would be detrimental to the harvesting industry and most importantly to help maintain population genetic diversity.

1.4 Objectives

1. To identify fish larvae using morphological characters and to quantify the diversity and distribution of fish larvae.

2. To apply DNA Barcoding method for fish larvae identification and phylogenetic comparison with their adult congeners

3. To develop and characterize microsatellite primers for Blue-spotted mudskipper, *Boleophthalmus boddarti.*

4. To examine patterns of genetic variation and population connectivity among Blue-spotted mudskipper using microsatellite markers developed from objective 3 and based on mitochondrial marker.

REFERENCES

Abdul Haris Hilmi, A. A. and Muhammad Faisal, M. S. (2006). "Study on density, distribution and species composition of fish larvae in the waters off the northwest coast of Peninsular Malaysia. In Status of fish larvae study in Malaysia" Retrieved from http://www.unepscs.org/Advanced_Larval_Fish_Training/Country%20 Reports %20on%20Larval%20Fish%20Sampling%202008/30-Status-Fish-LarvaeStudy-Malaysia.pdf

Abdul-Muneer, P. M. (2014). Application of microsatellite markers in conservation genetics and fisheries management: recent advances in population structure analysis and conservation strategies. *Genetics research international*, *2014*.

Abrogueña, J. B. R., Bagarinao, T. U. and Chícharo, L. (2012). Fish habitats in a small, human-impacted Sibunag mangrove creek (Guimaras, Philippines): a basis for mangrove resource enhancement. *Ecohydrology & Hydrobiology*, 12(4): 311-319.

Adams, M. D., Kelley, J. M., Gocayne, J. D., Dubnick, M., Polymeropoulos, M. H., Xiao, H., Merril, C. R., Wu, A., Olde, B. and Moreno, R. F. (1991). Complementary DNA sequencing: expressed sequence tags and human genome project. *Science*, 252(5013): 1651-1656.

Adrian-Kalchhauser, I., Svensson, O., Kutschera, V. E., Rosenblad, M. A., Pippel, M., Winkler, S., Schloissnig, S., Blomberg, A. and Burkhardt-Holm, P. (2017). The mitochondrial genome sequences of the round goby and the sand goby reveal patterns of recent evolution in gobiid fish. *BMC genomics*, 18(1): 177.

Agorreta, A., San Mauro, D., Schliewen, U., Van Tassell, J. L., Kovačić, M., Zardoya, R. and Rüber, L. (2013). Molecular phylogenetics of Gobioidei and phylogenetic placement of European gobies. *Molecular Phylogenetics and Evolution*, 69(3): 619-633.

Ahmad, S. (2009). Recreational values of mangrove forest in Larut Matang, Perak. *Journal of Tropical Forest Science, 21*(2), 81–87.

Ahn, Y. K., Tripathi, S., Cho, Y. I., Kim, J. H., Lee, H. E., Kim, D. S., Woo, J. G. and Cho, M. C. (2013). De novo transcriptome assembly and novel microsatellite marker information in *Capsicum annuum* varieties Saengryeg 211 and Saengryeg 213. *Botanical Studies*, 54(1): 58.

Ajmal Ali, M., Gyulai, G., Hidvegi, N., Kerti, B., Al Hemaid, F. M., Pandey, A. K. and Lee, J. (2014). The changing epitome of species identification–DNA barcoding. *Saudi journal of biological sciences*, 21(3): 204-231.

Akhir, M.M.F. (2008). Surface Circulation and Temperature Distribution of Southern South China Sea from Global Ocean Model (OCCAM). *Sains Malaysiana* 41(6)(2012): 701–714.

Al-Atiyat, R. M. (2015). The power of 28 microsatellite markers for parentage testing in sheep. *Electronic Journal of Biotechnology*, 18(2): 116-121.

Al-Behbehani, B. E. and Ebrahim, H. M. (2010). Environmental studies on the mudskippers in the intertidal zone of Kuwait Bay. *Nature and Science*, 8(5): 79-89.

Allendorf, G.R., Midgley, S.H. and Allen, M. (2001). The problems with hybrid setting conservation guidelines. *Trends in Ecology and Evolution* 16: 613-622.

Altinoz, M. A. and Tunalı, N. E. (2016). Trinucleotide repeat expansions in human breast cancer-susceptibility genes: relevant targets for aspirin chemoprevention. *Clinical and Translational Oncology*, 18(1): 9-17.

Ambreen, H., Kumar, S., Variath, M. T., Joshi, G., Bali, S., Agarwal, M. and Goel, S. (2015). Development of genomic microsatellite markers in *Carthamus tinctorius* L. (Safflower) using next generation sequencing and assessment of their cross-species transferability and utility for diversity analysis. *PloS one*, 10(8): e0135443.

An, H. S. and Lee, J. W. (2012). Development of microsatellite markers for the Korean mussel, *Mytilus coruscus* (Mytilidae) using next-generation sequencing. *International journal of molecular sciences*, 13(8): 10583-10593.

Ansari, A.A., Trivedi, S., Saggu, S. and Rehman, H. (2014). Mudskipper: A biological indicator for environmental monitoring and assessment of coastal waters. *Journal of Entomology and Zoology Studies*, 2 (6): 22-33.

Ara. R,, Arshad, A., Amin, S. M .N., Daud, S. K. and Ghaffar, M. A. (2011a). Environment and diversity of ichthyoplankton in the seagrass beds of Sungai Pulai estuary, Johor Peninsular Malaysia. *Journal of Food, Agriculture and Environment,* 9: 733-738.

Ara, R., Arshad, A., Amin, S. M. N., Daud, S. K. and Ghaffar, M. A. (2011b). Comparison of larval fish density between seagrass beds and outside

seagrass beds of the Southwestern Johor, Peninsular Malaysia. *Journal of Fisheries and Aquatic Science*, 6(7): 795

Ara, R., Amin, S. M. N., Mazlan, A. G. and Arshad, A. (2013). Morphometric Variation Among Six Families of Larval Fishes in the Seagrass-Mangrove Ecosystem of Gelang Patah, Johor, Malaysia. *Asian Journal of Animal and Veterinary Advances,* 8: 247-256.

Ardura, A., Morote, E., Kochzius, M. and Garcia-Vazquez, E. (2016). Diversity of planktonic fish larvae along a latitudinal gradient in the Eastern Atlantic Ocean estimated through DNA barcodes. *PeerJ*, *4*: e2438.

Arif, I. A. and Khan, H. A. (2009). Molecular markers for biodiversity analysis of wildlife animals: a brief review. *Animal Biodiversity and Conservation*, 32.1: 9–17.

Alexandris, N., Chatenoux, B., Lopez, T. L. and Peduzzi, P. (2013). Monitoring mangrove restoration from space. UNEP / GRID-Geneva.

Ara, R., Arshad, A., Amin, S. M. N. and Mazlan, A. G. (2013). Temporal and spatial distribution of larval fish assemblage in different ecological habitat in Johor Strait, Peninsular Malaysia. *Asian Journal of Animal and Veterinary Advances.* 8(1): 53-62.

Arshad, A., Ara, R., Amin, S.M.N., Daud, S.K. and Ghaffar, M.S. (2012). Larval fish composition and spatio-temporal variation in the estuary of Pendas River, southwestern Johor, Peninsular Malaysia. *Coastal Marine Science,* 35: 96-102.

Atan, Y., Jaafar, H. and Abdul Majid, A. R. (2010). *Ikan Laut Malaysia glosari nama sahih spesies ikan*. Dewan Bahasa dan Pustaka.

Auer, N. A. (1982). Identification of larval fishes of the Great Lakes basin with emphasis on the Lake Michigan drainage. Great Lakes Fishery Commission, Ann Arbor, MI 48105. Special Pub. 82-3, p. 8

Avise, J.C. and Felley, J. (1979). Population structure of freshwater fishes. I. Genetic variation of bluegill (*Lepomis macrochirus*) populations in man-made reservoirs. *Evolution*, 33:15-26.

Avise, J. C., Arnold, J., Ball, R. M., Bermingham, E., Lamb, T., Neigel, J. E., Reeb, C. A. and Saunders, N. C. (1987). Intraspecific phylogeography: the mitochondrial DNA bridge between population genetics and systematics. *Annual review of ecology and systematics*, 18(1): 489-522.

Avise, J.C. 1998. The history and purview of phylogeography: a personal reflection. *Molecular Ecology* 7:371-379.

Avise, J.C. and Tatarenkov, A. (2015). Population genetics and evolution of the mangrove rivulus (*Kryptolebias marmoratus*), the world's only self-fertilizing hermaphroditic vertebrate. *Journal of Fish Biology* 87:519-538.

Ayala, D., Riemann, L. and Munk, P. (2016). Species composition and diversity of fish larvae in the Subtropical Convergence Zone of the Sargasso Sea from morphology and DNA barcoding. *Fisheries oceanography*, 25(1): 85-104.

Aziz, N. M. A., Esa, Y. and Arshad, A. (2016). DNA barcoding and phylogenetic analysis of Malaysian groupers (Subfamily: Epinephelinae) using mitochondrial Cytochrome c oxidase I (COI) gene. *JOURNAL OF ENVIRONMENTAL BIOLOGY*, 37(4): 725-733.

Azwady, A. N. and Mazlan, A. G. (2009). Feeding habits and temporal variation of diet composition of fish larvae (Osteichthyes: Sparidae) in the Sungai Pulai seagrass bed, Johore, Peninsular Malaysia. *Journal of Biological Sciences*, 9(5): 445-451.

Bacher, J. W., Abdel Megid, W. M., Kent-First, M. G. and Halberg, R. B. (2005). Use of mononucleotide repeat markers for detection of microsatellite instability in mouse tumors. *Molecular carcinogenesis*, 44(4): 285-292.

Bader, J.M. (1998). Measuring genetic variability in natural populations by allozyme electrophoresis. Pages 25-42, *in* Tested studies for laboratory teaching, Volume 19 (S. J. Karcher, Editor). Proceedings of the 19th Workshop/Conference of the Association for Biology Laboratory Education (ABLE), 365 pages.

Badri, J., Yepuri, V., Ghanta, A., Siva, S. and Siddiq, E. A. (2014). Development of microsatellite markers in sesame (Sesamum indicum L.). *Turkish Journal of Agriculture and Forestry*, 38(5): 603-614.

Baldwin, C.C. and Johnson, G.D. (2014). Connectivity across the Caribbean Sea: DNA Barcoding and Morphology Unite an Enigmatic Fish Larva from the Florida Straits with a New Species of Sea Bass from Deep Reefs off Curac¸ao. PLoS ONE 9(5): e97661.

Bandelt, H., Forster, P. and Röhl, A. (1999). Median-joining networks for inferring intraspecific phylogenies. *Molecular Biology and Evolution*, 6: 37–48.

Bansidhar, B. J. and Silinsky, J. (2012). History and pathogenesis of lynch syndrome. *Clinics in colon and rectal surgery*, 25(02): 063-066.

Baran, E. (2002). The importance of non-commercial fish. *Fisheries and aquaculture: towards sustainable aquatic living resources management. UNESCO Encyclopaedia of Life Support Systems. EOLSS Publishers, Oxford*, 2-11.

Barbara, T., Palma-Silva, C., Paggi, G. M., Bered, F., Fay, M. F. and Lexer, C. (2007). Cross-species transfer of nuclear microsatellite markers: potential and limitations. *Molecular Ecology*, 16(18): 3759-3767.

Bardakci, F. (2001). Random Amplified Polymorphic DNA (RAPD) Markers. Turk J Biol 25:185-196

Barker, J. S. F. (1994). A global protocol for determining genetic distances among domestic livestock breeds. In *Proceedings of the 5th World Congress on Genetics Applied to Livestock Production, Guelph and Ontario, Canada* (Vol. 21, pp. 501-508).

Barton N. H. and Hewitt G. M. (1985). Analysis of hybrid zones. *Annual Review of Ecology and Systematics,* 16, 113–148.

Bayot, F. A., Joya, K. N. A. and Jacinto, W. R. (2014). Phylogenetic analysis and barcoding of gobies in Maragondon river, Cavite, Philippines. *International Journal of Current Science*, 12: 50-6.

Beer, A. (1852). Bestimmung der absorption des rothen lichts in farbigen flussigkeiten. *Ann. Physik*, 162: 78-88.

Bentzen, P., Taggart, C.T, Ruzzante, D.E. and Cook, D. 1996. Microsatellite polymorphism and the population structure of Atlantic cod (*Gadus morhua*) in the northwest Atlantic. *Anadian Journal of Fisheries and Aquatic Sciences,* 53: 2706-2721.

Berdugo, G.O. and Barandica, J.C.N., (2014). Genetic diversity and population structure of bocachico *Prochilodus magdalenae* (Pisces, Prochilodontidae) in the Magdalena River basin and its tributaries, Colombia. *Genetics and Molecular Biology*, 37(1): 37-45

Bernal, A., Viñas, J. and Olivar, M. P. (2014). Genetic support for the morphological identification of larvae of Myctophidae, Gonostomatidae, Sternoptychidae and Phosichthyidae (Pisces) from the western Mediterranean. *Scientia Marina*, 78(4): 461-471.

Bhattacharyya, U., Pandey, S. K. and Dasgupta, T. (2014). Identification of EST-SSRs and FDM in sesame (*Sesamum indicum* L.) through data mining. *Scholars Journal of Agriculture and Veterinary Sciences*, 4: 60-69.

Bianchi, F., Galizia, E., Catalani, R., Belvederesi, L., Ferretti, C., Corradini, F. and Cellerino, R. (2009). CAT25 is a mononucleotide marker to identify HNPCC patients. *The Journal of Molecular Diagnostics*, 11(3): 248-252.

Bird, C.E., Holland, B.S., Bowen, B.W. and Toonen, R.J. (2007). Contrasting phylogeography in three endemic Hawaiian limpets (*Cellana* spp.) with similar life histories. *Molecular Ecology*, 16:3173–3186.

Bisht, S.S. and Panda, A.K., (2014). DNA Sequencing: Methods and Application. Eds Ravi, I., Baunthiyal, M. and Saxena, *J. Advances in Biotechnology*. Springer New Delhi.

Blaber, S. J. M. and Milton, D. A. (1990). Species composition, community structure and zoogeography of fishes of mangrove estuaries in the Solomon Islands. *Marine Biology*, 105(2): 259-267.

Blaber, S. J., Milton, D. A., Pang, J., Wong, P., Boon-Teck, O., Nyigo, L. and Lubim, D. (1996). The life history of the tropical shad *Tenualosa toli* from Sarawak: First evidence of protandry in the Clupeiformes. *Environmental Biology of Fishes*, 46(3): 225-242.

Blaber, S. J. M., Farmer, M. J., Milton, D. A., Pang, J., Boon-Teck, O. and Wong, P. (1997). The ichthyoplankton of selected estuaries in Sarawak and Sabah: composition, distribution and habitat affinities. *Estuarine, Coastal and Shelf Science*, 45(2): 197-208.

Bonhomme, F., Rivals, E., Orth, A., Grant, G. R., Jeffreys, A. J. and Bois, P. R. (2007). Species-wide distribution of highly polymorphic minisatellite markers suggests past and present genetic exchanges among house mouse subspecies. *Genome biology*, 8(5): R80.

Bornet, B., Antoine, E., Bardouil, M. and Marcaillou-Le Baut, C. (2004). ISSR as new markers for genetic characterization and evaluation of relationships among phytoplankton. *Journal of Applied Phycology*, 16(4): 285-290.

Bouckaert, R., Heled, J., Kühnert, D., Vaughan, T., Wu, C-H., Xie, D., Suchard, M.A. Rambaut, A. and Drummond, A. J. (2014). BEAST 2: A Software Platform for Bayesian Evolutionary Analysis. *PLoS Computational Biology*, 10(4), e1003537.

Branicki, W., Kupiec, T. and Pawlowski, R. (2003). Validation of cytochrome b sequence analysis as a method of species identification. *Journal of Forensic Science*, 48(1): 1-5.

Brendtro, K.S., McDowell, J.R., and Graves, J.E. (2008). Population genetic structure of escolar (*Lepidocybium xavobrunneum*). *Marine Biology*, 155:11–22

Brook, B., Tonkyn, D., O'Grady, J. and Frankham, R. (2002). Contribution of inbreeding to extinction risk in threatened species. *Conservation Ecology*, 6(1).

Brouwer, J. R., Willemsen, R. and Oostra, B. A. (2009). Microsatellite repeat instability and neurological disease. *Bioessays*, 31(1): 71-83.

Brown, B. and Epifanio, J. (2003). Nuclear DNA. In: Hallermann, E.M. Ed., *Population Genetics*: *Principles and Applications for Fisheries Scientists*, American Fisheries Society, Bethesda, 458-472.

Bu-Olayan, A. H. and Thomas, B. V. (2008). Trace metals toxicity and bioaccumulation in mudskipper *Periophthalmus waltoni* Koumans 1941 (Gobiidae: Perciformes). *Turkish Journal of Fisheries and Aquatic Sciences*, 8: 215-218.

Cai, G., Leadbetter, C. W., Muehlbauer, M. F., Molnar, T. J. and Hillman, B. I. (2013). Genome-wide microsatellite identification in the fungus *Anisogramma anomala* using Illumina sequencing and genome assembly. *PloS one*, 8(11): e82408.

Calow, P. (1998). Encyclopedia of Ecology and Environmental Management. Blackwell Press. Pp 379-380

Carreon-Martinez, L. B., Walter, R. P., Johnson, T. B., Ludsin, S. A. and Heath, D. D. (2015). Benefits of turbid river plume habitat for Lake Erie yellow perch (*Perca flavescens*) recruitment determined by juvenile to larval genotype assignment. *PloS one*, 10(5): e0125234.

Castro, J. A., Picornell, A. and Ramon, M. (1998). Mitochondrial DNA: a tool for populational genetics studies. *International Microbiology*, *1*(4): 327-332.

Cavagnaro, P. F., Senalik, D. A., Yang, L., Simon, P. W. and Harkins, T. T. (2010). Genome-wide characterization of simple sequence repeats in cucumber (*Cucumis sativus* L.). *BMC genomics*, 11(1): 569.

Cao, L., Liang, X-F., Du, Y., Zheng, H., Yang, M. and Huang, W. (2013). Genetic population structure in *Siniperca scherzeri* (Perciformes: Siniperca) in China inferred from mitochondrial DNA sequences and microsatellite loci. *Biochemical Systematics and Ecology*, 51:160–170

Chong, V. C., Sasekumar, A., Leh, M. U. C. and Cruz, R. D. (1990). The fish and prawn communities of a Malaysian coastal mangrove system, with comparison to adjacent mud flats and inshore waters. *Estuarine Coastal and Shelf Science*. 31(5):703-722.

Carlsson, J. (2008). Effects of microsatellite null alleles on assignment testing. *Journal of Heredity*, 99(6): 616-623.

Carr, S.M. and Crutcher, D.C. (1998). Population genetic structure in Atlantic Cod (*Gadus morhua*) from the North Atlantic and Barents Sea: contrasting or concordant patterns in mtDNA sequence and microsatellite data. Pp. 91-103 In The Implications of Localized Fishery Stocks (I. Hunt von Herbing, I. Kornfield, M. Tupper, and J. Wilson. eds.). Northeast Regional Agricultural Engineering Service, Ithaca, New York.

Carvalho, G.R. and Hauser, L. 1995. *Molecular genetics and the stock concept in fisheries.* In Carvalho, G. R. and T. J. Pitcher (eds), Molecular Genetics in Fisheries.

Carvalho, G. R. and Hauser, L. (1998). Advances in the molecular analysis of fish population structure. *Italian Journal of Zoology*, 65(S1): 21-33.

Castro, J.A., Picornell, A. and Ramon, M. (1998). Mitochondrial DNA: a tool for populational genetics studies. *International Microbiology,* 1:327–332.

Census of Marine Life (2010). Census Of Marine Life 2007/2008 Highlights Report. Accessed on 1st February 2017. Retrieved from http://www.coml.org/pressreleases/highlights08/coml_highlights Report08-sm.pdf.

Chabarria, R.E. and Pezold, F. (2013). Phylogeography and historical demography of *Sicydium salvini* in the eastern Pacific. *Ichthyological Research*, 60(4): 353-362.

Chang, J. T. and Lee, S. C. (1994). Genetic variation of the Chinese mudskipper, *Periophthalmus cantonensis* (Osbeck, 1762)(Pisces; Perciformes, Gobiidae) from Taiwan. *Zoological studies*, 33(1): 34-43.

Chapuis, M. P. and Estoup, A. (2006). Microsatellite null alleles and estimation of population differentiation. *Molecular biology and evolution*, 24(3): 621-631

Chen, W., Hong, W., Chen, S., Wang, Q. and Zhang, Q. (2015). Population genetic structure and demographic history of the mudskipper *Boleophthalmus pectinirostris* on the northwestern pacific coast. *Environmental biology of fishes*, 98:845–856

Chauhan, T. and Rajiv, K. (2010). Molecular markers and their applications in fisheries and aquaculture. *Advances in Bioscience and Biotechnology*, 1: 281-291.

Chen, I-S., Shao, K-T., Hsu, S-L., Gong, G-C., Chen, Y-C. and Liu, T-K. (2013). Dna barcoding of coastal larval fish communities of Dongsha Island, South China Sea Revealed by mitochondrial COI Sequences. *Journal of Marine Science and Technology*, 21(Suppl.): 252-257.

Chen, W., Hong, W., Chen, S., Wang, Q. and Zhang, Q. (2015). Population genetic structure and demographic history of the mudskipper *Boleophthalmus pectinirostris* on the Northwestern Pacific coast. *Environmental Biology of Fishes.* 98: 845.

Chong, V. C. (2007a). Mangroves-fisheries linkages—the Malaysian perspective. *Bulletin of Marine Science*, 80(3): 755-772.

Chong, V. C. (2007b). Fifteen years of fisheries research in the Matang mangroves: What have we learnt. In: Shaharuddin MI, Azahar M, Razani U Kamaruzzaman AB, Lim KL, Suhaili R, Jalil MS, Latiff a. (eds.) Sustainable Management of Matang Mangroves: 100 Years and Beyond. Forest Biodiversity Series 4. Forestry Department Peninsular Malaysia. pp 411-429.

Choudhary, O. P. and Trivedi, S. (2010). Microsatellite or simple sequence repeat (SSR) instability depends on repeat characteristics during replication and repair. *Journal of Cell and Molecular Biology*, 8(2): 21-34.

Chua, J.L.T. (2009). Tidal migration of the giant mudskipper, *Periophthalmodon schlosseri* (Pallas, 1770) in a Singapore Mangrove. Unpublished Undergraduate Research Opportunities in Science Report. National University of Singapore, Singapore, 30 pp.

Cifarelli, R. A., Gallitelli, M. and Cellini, F. (1995). Random amplified hybridization microsatellites (RAHM): isolation of a new class of

microsatellite-containing DNA clones. *Nucleic Acids Research*, 23(18): 3802.

Ciftci, Y. and Okumus, I. (2002). Fish Population Genetics and Applications of Molecular Markers to Fisheries and Aquaculture: I- Basic Principles of Fish Population Genetics. *Turkish Journal of Fisheries and Aquatic Sciences* 2: 145-155.

Clayton, D.A. and Vaughan, T.C. (1988). Ethogram of *Boleophthalmus boddarti* (Pallas), a mudskipper found on the mudflats of Kuwait. *Kuwait Journal of Sciences*, 15(1):115-138.

Clayton, D. A. and Wright, J. M. (1989). Mud-walled territories and feeding behaviour ofBoleophthalmus boddarti (Pisces: Gobiidae) on the mudflats of Kuwait. *Journal of Ethology*, *7*(2), 91-95.

Coates, B.S., Bayles, D.O., Wanner, K.W., Robertson, H.M., Hellmich, R.L. and Sappington, T.W. (2011). The Application and Performance of Single Nucleotide Polymorphism Markers for Population Genetic Analyses of Lepidoptera. *Frontiers in Genetics,* 2: 38.

Coddington, J. A., Agnarsson, I., Miller, J. A., Kuntner, M. and Hormiga, G. (2009). Undersampling bias: the null hypothesis for singleton species in tropical arthropod surveys. *Journal of animal ecology*, 78(3): 573-584.

Coelho, P., Sousa, P., Harris, D. J. and Van der Meijden, A. (2014). Deep intraspecific divergences in the medically relevant fat-tailed scorpions (Androctonus, Scorpiones). *Acta tropica*, 134: 43-51.

Collins, R. A. and Cruickshank, R. H. (2012). The seven deadly sins of DNA barcoding. *Molecular ecology resources*, 13(6): 969-975.

Collins, S.M.B., McIntyre, N., Coulon, P.B., Ulseth, A., Taphorn, A.J., Flecker, D.C. and Alexander, S. (2013). Population structure of a neotropical migratory fish: contrasting perspectives from genetics and otolith microchemistry. *Transactions of the American Fisheries Society* , 142(5).

Cooke, G.M., Chao, N.L. and Beheregaray, L.B. (2012). five cryptic species in the amazonian catfish *Centromochlus existimatus* identified based on biogeographic predictions and genetic data. *PLoS ONE* 7(11): e48800.

Cornuet, J. M. and Luikart, G. (1996). Description and power analysis of two tests for detecting recent population bottlenecks from allele frequency data. *Genetics*, 144(4): 2001-2014.

Costa, F. O., DeWaard, J. R., Boutillier, J., Ratnasingham, S., Dooh, R. T., Hajibabaei, M. and Hebert, P. D. (2007). Biological identifications through DNA barcodes: the case of the Crustacea. *Canadian Journal of Fisheries and Aquatic Sciences*, 64(2): 272-295.

Couceiro, L., Maneiro, I., Mauger, S., Valero, M., Ruiz, J. M., and Barreiro, R. (2011). Microsatellite development in rhodophyta using high-throughput sequence data. *Journal of phycology*, 47(6): 1258-1265.

Cowen, R. K., Paris, C. B. and Srinivasan, A. (2006). Scaling of connectivity in marine populations. *Science*, 311(5760): 522-527.

Coyne, J. A. and Orr, H. A. (2004). *Speciation*. Sinauer Associates, Sunderland, MA. 545 pp.

Craft, K. J., Pauls, S. U., Darrow, K., Miller, S. E., Hebert, P. D., Helgen, L. E., Novotny, V. and Weiblen, G. D. (2010). Population genetics of ecological communities with DNA barcodes: An example from New Guinea Lepidoptera. *Proceedings of the National Academy of Sciences*, 107(11), 5041-5046.

Crandall, E.D., Taffel, J.R. and Barber, P.H. (2009). High gene flow due to pelagic larval dispersal among South Pacific archipelagos in two amphidromous gastropods (Neritomorpha: Neritidae). *Heredity*, 104: 563–572.

Crawford, M. H. (Ed.). (2007). *Anthropological genetics: theory, methods and applications*. Cambridge University Press.

Cunningham, M.K., Granberry, W.F. and Pope, K.L. (2000). Shrinkage of inland silverside larvae preserved in ethanol and formalin. Nebraska Cooperative Fish & Wildlife Research Unit -- Staff Publications. Paper 14.

Dang, N-X., Sun, F-H., Lv, Y-Y., Zhao, B-H., Wang, J-C., Murphy, R.W., Wang, W-Z. and Jia-Tang. (2015). DNA barcoding and the identification of tree frogs (Amphibia: Anura: Rhacophoridae) *Mitochondrial DNA*, Early Online: 1–11

Daud, S. K., Mohammadi, M. E. H. D. I., Siraj, S. S. and Zakaria, M. P. (2005). Morphometric analysis of Malaysian oxudercine goby, *Boleophthalmus boddarti* (Pallas, 1770). *Pertanika Journal of Tropical Agricultural Science*, 28(2): 121.

Davis, M. J. J., Bailey, C. S. and Smith, C. K. (1996). Increased informativeness of RAPD analysis by detection of microsatellite motifs. *BioTechniques*, 23: 285-290.

De Carvalho, D. C., Oliveira, D. A., Pompeu, P. S., Leal, C. G., Oliveira, C. and Hanner, R. (2011). Deep barcode divergence in Brazilian freshwater fishes: the case of the São Francisco River basin. *Mitochondrial Dna, 22(sup1*): 80-86.

Decru, E., Moelants, T., De Gelas, K., Vreven, E., Verheyen, E. and Snoeks, J. (2016). Taxonomic challenges in freshwater fishes: a mismatch between morphology and DNA barcoding in fish of the north-eastern part of the Congo basin. *Molecular ecology resources*, 16(1): 342-352.

Delrieu-Trottin, E., Mona, S., Maynard, J., Neglia, V., Veuille, M. and Planes, S. (2017). Population expansions dominate demographic histories of endemic and widespread Pacific reef fishes. *Scientific reports*, 7: 40519.

Denney, N.H. Jennings, S. and Reynolds, J.D. (2002). Life-history correlates of maximum population growth rates in marine fishes. *Proceedings of the royal society of London B: Biological sciences* 269: 2229–2237

DeWoody, J. A. and Avise, J. C. (2000). Microsatellite variation in marine, freshwater and anadromous fishes compared with other animals. *Journal of fish biology*, 56(3): 461-473.

Di Rienzo, A., Peterson, A. C., Garza, J. C., Valdes, A. M., Slatkin, M. and Freimer, N. B. (1994). Mutational processes of simple-sequence repeat loci in human populations. *Proceedings of the National Academy of Sciences*, 91(8): 3166-3170.

Díaz, J., Villanova, G. V., Brancolini, F., del Pazo, F., Posner, V. M., Grimberg, A. and Arranz, S. E. (2016). First DNA barcode reference library for the identification of South American freshwater fish from the lower Paraná river. *PloS one*, 11(7): e0157419.

Dinh, Q. M. (2014). A preliminary study on length-weight relationship of the mudskipper *Boleopthalmus boddarti* in Soc Trang. *Journal of Biological studies*, 36(1): 88-92.

Dinh, Q. M., Tra Giang, N. T. and Kieu Tien, N. T. (2015). Reproductive biology of the mudskipper *Bolepthalmus boddarti* in Soc Trang. *Journal of Biology studies*. 37(3): 362-369.

Dixon, P. I., Crozier, R. H., Black, M. and Church, A. (1987). Stock identification and discrimination of commercially important whitings in Australian waters using genetic criteria. *Centre for Marine Science, University of New South Wales, FIRTA Project*, 87(11).

do Amaral Crispim, B., de Oliveira Seno, L., do Egito, A. A., de Vargas Junior, F. M. and Grisolia, A. B. (2014). Application of microsatellite markers for breeding and genetic conservation of herds of Pantaneiro sheep. *Electronic Journal of Biotechnology*, 17(6): 317-321.

Dove, C.J., Rotzel, N.C., Heacker, M. and Weight, L.A. (2008). Using DNA barcodes to identify bird species involved in birdstrikes. *Journal of Wildlife Management*, 72: 1231-1236.

Dubut, V., Sinama, M., Martin, J. F., Meglécz, E., Fernandez, J., Chappaz, R., Gilles, A. and Costedoat, C. (2010). Cross-species amplification of 41 microsatellites in European cyprinids: a tool for evolutionary, population genetics and hybridization studies. *BMC research notes*, 3(1): 135.

Ebach, M.C. and de Carvalho, R. (2010). Anti-intellectualism in the DNA Barcoding Enterprise. *ZOOLOGIA* 27(2):165-178.

Edgar, G. J. and Shaw, C. (1995). The production and trophic ecology of shallow-water fish assemblages in southern Australia II. Diets of fishes and trophic relationships between fishes and benthos at Western Port, Victoria. *Journal of Experimental Marine Biology and Ecology*, 194(1): 83-106

Esa, Y. B., Siraj, S. S., Daud, S. K., Khairul Adha, A. R., Jeffrine, R. J. R. and Tan, S. G. (2008). Mitochondrial DNA Diversity of *Tor tambroides* Valenciennes (Cyprinidae) from Five Natural Populations in Malaysia. *Zoological Studies* 47(3): 360-367.

Eisen, J. A. (1999). *Mechanistic basis for microsatellite instability. Eds Goldstein DB & Schlötterer C, in Microsatellites: Evolution and applications*. Oxford University Press, Oxford, UK, pp. 34-48.

El-Regal, M. A. A. and Ibrahim, N. K. (2014). Role of mangroves as a nursery ground for juvenile reef fishes in the southern Egyptian Red Sea. *The Egyptian Journal of Aquatic Research*, 40(1): 71-78.

Ellegren, H. (2004). Microsatellites: Simple sequences with complex evolution. *Nat. Rev. Genet*. 5, 435–445.

Ender, A., Schwenk, K., Städler, T., Streit, B. and Schierwater, B. (1996). RAPD identification of microsatellites in Daphnia. *Molecular Ecology*, 5(3): 437-441.

Estoup, A. and Cornuet, J-M. (1998). Microsatellite evolution: inferences from population data. *Microsatellites: evolution and applications*. In Microsatelliies Evolution and Applications, (eds. Goldstein DB, Schlotterer C), Oxford University Press, Oxford, in press.

Excoffier, L. (2004). Patterns of DNA sequence diversity and genetic structure after a range expansion: lessons from the infinite-island model. *Molecular Ecology*, 13(4): 853-864.

Excoffier, L. and Lischer, H. E. (2010). Arlequin suite ver 3.5: a new series of programs to perform population genetics analyses under Linux and Windows. *Molecular ecology resources*, 10(3): 564-567.

Faircloth, B. C. (2008). Msatcommander: detection of microsatellite repeat arrays and automated, locus-specific primer design. *Molecular ecology resources*, 8(1): 92-94.

Fang, D. A., Zhou, Y. F., Duan, J. R., Zhang, M. Y., Xu, D. P., Liu, K., Xul, P., and Wei, Q. (2015). Screening potential SSR markers of the anadromous fish *Coilia nasus* by de novo transcriptome analysis using Illumina sequencing. *Genetics and Molecular Research*, 14(4): 14181-14188.

Fedrizzi, N., Stiassny, M. L., Boehm, J. T., Dougherty, E. R., Amato, G. and Mendez, M. (2015). Population genetic structure of the dwarf seahorse (*Hippocampus zosterae*) in Florida. *PloS one*, 10(7): e0132308.

Felsenstein, J. (1981). Evolutionary trees from DNA sequences: a maximum likelihood approach. *Journal of molecular evolution, 17(*6): 368-376.

Fishbase. *Boleophthalmus boddarti*. Accessed on 26th May 2017. http://www.fishbase.org/summary/Boleophthalmus-boddarti.html

Fong, C. O. (1984). Johore Port: its role in the growth of south Peninsular Malaysia. *The Developing Economies.* 21: 185-187.

Foran, D.R., Fischer, A.B. and Stoloff, .E. A. (2015). Comparison of mitochondrial DNA amplification strategies for species identification. *Journal of Forensic Investigation*. 3(2): 7.

Freitas, D. M. and Muelbert, J. H. 2004. Ichthyoplankton distribution and abundance off Southeastern and Southern Brazil. *Brazilian Archives of Biology and Technology*, 47 (4): 601-612.

Fu, Y. X. (1997). Statistical tests of neutrality of mutations against population growth, hitchhiking and background selection. *Genetics, 147(*2): 915-925.

Fuller, R. S., Frietze, S. and McGlaughlin, M. E. (2015). Characterization of 13 microsatellite markers for *Calochortus gunnisonii* (Liliaceae) from Illumina MiSeq sequencing. *Applications in plant sciences*, 3(8): 1500051.

Galarza, J. A., Mappes, J., and Valkonen, J. K. (2015). Biogeography of the smooth snake (*Coronella austriaca*): origin and conservation of the northernmost population. *Biological journal of the Linnean Society,* 114(2): 426-435.

Gall, G. A. E. (1987). *Inbreeding.* N. Ryman and F.M. Utter (Eds.), Population Genetics and Fishery Management. Washington: University of Washington: 47-88.

Galtier, N., Nabholz, B., Min, S. G. and Hurst. G.D.D. (2009). Mitochondrial DNA as a marker of molecular diversity: a reappraisal. *Molecular Ecology*, 18:4541–4550.

Grabherr, M. G., Haas, B. J., Yassour, M., Levin, J. Z., Thompson, D. A., Amit, I., Adiconis, X., Fan, L., Raychowdhury, R., Zeng, Q., Chen, Z., Mauceli, E., Hacohen, N., Gnirke, A., Rhind, N., di Palma, F., Birren, B. W., Nusbaum, C., Lindblad-Toh, K., Friedman, N., Regev, A. (2011). Full-length transcriptome assembly from RNA-Seq data without a reference genome. *Nature Biotechnology,* 29, 644–652.

Gascuel, O. and Steel, M. (2006). Neighbor-joining revealed. *Molecular biology and evolution*, 23(11): 1997-2000.

Gaylord, B. Gaines, S. D., Siegel, D.A. and Carr, M.H. (2005). Marine reserves exploit population structure and life history in potentially improving fisheries yields. *Ecological Application*s, 15(6): 2180–2191

Ghaffar, M. A., Teck, L. W. and Talib, Z. (2010). *A Field Guide for Sampling and Identification of Larval Fish from Coastal Waters of Southeastern Peninsular Malaysia*. Universiti Kebangsaan Press, Malaysia. p 55.

Gilka, S. E., Wanga, I. A., Hoovera, C. L., Smokera, W.W., Taylorb, S. G., Graya, A. K. and Gharretta, A. J. (2003). Outbreeding depression in hybrids between spatially separated pink salmon, Oncorhynchus gorbuscha, populations: marine survival, homing ability, and variability in family size. *Environmental Biology of Fishes* 69: 287–297.

Gonzalez, E. B., Knutsen, H. and Jorde, P. E. (2016). Habitat discontinuities separate genetically divergent populations of a rocky shore marine fish. *PloS one*, 11(10): e0163052.

Goodall-Copestake, W. P., Tarling, G. A. and Murphy, E. J. (2012). On the comparison of population-level estimates of haplotype and nucleotide diversity: a case study using the gene cox1 in animals. *Heredity*, 109(1): 50.

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 lessons for conservation. *Journal of Heredity*, 89(5): 415-426.

Grubisha, L. C., Nelson, B. A., Dowie, N. J., Miller, S. L. and Klooster, M. R. (2014). Characterization of microsatellite markers for pinedrops, *Pterospora andromedea* (Ericaceae), from Illumina MiSeq sequencing.

Grzimek's Animal Life Encyclopedia. (2004). Clupeiformes (Herrings). Encyclopedia.com.http://www.encyclopedia.com/article-1G23406700261/clupeiformes-herrings.html. Accessed 1 may 2016

Gu, Q. H., Husemann, M., Ding, B., Luo, Z. and Xiong, B. X. (2015). Population genetic structure of *Bellamya aeruginosa* (Mollusca: Gastropoda: Viviparidae) in China: weak divergence across large geographic distances. *Ecology and Evolution*, 5(21): 4906–4919.

Gürcan, K., Mehlenbacher, S. A. and Cristofori, V. (2008, June). Inter-simple sequence repeat (ISSR) markers in hazelnut. In *VII International Congress on Hazelnut 845* (pp. 159-162).

Gutierrez-Rodriguez, C. (2003). Reproductive biology of the Caribbean gorgonian Pseudopterogorgia elisabethae and its effects on genetic variation.

Gutiérrez-Rodríguez, C. and Lasker, H. R. (2004). Microsatellite variation reveals high levels of genetic variability and population structure in the gorgonian coral Pseudopterogorgia elisabethae across the Bahamas. *Molecular Ecology*, 13(8): 2211-2221.

Hajisamae, S., Yeesin, P. and Chaimongkol, S. (2006). Habitat utilization by fishes in a shallow, semi-enclosed estuarine bay in southern Gulf of Thailand. *Estuarine Coastal and Shelf Science*. 68(3-4):647-655.

Hakki, E., Christo, P., Luchezar, K. and Mahinur, A. (2002). Isolation of wheat microsatellite DNA fragments by hybridization selection. *Bulgarian Journal of Plant physiology*, 28: 3-10.

Hakki, E. E. and Akkaya, M. S. (2000). Microsatellite isolation using amplified fragment length polymorphism markers: no cloning, no screening. *Molecular Ecology*, 9(12): 2152-2154.

Hall, T. A. (1999, January). BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. In *Nucleic acids symposium series* (Vol. 41, No. 41, pp. 95-98). [London]: Information Retrieval Ltd., c1979-c2000.

Hansen, M. M. (2003). Application of molecular markers in population and conservation genetics, with special emphasis on fishes (Doctoral desertion). Retrieved from http://s3.amazonaws.com/publicationslist.org/data/Michael.M.Hansen/ref-77/DSc%20thesis.pdf

Hanzawa, N., Gotoh, R. O., Sekimoto, H., Goto, T. V., Chiba, S. N., Kuriiwa, K. and Tamate, H. B. (2012). Genetic diversity and evolution of marine animals isolated in marine lakes. In *Analysis of Genetic Variation in Animals*. InTech.

Hasegawa, M., Kishino, H. and Saitou, N. (1991). On the maximum likelihood method in molecular phylogenetics. *Journal of molecular evolution*, 32(5): 443-445.

He, L., Mukai, T., Chu, K. H., Ma, Q. and Zhang, J. (2015). Biogeographical role of the Kuroshio Current in the amphibious mudskipper *Periophthalmus modestus* indicated by mitochondrial DNA data. *Scientific reports*, *5*, 15645.

Heath, D. D., Pollard, S. and Herbinger, C. (2001). Genetic structure and relationships among steelhead trout (*Oncorhynchus mykiss*) populations in British Columbia. *Heredity*, 86**:** 618–627.

Hebert, P. D., Cywinska, A., Ball, S. L. and DeWaard, J. R. (2003). Biological identifications through DNA barcodes. *Proceedings of the Royal Society of London B: Biological sciences*, 270(1512): 313-21.

Hebert, P. D., Penton, E. H., Burns, J. M., Janzen, D. H. and Hallwachs, W. (2004a). Ten species in one: DNA barcoding reveals cryptic species in the neotropical skipper butterfly *Astraptes fulgerator*. *Proceedings of the National Academy of Sciences of the United States of America*, 101(41): 14812-14817.

Hebert, P. D., Stoeckle, M. Y., Zemlak, T. S. and Francis, C. M. (2004b). Identification of birds through DNA barcodes. *PLoS biology*, 2(10): e312.

Hedrick, P. W. (2005). A standardized genetic differentiation measure. *Evolution*, 59(8) 1633-1638.

Henriksson, O. (2013). Genetic connectivity of fish in the Western Indian Ocean. (Doctoral dissertation). Retrieved from https://www.diva-portal.org/smash/get/diva2:641068/FULLTEXT01.pdf

Hobbs, J. P. A., van Herwerden, L., Jerry, D. R., Jones, G. P. and Munday, P. L. (2013). High genetic diversity in geographically remote populations of endemic and widespread coral reef angelfishes (genus: Centropyge). *Diversity*, 5(1): 39-50.

Hobbs, J. P., Jones, G. P. and Munday, P. L. (2011). Extinction risk in endemic marine fishes. *Conservation biology*, 25(5): 1053-1055.

Hogg, I. D. and Hebert, P. D. (2004). Biological identification of springtails (Hexapoda: Collembola) from the Canadian Arctic, using mitochondrial DNA barcodes. *canadian Journal of Zoology*, 82(5): 749-754.

Holcroft, N. I. (2005). A molecular analysis of the interrelationships of tetraodontiform fishes (Acanthomorpha: Tetraodontiformes). *Molecular phylogenetics and evolution*, 34(3): 525-544.

Honda, K., Nakamura, Y., Nakaoka, M., Uy, W. H. and Fortes, M. D. (2013) Habitat use by fishes in coral reefs, seagrass beds and mangrove habitats in the Philippines. *PLoS ONE* 8(8): e65735.

Hong, L. Y., Hong, W. S., Zhu, W. B., Shi, Q., You, X. X. and Chen, S. X. (2014). Cloning and expression of melatonin receptors in the mudskipper *Boleophthalmus pectinirostris*: their role in synchronizing its semilunar spawning rhythm. *General and comparative endocrinology*, 195: 138-150.

Hossain, M.A.R., Nahiduzzaman, M., Saha, D., Khanam, M.U.H. and Alam, M.S. (2010). 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.

Huang, S. P., Zeehan, J. and Chen, I. S. (2013). A new genus of Hemigobius generic group goby based on morphological and molecular evidence, with description of a new species. *Journal of Marine Science and Technology*, 21: 146-155.

Hubby, J. L. and Lewontin, R.C. (1966). A molecular approach to the study of genic heterozygosity in natural populations. I. The number of alleles at different loci in *Drosophila pseudoobscura*. *Genetics,* 54: 577-594.

Hubert, S. and Hedgecock, D. (2004). Linkage maps of microsatellite DNA markers for the Pacific oyster *Crassostrea gigas*. *Genetics*, 168(1): 351-362.

Hubert, N., Meyer, C.P., Bruggemann, H. J., Guérin, F., Komeno, R. J. L., Espiau, B., Causse, R., Williams, J. T. and Planes, S. (2012). Cryptic diversity in Indo Pacific coral-reef fishes revealed by DNA-barcoding provides new support to the centre-of-overlap hypothesis. *PLoS ONE* 7(3): e28987.

Huelsenbeck, J. P. and Ronquist, F. (2001). MRBAYES: Bayesian inference of phylogenetic trees. *Bioinformatics*, 17(8): 754-755.

Hughes, G. M. and Kadhomiy-Al, N. K. (1986). Gill morphometry of the mudskipper, *Boleophthalmus boddarti*. *Journal of the Marine Biological Association of the United Kingdom*, 66(3): 671-682.

Hunter, M. E., and Hart, K. M. (2013). Rapid microsatellite marker development using next generation pyrosequencing to inform invasive Burmese python—*Python molurus bivittatus* management. *International journal of molecular sciences*, 14(3): 4793-4804.

Hurst, G. D. D. and Jiggins, F.M. (2005). Problems with mitochondrial DNA as a marker in population, phylogeographic and phylogenetic studies: the effects of inherited symbionts. *Proceedings of the Royal Society of London B: Biological Sciences*, 272: 1525–1534.

Ihssen, P. E., Booke, H. E., Casselman, J. M., McGlade, J. M., Payne, N. R. and Utter, F. M. (1981). Stock identification: materials and methods. *Canadian Journal of Fisheries and Aquatic Science*, 38: 1838- 1855.

Iorgu, E. I., Popa, O. P., Petrescu, A. M. and Popa, L. O. (2011). Cross-amplification of microsatellite loci in the endangered stone-crayfish *Austropotamobius torrentium* (Crustacea: Decapoda). *Knowledge and Management of Aquatic Ecosystems*, 401 :08.

Iseli, C., Jongeneel, C. V. and Bucher, P. (1999). ESTScan: a program for detecting, evaluating, and reconstructing potential coding regions in EST sequences. In *ISMB*. 99, pp. 138-148.

Jaafar, T. N. A. M., Taylor, M. I., Nor, S. A. M., De Bruyn, M. and Carvalho, G. R. (2012). DNA barcoding reveals cryptic diversity within commercially exploited Indo-Malay Carangidae (Teleosteii: Perciformes). *PLoS One*, 7(11): e49623.

Jain, A., Chaudhary, S. and Prakash, C. S. (2014). Mining of microsatellites using next generation sequencing of seabuckthorn (*Hippophae rhamnoides* L.) transcriptome. *Physiology and Molecular Biology of Plants*, 20(1): 115–123.

Jayashree, B., Punna, R., Prasad, P., Bantte, K., Hash, C. T., Chandra, S.,Hoisington, D. A. and Varshney, R. K. (2006). A database of simple sequence repeats from cereal and legume expressed sequence tags mined in silico: survey and evaluation. *In silico biology*, 6(6): 607-620.

Jeffrey, N. W. (2015). Genome size diversity and evolution in the Crustacea. A Thesis Presented to The Faculty of Graduate Studies of The University of Guelph, Guelph Ontario Canada.

Jensen, T., Nutt, K. J., Seal, B. S., Fernandes, L. B. and Durrant, B. (2008). Permanent Genetic Resources: Isolation and characterization of microsatellite loci in the North Island brown kiwi, *Apteryx mantelli*. *Molecular ecology resources*, 8(2): 399-401.

Jeyaseelan, M. J. P. (1998).). Manual of fish eggs and larvae from Asian mangrove waters. *United Nations Educational, Scientific and Cultural Organization, Paris.* 193 pp.

Jin-Eong, O. (1995). The ecology of mangrove conservation & management. *Hydrobiologia, 295(*1-3): 343-351.

John, A., Kumar, C. P., Khan, S. A., Lyla, P. S., Murugan, S., Mohamed, R. and Khan Chowdhury, A. J. (2011). Efficiency of universal barcode gene (Coxi) on morphologically cryptic mugilidae fishes delineation. *Trends in Applied Sciences Research*, 6(9): 1028-1036.

Johnsen, A., Rindal, E., Ericson, P. G., Zuccon, D., Kerr, K. C., Stoeckle, M. Y. and Lifjeld, J. T. (2010). DNA barcoding of Scandinavian birds reveals divergent lineages in trans-Atlantic species. *Journal of Ornithology*, 151(3): 565-578.

Ju, Y. M., Hsu, C. H., Fang, L. S., Lin, H. D., Wu, J. H., Han, C. C., Chen, I. S. and Chiang, T. Y. (2013). Population structure and demographic history of *Sicyopterus japonicus* (Perciformes; Gobiidae) in Taiwan inferred from mitochondrial control region sequences. *Genetics and Molecular Research*, 12(3): 4046-4059.

Kaga, T. (2013). Phylogenetic systematics of the family Sillaginidae (Percomorpha: order Perciformes). *Zootaxa*, 3642(1): 1-105.

Kamaruzzaman, B. A., John, M.H., Aqilah, M. and K. Zaleha. (2011). Bioaccumulation of heavy metals in horseshoe crabs (*Tachypleus gigas*) from Pekan, Pahang, Malaysia. *Research Journal of Environmental Toxicology, 5: 222-228.*

Kandpal, R. P., Kandpal, G. and Weissman, S. M. (1994). Construction of libraries enriched for sequence repeats and jumping clones, and hybridization selection for region-specific markers. *Proceedings of the National Academy of Sciences*, 91(1): 88-92.

Kang, T. H., Han, S. H. and Park, S. J. (2015). Development of seven microsatellite markers using next generation sequencing for the conservation on the Korean population of *Dorcus hopei* (E. Saunders, 1854) (Coleoptera, Lucanidae). *International journal of molecular sciences*, 16(9): 21330-21341.

Karl, S. A., Toonen, R. J., Grant, W. S. and Bowen, B. W. (2012). Common misconceptions in molecular ecology: echoes of the modern synthesis. *Molecular Ecology*, 21(17): 4171-4189.

Karthika, P., Krishnaveni, N., Vadivalagan, C., Murugan, K., Nicoletti, M. and Giovanni, B. (2016). DNA barcoding and evolutionary lineage of 15 insect pests of horticultural crops in South India Karbala. *International Journal of Modern Science*. 2(3): 156–168.

Katsuragawa, M., Dias, J. F., Harari, J., Namiki, C. and Zani-Teixeira, M. L. (2014). Patterns in larval fish assemblages under the influence of the Brazil current. *Continental Shelf Research*, 89: 103-117.

Kawaguchi, K. (2002). Guide for sampling and identification of fish larvae in the straits of Malacca. JICA-MASDEC project, Universiti Putra Malaysia, Malaysia.

Kendall Jr, A. W. and Ahlstrom, E. H. (1984). Early life history stages of fishes and their characters. Pages 11–22 in HG Moser, WJ Richards, DM Cohen, MP Fahay, AW Kendall, Jr. and SL Richardson, eds. Ontogeny and systematics of fishes. *Am. Soc. Ichthyol. Herpetol. Spec. Publ*, *1*.

Khaironizam, M. Z. and Norma-Rashid, Y. (2002). Length-weight relationship of mudskippers (Gobiidae: Oxudercinae) in the coastal areas of Selangor, Malaysia. *Naga, WorldFish Center Quarterly*, 25(3-4): 20-22.

Khaironizam, M. Z. and Norma-Rashid, Y. (2005). Distribution of mudskippers (Gobiidae: Oxudercinae) on the Selangor coast. *Ecology of the Klang Strait. Faculty of Science, University of Malaya, Kuala Lumpur*, 101-114.

Khan, S. A., Kumar, C. P., Lyla, P. S. and Murugan, S. (2011). Identifying marine fin fishes using DNA barcodes. *Current Science*, 101(9): 1152-1154.

Kim, K. S., Min, M. S., An, J. H. and Lee, H. (2004). Cross-species amplification of Bovidae microsatellites and low diversity of the endangered Korean goral. *Journal of Heredity*, 95(6): 521-525.

Kimberly, A. T., Brian, W. B. and Giacomo, B. (2016) Reef fish dispersal in the Hawaiian Archipelago: Comparative phylogeography of three endemis damselfishes. *Journal of Marine Biology*, 2016.

Kimura, M. (1980). A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. *Journal of molecular evolution*, 16(2): 111-120.

Klangnurak, W., Phinchongsakuldit, J. and James, T. (2012). Population structure and genetic connectivity of *Lutjanus russelli* (Lutjanidae) in Thailand. In *Proceedings of the 12th International Coral Reef Symposium, Cairns*.

Knebelsberger, T., Landi, M., Neumann, H., Kloppmann, M., Sell, A. F., Campbell, P. D., Laakmann, S., Raupach, M. J., Carvalho, R. and Costa, F. O. (2014). A reliable DNA barcode reference library for the identification of the North European shelf fish fauna. *Molecular ecology resources*, 14(5): 1060-1071.

Krishna, P. V., Madhusudhana Rao, K. and Srinivasa Rao, D. (2012). Identification of selected estuarine fishes by DNA barcoding from river Krishna region, Andhra Pradesh, India, *International Journal of Research in Pharmaceutical and Biomedical Sciences*, 3(3): 1044-1049.

Krishnamurthy, P. K. and Francis, R. A. (2012). A critical review on the utility of DNA barcoding in biodiversity conservation. *Biodiversity and Conservation*, 21(8): 1901-1919.

Ko, H. L., Wang, Y. T., Chiu, T. S., Lee, M. A., Leu, M. Y., Chang, K. Z. and Shao, K. T. (2013). Evaluating the accuracy of morphological identification of larval fishes by applying DNA barcoding. *PLoS One*, 8(1): e53451.

Kochzius, M., Seidel, C., Antoniou, A., Botla, S.K., Campo, D., Cariani, A., Vazquez, E.G., Hauschild, J., Hervet, C., Hjörleifsdottir, S., Hreggvidsson, G., Kappel, K., Landi, M., Magoulas, A., Marteinsson, V., Nölte, M., Planes, S., Tinti, F., Turan, C., Venugopal, M.N., Weber, H. and Blohm, D. (2010). Identifying fishes through DNA Barcodes and microarrays. *PLoS ONE,* 5(9): e12620.

Kofler, R., Schlötterer, C. and Lelley, T. (2007). SciRoKo: a new tool for whole genome microsatellite search and investigation. *Bioinformatics*, 23(13): 1683-1685.

Kourous, G. (2005). Many of the world's poorest people depend on fish. *FAO Newsroom.* Retrieved 1 December 2017, from http://www.fao.org/Newsroom/en/news/2005/102911/index.html.

Koutrakis, E. T., Kallianiotis, A. A. and Tsikliras, A. C. (2004). Temporal patterns of larval fish distribution and abundance in a coastal area of northern Greece. *Scientia Marina*. 68(4): 585-595.

Kumar, N. S. and Gurusubramanian, G. (2011). Random amplified polymorphic DNA (RAPD) markers and its applications. *Sci Vis,* 11(3): 116-124.

Laegdsgaard, P. and Johnson, C. (1995). Mangrove habitats as nurseries: unique assemblages of juvenile fish in subtropical mangroves in eastern Australia. *Marine Ecology Progress Series*. 126:67-81.

Laegsdgaard, P. and Johnson, C. (2001). Why do juvenile fish utilize mangrove habitats?. *Journal of Experimental Biology and Ecology*. 257: 229-253.

Laiho, J. and Ståhls, G. (2013). DNA barcodes identify Central Asian *Colias* butterflies (Lepidoptera, Pieridae) *Zookeys*. 365: 175–196.

Laikre, L., Palm, S. and Ryman, N. (2005). Genetic population structure of fishes: implications for coastal zone management. *Ambio*. 34(2): 111-119.

Lakra, W. S., Mohindra, V. and Lal, K. K. (2007). Fish genetics and conservation research in India: status and perspectives. *Fish Physiol Biochem,* 33:475–487.

Landi, M., Dimech, M., Arculeo, M., Biondo, G., Martins, R., Carneiro, M., Carvalho, G. R., Brutto, S. L. and Costa, F. O. (2014). DNA barcoding for species assignment: the case of Mediterranean marine fishes. *PLoS One*, *9*(9): e106135.

Langen, K., Schwarzer, J., Kullmann, H., Bakker, T. C. and Thünken, T. (2011). Microsatellite support for active inbreeding in a cichlid fish. *PLoS One*, 6(9): e24689.

Larget, B. and Simon, D. L. (1999). Markov chain Monte Carlo algorithms for the Bayesian analysis of phylogenetic trees. *Molecular biology and evolution*, 16(6): 750-759.

Larkin, M. A., Blackshields, G., Brown, N. P., Chenna, R., McGettigan, P. A., McWilliam, H., Valentin, F., Wallace, I. M., Wilm, A., Lopez, R. and Thompson, J. D. (2007). Clustal W and Clustal X version 2.0. *bioinformatics*, 23(21): 2947-2948.

Larson, A., Wake, D. B. and Yanev, K. P. (1984). Measuring gene flow among populations having high levels of genetic fragmentation. *Genetics*, 106(2): 293-308.

Laurent, V., Devaux, P., Thiel, T., Viard, F., Mielordt, S., Touzet, P. and Quillet, M. C. (2007). Comparative effectiveness of sugar beet microsatellite markers isolated from genomic libraries and GenBank ESTs to map the sugar beet genome. *Theoretical and applied genetics*, 115(6): 793-805.

Lee, S. J. and Kim, J. K. (2014). Identification of Trichiurus (Pisces: Trichiuridae) eggs and larvae from Korea, with a taxonomic note. *Fisheries and aquatic sciences*, 17(1): 137-143.

Leis, J. M. and Goldman, B. (1983). Studies on the biology of larval fishes in the Lizard Island area, northern Great Barrier Reef. In *Proceedings: Inaugural Great Barrier Reef Conference, Townsville, 28 Aug.–2 Sept* (pp. 221-225).

Leis, J. M. and Rennis, D. S. (1983). The larvae of Indo-Pacific coral reef fishes. New South Wales University Press and University Press of Hawaii: Sydney and Honolulu. p269.

Leis, J. M. (1993). Larval fish assemblages near Indo-Pacific coral reefs. *Bulletin of Marine Science*, 53(2): 362-392.

Leis, J. M. and Carson-Ewart, B. M. (2000). *The Larvae of Indo-Pacific Coastal Fishes: An Identification Guide to Marine Fish Larvae.* Brill Publisher, Leiden, The Netherlands. p 850.

Leis, J. M. (2015). Taxonomy and systematics of larval Indo-Pacific fishes: a review of progress since 1981*. Ichthyological Research*. 62(1): 9-28.

Lennaton, R. C. J. and Potter, I. C. (1987). Contribution of estuaries to commercial fisheries in temperate Western Australia and the concept of estuarine dependence. *Estuaries*. 10: 28-35.

Lewallen, E. A., Bohonak, A. J., Bonin, C. A., van Wijnen, A. J., Pitman, R. L. and Lovejoy, N. R. (2016). Population genetic structure of the tropical two-wing Flyingfish (Exocoetus volitans). *PloS one*, 11(10): e0163198.

Lewis, L. A., Richardson, D. E., Zakharov, E. V. and Hanner, R. (2016). Integrating DNA barcoding of fish eggs into ichthyoplankton monitoring programs. *Fishery Bulletin*, *114*(2): 153-166.

Li, C. and Ortí, G. (2007). Molecular phylogeny of Clupeiformes (Actinopterygii) inferred from nuclear and mitochondrial DNA sequences. *Molecular phylogenetics and evolution*, 44(1): 386-398.

Li, Y., Ludwig, A. and Peng, Z. (2017). Geographical differentiation of the Euchiloglanis fish complex (Teleostei: Siluriformes) in the Hengduan Mountain Region, China: Phylogeographic evidence of altered drainage patterns. *Ecology and evolution*, 7(3): 928-940.

Lian, C., Zhou, Z. and Hogetsu, T. (2001). A simple method for developing microsatellite markers using amplified fragments of inter-simple sequence repeat (ISSR). *Journal of plant research*, 114(3): 381-385.

Librado, P. and Rozas, J. (2009). DnaSP v5: a software for comprehensive analysis of DNA polymorphism data. *Bioinformatics*, 25(11): 1451-1452.

Liew, K. S., Ho, W. S., Pang, S. L. and Julaihi, A. (2015). Development and characterization of microsatellite markers in sawih tree (*Duabanga moluccana* Blume) using ISSR-suppression PCR techniques. *Physiology and Molecular Biology of Plants*, 21(1): 163-165.

Lim, G. S., Balke, M. and Meier, R. (2011). Determining species boundaries in a world full of rarity: singletons, species delimitation methods. *Systematic biology*, 61(1): 165-169.

Lima, A. R. A., Barletta, M., Costa, M. F., Ramos, J. A. A., Dantas, D. V., Melo, P. A. M. C., Justino, A. K. S. and Ferreira, G. V. B. (2016). Changes in the composition of ichthyoplankton assemblage and plastic debris in mangrove creeks relative to moon phases. *Journal of fish biology*, 89(1): 619-640.

Lin, Y., Hubert, L. and Wilson, J. H. (2009). Transcription destabilizes triplet repeats. *Molecular carcinogenesis*, 48(4): 350-361.

Lin, H. S. and Chang, S. B. (2013). PCR-Based Isolation of Microsatellite Arrays (PIMA). *Microsatellites: Methods and Protocols*, 25-55.

Lindstrom, D. P. (1999). Molecular species identification of newly hatched Hawaiian amphidromous gobioid larvae. *Marine Biotechnology*, 1(2): 167-174.

Liu, F., Hu, Z., Liu, W., Li, J., Wang, W., Liang, Z., Wang, F. and Sun, X. (2016). Distribution, function and evolution characterization of microsatellite in *Sargassum thunbergii* (Fucales, Phaeophyta) transcriptome and their application in marker development. *Scientific reports*, *6*, 18947.

Liu, X., Luo, W., Zeng, C., Wang, W. and Gao, Z. (2011). Isolation of new 40 microsatellite markers in mandarin fish (*Siniperca chuatsi*). *International journal of molecular sciences*, 12(7): 4180-4189.

Lunt, D. H., Hutchinson, W. F. and Carvalho, G. R. (1999). An efficient method for PCR-based isolation of microsatellite arrays (PIMA). *Molecular Ecology*, 8(5): 891-894.

Mabragaña, E., de Astarloa, J. M. D., Hanner, R., Zhang, J. and Castro, M. G. (2011). DNA barcoding identifies Argentine fishes from marine and brackish waters. *PLoS One*, 6(12): e28655.

Maduna, S. N., Rossouw, C., Roodt-Wilding, R. and Bester-van der Merwe, A. E. (2014). Microsatellite cross-species amplification and utility in Southern African elasmobranchs: a valuable resource for fisheries management and conservation. *BMC research notes*, 7(1): 352.

Magurran, A. E. (1988). *Ecological Diversity and Its Measurement*. Princeton University Press.

Mai, A. C. G. and Vieira, J. P. (2013). Review and consideration on habitat use, distribution and life history of *Lycengraulis grossidens* (Agassiz, 1829) (Actinopterygii, Clupeiformes, Engraulididae). *Biota Neotropica*, 13(3): 121-130.

Mailund, T., Brodal, G. S., Fagerberg, R., Pedersen, C. N., and Phillips, D. (2006). Recrafting the neighbor-joining method. *BMC bioinformatics*, 7(1): 29.

Mansor, M. I., Kohno, H., Ida, H., Nakamura, H. T., Aznan, Z. and Abdullah, S. (1998). Field Guide to Important Commercial Marine Fishes of the South China Sea. Malaysia: *Marine Fishery Resources Development and Management SEAFDEC.* MFRDMD/SP/2.

Marosi, B. A., Sos, T., Ghira, I. V. and Popescu, O. (2013). COI based phylogeography and intraspecific genetic variation of *Rana dalmatina* populations in the vicinity of the Carpathians. *German Journal of Zoology Research*, 1: 7-16.

Marsjan, P.A. and Oldenbroek, J.K. (2007). Molecular markers, a tool for exploring genetic diversity (Section C in part 4). In: The State of the World's Animal Genetic Resources for Food and Agriculture. - Rome : FAO - ISBN 9789251057629.

Martin, A. P., Pardini, A. T., Noble, L. R. and Jones, C. S. (2002). Conservation of a dinucleotide simple sequence repeat locus in sharks. *Molecular Phylogenetics and Evolution*, 23(2): 205-213.

Mat Jaafar, T.N., Taylor, M.I., Mohd Nor, S.A., de Bruyn, M. and Carvalho, G.R. (2012). DNA barcoding reveals cryptic diversity within commercially exploited Indo-Malay Carangidae (Teleosteii: Perciformes). *PLoS One*, 7(11): e49623

Matarese, A. C., Spies, I. B., Busby, M. S. and Orr, J. W. (2011). Early larvae of *Zesticelus profundorum* (family Cottidae) identified using DNA barcoding. *Ichthyological research*, *58*(2): 170-174.

Matsuura, K. (2015). Taxonomy and systematics of tetraodontiform fishes: a review focusing primarily on progress in the period from 1980 to 2014. *Ichthyological Research*, 62(1): 72-113.

Mcglashan, D.J. and Hughes, J.M. (2001). Low levels of genetic differentiation among populations of the freshwater fish *Hypseleotris compressa* (Gobiidae: Eleotridinae): implications for its biology, population connectivity and history. *Heredity,* 86: 222-233.

McKay, R. J. (2002). FAO species catalogue Vol. 14, Sillaginid fishes of the world, Food and Agriculture Organization of the United Nations, FAO Fisheries Synopsis, 14(125).

McLeod, L. E., and Costello, M. J. (2017). Light traps for sampling marine biodiversity. *Helgoland Marine Research*, 71(1): 2.

M.C.R.S.T. (Malaysian Coastal Resource Study Team), Ministry of Science, Technology and Environment, Malaysia. (1992). The coastal resources management plant for South Johore, Malaysia. ICLARM Tech. Rep. *33*, 291 p.

Meglecz, E., Petenian, F., Danchin, E., D'acier, A. C., Rasplus, J. Y. and Faure, E. (2004). High similarity between flanking regions of different microsatellites detected within each of two species of Lepidoptera: *Parnassius Apollo* and *Euphydryas aurinia*. *Molecular Ecology*. 13: 1693-1700.

Meglecz, E., Anderson, S. J., Bourguet, D., Butcher, R., Caldas, A., Cassel-Lundhagen, A., d'Acier, A. C., Dawson, D. A., Faure, N., Fauvelot, C., Franck, P., Harper, G., Keyghobadi, N., Kluetsh, C., Muthulakshmi, M., Nagaraju, J., Patt, A., Petenian, F., Silvain, J-F. and Wilcock, H. R. (2007). Microsatellite flanking region similarities among different loci within insect species. *Insect Molecular Biology*. 16(2):175-85

Meii, M.N. and Ali, A.B. (2000). Preliminary study on fish larvae distribution at Pulau Payar Marine Park, Kedah, Malaysia. pp. 69-72. In Ali, A. B., M.A. Arshad, I. Zaidnuddin and S.A. Mohd Sah (eds.). Proceedings of National Symposium On Pulau Payar Marine Park. Fisheries Research Institute, Batu Maung, Pulau Pinang.

Michelmore, R. W., Paran, I. and Kesseli, R. V. (1991). Identification of markers linked to disease-resistance genes by bulked segregant analysis: a rapid method to detect markers in specific genomic regions by using segregating populations. *Proceedings of the national academy of sciences*, 88(21): 9828-9832.

Milá, B., Tavares, E. S., Saldaña, A. M., Karubian, J., Smith, T. B. and Baker, A. J. (2012). A trans-Amazonian screening of mtDNA reveals deep intraspecific divergence in forest birds and suggests a vast underestimation of species diversity. *PLoS One*, 7(7): e40541.

Milá, B., Van Tassell, J.L., Calderón, J.A., Rüber, L. and Zardoya, R. (2017) Cryptic lineage divergence in marine environments: genetic differentiation at multiple spatial and temporal scales in the widespread intertidal goby *Gobiosoma bosc*. *Ecol Evol*. (14): 5514–552.

Mills, C.E., Hadwen, W.L. and Hughes, J. (2008). Looking through glassfish: marine genetic structure in an estuarine species. *Marine and Freshwater Research*, 59: 627–637.

Minh, T. H., Gallardo, W. G. and Phuong, N. T. (2010). Fishery and aquaculture of juvenile mudskipper *Pseudapocryptes elongatus* (Cuvier, 1816) in the coastal zone of Mekong Delta, Vietnam. *Asian Fisheries Science*, 23(2): 224-239.

Mitas, M. (1997). Trinucleotide repeats associated with human disease. *Nucleic acids research*, 25(12): 2245-2253.

Mohammadi, M. (2007). Genetic diversity of *Boleophthalmus boddarti* and other Malaysian gobies. (Unpublished doctoral dissertation). Universiti Putra Malaysia, Serdang, Selangor, Malaysia.

Mojekwu, T.O. and Anumudu, C.I. (2013). Microsatellite markers in Aquaculture: Application in fish population genetics. *IOSR Journal Of Environmental Science, Toxicology And Food Technology (IOSR-JESTFT),* 5(4): 43-48.

Moniruzzaman, M., Khatun, R., Yaakob, Z., Khan, M. S. and Mintoo, A. A. (2016). Development of microsatellites: a powerful genetic marker. *The Agriculturists*, 13(1): 152-172.

Morin, P. A., Leduc, R. G., Archer, F. I., Martien, K. K., Huebinger, R., Bickham, J. W. and Taylor, B. L. (2009). Significant deviations from Hardy–Weinberg equilibrium caused by low levels of microsatellite genotyping errors. *Molecular Ecology Resources*, 9(2): 498-504.

Moser, H. G. (1992). The early stages of fishes in the California current. *CALCOFI Atlas no 33*(p32). Allen Press, Inc, Lawrence, Kansas.

Muhammad, N. and Rahim, S. A. K. (2014). Preliminary study on fish larvae at selected coastal waters of Sarawak. *Borneo Journal of Resource Science and Technology,* 4(2):1-8.

Mumby, P.J., Edwards, A.J., Arias-González, J.E., Lindeman, K.C., Blackwell, P.G., Gall, A., Gorczynska, M.I. Harborne, A.R., Pescod, C.L., Renken, H., Wabnitz, C.C.C. and Llewellyn, G. (2004). Mangroves enhance the biomass of coral reef fish communities in the Caribbean. *Nature* 427: 533-536.

Murdy, E. O. (1989). *A taxonomic revision and cladistic analysis of the oxudercine gobies (Gobiidae: Oxudercinae)*. Australian Museum.

Mutanen, M., Kivelä, S. M., Vos, R. A., Doorenweerd, C., Ratnasingham, S., Hausmann, A., Huemer, P., Dinca, V., Van Nieukerken, E. J., Lopez-Vaamonde, C., Vila, R., Aarvik, L., Decaëns, T., Efetov, K. A., Hebert, P. D. N., Johnsen, A., Karsholt, O., Pentinsaari, M., Rougerie, R.,

Segerer, A., Tarmann, G., Zahiri, R. and Godfray, H. C. J. (2016). Species-level para-and polyphyly in DNA barcode gene trees: strong operational bias in European Lepidoptera. *Systematic biology*, 65(6): 1024-1040.

Mwaluma, J. M., Kaunda-Arara, B. and Strydom, N. A. (2014). A guide to commonly occurring larval stages of fishes in Kenyan coastal waters. *WIOMSA Book series No 15* (xvi + pp73).

Na-Nakorn, U., Taniguchi, N., Nugroho, E., Seki, S. and Kamonrat, W. (1999). Isolation and characterization of microsatellite loci of *Clarias macrocephalus* and their application to genetic diversity study. *Fisheries science*, 65(4): 520-526.

National Hydrographic Malaysia. (2015). *Tide Tables Malaysia 2015.* Volume 1. Malaysia.

Nagelkerken, I., Robert, C. M., Van der Velde, G., Dorenbosc, M., Van Riel, M. C., De la Morinière, C. E. and Nienhuis, P. H. (2002). How important are mangroves and seagrass beds for coralreef fish? The nursery hypothesis tested on an island scale. *Marine Ecology Progress Series.* 244: 299-305.

Nagelkerken, I., Blaber, S. J. M., Bouillon, S., Green, P., Haywood, M., Kirton, L. G., Meynecke, J-O., Pawlik, J., Penrose, H. M., Sasekumar, A. and Somerfield, P. J. (2008). The habitat function of mangroves for terrestrial and marine fauna: a review. *Aquatic Botany*. 89: 155-185.

Neave, F. B., Mandrak, N. E., Docker, M. F. and Noakes, D. L. (2006). Effects of preservation on pigmentation and length measurements in larval lampreys. *Journal of fish biology*, *68*(4): 991-1001.

Nei, M. and Li, W. H. (1979). Mathematical model for studying genetic variation in terms of restriction endonucleases. *Proceedings of the National Academy of Sciences*, 76(10): 5269-5273.

Nei, M. (1987). *Molecular evolutionary genetics*. Columbia university press.

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.

Neira, F. J., Perry, R. A., Burridge, C. P., Lyle, J. M. and Keane, J. P. (2014). Molecular discrimination of shelf-spawned eggs of two co-occurring *Trachurus* spp.(Carangidae) in southeastern Australia: a key step to

future egg-based biomass estimates. *ICES Journal of Marine Science*, 72(2): 614-624.

Nelson, D. L., Orr, H. T. and Warren, S. T. (2013). The unstable repeats—three evolving faces of neurological disease. *Neuron*, 77(5): 825-843.

Ng, H. H., Tan, H. H., Lim, K. K. P., Ludt, W. and Chakrabarty, P. (2015). Fishes of the Eastern Johor Strait. *Raffles Bulletin of Zoology*. pp 303-337.

Nielsen, E. E., Hemmer-Hansen, J., Larsen, P. F. and Bekkevold, D. (2009). Population genomics of marine fishes: identifying adaptive variation in space and time. *Molecular ecology*, 18(15): 3128-3150.

Norma-Rashid, Y. and Khaironizam, M. Z. (1970). Some biological aspects of mudskippers (Gobiidae, Oxudercinae) from Langkawi Island. *Malaysian Journal of Science*, 24: 139-144.

O'Brien, S. J. (1991). Molecular genome mapping: lessons and prospects. *Current Opinion in Genetic Development*, 1(1):105-111.

Oates, D. W., Krings, L. M. and Ditz, K. L. (1993). Field manual for the identification of selected North American freshwater fish by fillets and scales. *Other publications in wildlife management*, Paper 13.

Odom, M. C. (1987). *Distribution of larval fishes in the Winfield Pool, Kanawha River, and direct impacts of commercial navigation traffic on larval fish survival*. Virginia Polytechnic Institute and State University, Blacksburg, Virginia.

Okiyama, M. (1988). An atlas of the early stage fishes in japan. Tokai University Press, Tokyo, Japan. p1154

Okumuş, İ. and Çiftci, Y. (2003). Fish population genetics and molecular markers: II-molecular markers and their applications in fisheries and aquaculture. *Turkish Journal of Fisheries and Aquatic Sciences*, 3(1): 51-79.

Oliveira, E. J., Pádua, J. G., Zucchi, M. I., Vencovsky, R. and Vieira, M. L. C. (2006). Origin, evolution and genome distribution of microsatellites. *Genetics and Molecular Biology*, 29(2): 294-307.

Oliveira, G. A. F., Pádua, J. G., Costa, J. L., Jesus, O. N. D., Carvalho, F. M. D. and Oliveira, E. J. D. (2013). Cross-species amplification of microsatellite loci developed for *Passiflora edulis* Sims. in related Passiflora Species. *Brazilian Archives of Biology and Technology*, 56(5): 785-792.

Ong, J. E. (2003). Plants of the Merbok mangrove, Kedah, Malaysia and the urgent need for their conservation. *Folia malaysiana*, 4(1): 1-18.

Ooi, A. L. and Chong, V. C. (2011). Larval fish assemblages in a tropical mangrove estuary and adjacent coastal waters: Offshore–inshore flux of marine and estuarine species. *Continental Shelf Research*, *31*(15): 1599-1610.

Ovenden, J.R. and Street, R. (2003). Genetic population structure of mangrove jack, *Lutjanus argentimaculatus. Marine and Freshwater,* 54, 127-137.

Pace, C. M. and Gibb, A. C. (2009). Mudskipper pectoral fin kinematics in aquatic and terrestrial environments. *Journal of Experimental Biology*, 212(14) 2279-2286.

Pagin, A., Zerimech, F., Leclerc, J., Wacrenier, A., Lejeune, S., Descarpentries, C., Escande, F., Porchet, N. and Buisine, M. P. (2013). Evaluation of a new panel of six mononucleotide repeat markers for the detection of DNA mismatch repair-deficient tumours. *British journal of cancer*, 108(10): 2079.

Palumbi, S. R. (1994). Genetic divergence, reproductive isolation, and marine speciation. *Annual review of ecology and systematics*, 25(1): 547-572.

Palumbi, S. R. (2004). Marine reserves and ocean neighborhoods: the spatial scale of marine populations and their management. *Annal Review of Environment and Resources, 29:* 31-68.

Panzer, S., Kuhl, D. and Caskey, C. T. (1995). Unstable triplet repeat sequences: a source of cancer mutations. *Stem cells*, 13(2): 146-157.

Pappalardo, A. M., Cuttitta, A., Sardella, A., Musco, M., Maggio, T., Patti, B., Mazzola, S. and Ferrito, V. 2015. DNA barcoding and *COI* sequence variation in Mediterranean lanternfishes larvae. *Hydrobiologia*, 749(1): 155-167.

Patel, S., Thompson, K., Williams, L., Tsai, P., Constantine, R. and Millar, C. (2014). Mining microsatellites for Gray's beaked whale from second-generation sequencing data. *Conservation genetics resources*, 6(3): 657-659.

Patrelle, C., Jouet, D., Lehrter, V. and Ferté, H. (2014). Development of 12 novel polymorphic microsatellite markers using a next generation sequencing approach for *Spiculopteragia spiculoptera*, a nematode parasite of deer. *Molecular and biochemical parasitology*, 196(2): 122-125.

Pearson, W. R., Robins, G. and Zhang, T. (1999). Generalized neighbor-joining: more reliable phylogenetic tree reconstruction. *Molecular Biology and Evolution*, 16(6): 806-816.

Pedrosa-Gerasmio, I.R., Agmata, A.B. and Santos, M.D. (2015). Genetic diversity, population genetic structure, and demographic history of *Auxis thazard* (Perciformes), *Selar crumenophthalmus* (Perciformes), *Rastrelliger kanagurta* (Perciformes) and *Sardinella lemuru* (Clupeiformes) in Sulu-Celebes Sea inferred by mitochondrial DNA sequences. *Fisheries Research*, 162: 64–74.

Pereira, L. H., Hanner, R., Foresti, F. and Oliveira, C. (2013). Can DNA barcoding accurately discriminate megadiverse Neotropical freshwater fish fauna. *BMC genetics*, 14(1): 20.

Parreira, B. R. and Chikhi, L. (2015). On some genetic consequences of social structure, mating systems, dispersal, and sampling. *Proceedings of the National Academy of Sciences*, 112(26): E3318-E3326.

Perry, J. C. and Rowe, L. (2010). Rapid microsatellite development for water striders by next-generation sequencing. *Journal of Heredity*, 102(1): 125-129.

Piper, R. (2007). *Extraordinary animals: An encyclopedia of curious and unusual animals*. Greenwood Publishing Group.

Pradhan, V., Kamble, Y., Ladniya, V. and Mogul, M. 2015. An overview of Species Identification by DNA Barcoding. *International Journal of current microbiology and Applied sciences,* 4(4): 127-140.

Prakash, C. S., Grover, A. and Kahl, G. (2007). Mining microsatellites in eukaryotic genomes. *TRENDS in Biotechnology*, 25: 11.

Prasanna-Kumar, C., Akbar-John, B., Ajmal-Khan, S., Lyla, P. S., Murugan, S., Rozihan, M. and Jala, K. C. A. (2011). Efficiency of universal barcode gene (Coxi) on morphologically cryptic Mugilidae fishes delineation. *Trends in Applied Sciences Research.* 6: 1028-1036.

Primmer, C.R. (2005). Genetic characterisation of populations and its use in conservation decision making in fish. The Role of Biotechnology Villa Gualino, Turin, Italy – 5-7 March, 2005.

Primmer, C. R., Painter, J. N., Koskinen, M. T., Palo, U. J. and Merilä, J. (2005). Factors affecting avian cross-species microsatellite amplification. *Journal of Avian Biology*, 36(4): 348-360.

Polgar, G. and Bartolino, V. (2010). Size variation of six species of Oxudercine gobies along the intertidal zone in a Malayan coastal swamp. *Marine Ecology Progress Series*, 409: 199-212.

Polgar, G., Ghanbarifardi, M., Milli, S., Agorreta, A., Aliabadian, M., Esmaeili, H. R. and Khang, T. F. (2017). Ecomorphological adaptation in three mudskippers (Teleostei: Gobioidei: Gobiidae) from the Persian Gulf and the Gulf of Oman. *Hydrobiologia*, 795(1): 91-111.

Porras-Hurtado, L., Ruiz, Y., Santos, C., Phillips, C., Carracedo, Á. and Lareu, M. V. (2013). An overview of STRUCTURE: applications, parameter settings, and supporting software. *Frontiers in genetics*, *4*.

Posada, D. and Crandall, K. A. (1998). Modeltest: testing the model of DNA substitution. *Bioinformatics (Oxford, England)*, 14(9): 817-818.

Pudake, R. N. and Kumari, M. (2016). Assessment of genetic diversity and indegenious plants from Northeast India using molecular marker technology. Eds Purkayastha, J. Bioprospecting of Indegenious Bioresources of North-East India. Springer Science+Business Media Singapore.

Pusey, B. (2001). The new and the known: describing freshwater fish species. *Using Rainforest Research.* p2. Retrieved from http://www.wettropics.gov.au/site/user-assets/docs/newFishes.pdf

Qi, P., Qin, J. and Xie, C. (2015). Determination of genetic diversity of wild and cultured topmouth culter (*Culter alburnus*) inhabiting China using mitochondrial DNA and microsatellites. *Biochemical Systematics and Ecology*, 61: 232-239.

Quang, D. M., Tra Giang, N. T. and Kieu Tien, N. T. (2016). Reproductive biology of the mudskipper *Boleophthalmus boddarti* in Soc Trang. *Tap chi Sinh hoc*, 37(3),: 362-369.

Quentin, C., Martin, P. A. C., Emma, T. S., Osmond,X. M., Gifty, N. A. H., Michael, J. W. and Brenda, D. W. (2009). Microsatellite discovery by deep sequencing of enriched genomic libraries. *BioTechniques*. 46: 217-223.

Rabbaniha, M. and Owfi, F. (2010). Ecological and habitat diversity of ichthyoplankton / fish larvae families in Bushehr province waters (Persian Gulf). INOC-Tischreen University, International conference on Biodiversity of the Aquatic Environment.

Rabbaniha, M., Owfi, F. and Saraji, F. (2014). Abundance and diversity of fish larval assemblages in Iranian waters of the Oman Sea. *Iranian Journal of Ichthyology,* 1(3): 185–190.

Radulovici, A. E., Archambault, P. and Dufresne, F. (2010). DNA barcodes for marine biodiversity: moving fast forward. *Diversity*, 2(4): 450-472.

Rainboth, W. J. (1996). *Fishes of the Cambodian Mekong*. Food & Agriculture Org.

Ramanadevi, V., Thangaraj, M., Sureshkumar, A. and Subburaj, J. (2013). Detection of genetic variation and genetic diversity in two Indian mudskipper species (*Boleophthalmus boddarti*, *B. dussumieri*) using RAPD Marker. *Notulae Scientia Biologicae*, 5(2): 139.

Ramos, S., Cowen, R. K., Re´, P. and Bordalo, A. A. (2006). Temporal and spatial distributions of larval fish assemblages in the Lima estuary (Portugal). *Estuarine, Coastal and Shelf Science*, 66: 303-314.

Ransangan, J. and Hui, S. S. (2003). Genetic erosion due to founder effect in hatchery stock of red tilapia (*Oreochromis* sp.) in Sabah. *Borneo science*, 14: 15-21.

Rassmann, K., Schlötterer, C. and Tautz, D. (1991). Isolation of simple-sequence loci for use in polymerase chain reaction-based DNA fingerprinting. *Electrophoresis*, 12: 113–118.

Ratnasingham, S. and Hebert, P.D.N. 2007. Barcoding Bold: The Barcode of Life Data System (www.barcodinglife.org). Molecular Ecology Notes (2007) 7: 355–364.

Ravi, V. (2005). Post- Tsunami studies on the mudskipper *Boleophthalmus boddarti* (Pallas, 1770) from Mudasalodai, Tamil Nadu, Southeast coast of India. *JIGS*, 4(1).

Ravi, V. (2013). Food and feeding habits of the mudskipper, *Boleophthalmus boddarti* (Pallas, 1770) from Pichavaram mangroves, southeast coast of India. *International Journal of Marine Science*, *3*.

Reiss, H., Hoarau, G., Dickey-Collas, M. and Wolff, W. J. (2009). Genetic population structure of marine fish: mismatch between biological and fisheries management units. *Fish and Fisheries*, 10(4): 361-395.

Rezagholinejad, S., Arshad, A., Nurul-Amin, S. M. and Ehteshami, F. (2016a). The influence of environmental parameters on fish larval distribution

and abundance in the mangrove estuarine area of Marudu bay, Sabah, Malaysia. *Journal of Survey in Fisheries Sciences,* 2(2):67-78.

Rezagholinejad, S., Ehteshami, F., Arshad, A., Amin S. M. N. and Ara, R. (2016b). Identification and morphometric descriptions of four dominant families of larval fishes in the estuary of Marudu Bay, Sabah, East Malaysia. *Iranian Journal of Fisheries Sciences.* 15(3):1262-1268.

Richardson, T., Cato, S., Ramser, J., Kahl, G. and Weising, K. (1995). Hybridization of microsatellites to RAPD: a new source of polymorphic markers. *Nucleic acids research*, 23(18): 3798-3799.

Rico, C., Rico, I. and Hewitt, G. (1996). 470 million years of conservation of microsatellite loci among fish species. *Proceedings of the Royal Society of London B: Biological Sciences*, 263(1370): 549-557.

Riju, A., Rajesh, M. K., Sherin, P. T. F., Chandrasekar, A., Apshara, S. E. and Arunachalam, V. (2009). Mining of expressed sequence tag libraries of cacao for microsatellite markers using five computational tools. *Journal of genetics*, 88(2): 217-225

Rochet. M-J. (2000). May life history traits be used as indices of population viability*. Journal of Sea Research*, 44: 145–157.

Rodrigues, R., Schneider, H., Santos, S., Vallinoto, M., Sain-Paul, U. and Sampaio, I. (2008). Low levels of genetic diversity depicted from mitochondrial DNA sequences in a heavily exploited marine fish (*Cynoscion acoupa*, Sciaenidae) from the Northern coast of Brazil. *Genetics and Molecular Biology*, 31(2): 487-492.

Roberts, D.G. and Ayre. D.J. (2010). Panmictic population structure in the migratory marine sparid *Acanthopagrus australis* despite its close association with estuaries. *Marine Ecology Progress Series*, 412: 223–230.

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

Russell, F. S. (1976). *The Eggs and Planktonic Stages of British Marine Fish.* Academic Press, London, New York, San Francisco. p 524.

Rutkowski, R., Olejniczak, I., Boniecki, P., Tereba, A., Cybulska., M. and Parys, A. (2007). Cross-species amplification of microsatellite loci in *Orchesella flavescens* (Apterygota: Collembola). In: Proceedings of the 8th Conference of the Polish Taxonomical Society, Wiechlice 18-20.

Saccone, C., Gissi, C., Lanave, C., Larizza, A., Pesole, G. and Reyes, A. (2000). Evolution of the mitochondrial genetic system: an overview. *Gene,* 261: 153−159

Saitou, N. and Nei, M. (1987). The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Molecular biology and evolution*, 4(4): 406-425.

Saitou, N. and Nei, M. (1987). The neighbor-joining method: A new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution* **4**:406-425.

Sakamoto, T., Nishiyama, Y., Ikeda, A., Takahashi, H., Hyodo, S., Kagawa, N. and Sakamoto, H. (2015). Neurohypophysial hormones regulate amphibious behaviour in the mudskipper goby. *PloS one*, 10(7): e0134605.

Sakaoka, K., Suzuki, I., Kasugai, N. and Fukumoto, Y. (2014). Paternity testing using microsatellite DNA markers in captive Adélie penguins (Pygoscelis adeliae). *Zoo biology*, 33(5): 463-470.

Samani, N. K., Esa, Y., Amin, S. N., and Ikhsan, N. F. M. (2016). Phylogenetics and population genetics of *Plotosus canius* (Siluriformes: Plotosidae) from Malaysian coastal waters. *PeerJ*, *:* e1930.

Samaradivakara, S. P., Hirimuthugoda, N. Y., Gunawaradana,R. H., Illeperuma,R. J., Fernandopulle N. D., De Silva, A. D. and Alexander, P. A. (2012).Morphological variation of four Tilapia population in selected Reservoirs in Sri lanka. *Tropical Agriculture Research* 23(2): 105 -116.

Sanches, A., Galetti Jr, P. M., Galzerani, F., Derazo, J., Cutilak-Bianchi, B. and Hatanaka, T. (2012). Genetic population structure of two migratory freshwater fish species (*Brycon orthotaenia* and *Prochilodus argenteus*) from the São Francisco River in Brazil and its significance for conservation. *Latin American Journal of Aquatic Research*, 40(1).

Sandilyan, S. and Kathiresan, K. (2014). Decline of mangroves – A threat of heavy metal poisoning. *Ocean & Coastal Management*. 102: 161-168.

Schoebel, C. N., Brodbeck, S., Buehler, D., Cornejo, C., Gajurel, J., Hartikainen, H., Keller, H., Leys, D., Ricanova, M., Segelbacher, S., Werth, S. and Csensics, D. (2013). Lessons learned from microsatellite development for nonmodel organisms using 454 pyrosequencing. *Journal of Evolutionary Biology*, 26(3): 600-611.

Schwenkenbecher, J. M. and Kaplan, R. M. (2007). Development and characterization of microsatellite markers for the canine hookworm, *Ancylostoma caninum*. *Parasitology research*, 100(5): 1015.

Scribner, K. T. and Pearce, J. M. (2000). Microsatellites: evolutionary and methodological background and empirical applications at individual, population, and phylogenetic levels. *Molecular methods in ecology*, 235-273.

Shaklee, J. B. and Bentzen, P. (1998). Genetic identification of stocks of marine fish and shellfish. *Bulletin of Marine Science*, 62(2): 589–621.

Shannon, C. E. and Weaver, W. (1949). *The Mathematical Theory of Communication.* Urbana: University of Illinois Press.

Shao'e Sun, Q. L., Kong, L., Yu, H., Zheng, X., Yu, R., Dai, L., Sun, Y., Chen, J., Liu, J., Ni, L., Feng, Y., Yu, Z., Zou, S. and Lin, J. (2016). DNA barcoding reveal patterns of species diversity among northwestern Pacific molluscs. *Scientific reports*, 6.

Senan, S., Kizhakayil, D., Sasikumar, B. and Sheeja, T. E. (2014). Methods for development of microsatellite markers: An Overview. *Notulae Scientia Biologicae*, 6(1): 1.

Sene, K. H. and Admassu, B. (2012). Analysis of Diversity of Nuclear Microsatellite of *Coffea arabica* as Revealed by Data Mining. *Journal of Biotechnology Letters,* 3(1): 28-31.

Senta, T. and Kinoshita, I. (1985). Larval and juvenile fishes occurring in surf zones of western Japan. *Transactions of the American Fisheries Society*, 114(4): 609-618.

Shao, K. T., Chen, K. C. and Wu, J. H. (2002). Identification of marine fish eggs in Taiwan using light microscopy, scanning electric microscopy and mtDNA sequencing. *Marine and Freshwater Research*, *53*(2):, 355-365.

Sharma, R., Kumar, B., Arora, R., Ahlawat, S., Mishra, A. K. and Tantia, M. S. (2016). Genetic diversity estimates point to immediate efforts for conserving the endangered Tibetan sheep of India. *Meta gene*, 8: 14-20.

Shen, Y., Guan, L., Wang, D. and Gan, X. (2016). DNA barcoding and evaluation of genetic diversity in Cyprinidae fish in the midstream of the Yangtze River. *Ecology and evolution*, 6(9): 2702-2713.

Shields, P. A. and Carlson, S. R. (1996). Effects of formalin and alcohol preservation on lengths and weights of juvenile sockeye salmon. *Alaska Fishery Research Bulletin*, 3(2): 81-93.

Shukla, M. L., Trivedi, J. N., Soni, G. M., Patel, B. K. and Vachhrajani, K. D. (2014). Mudskipper (Gobiidae: Oxudercinae) fauna of Northern Gulf of Khambhat with two new record of the species from Gujarat, India. *European Journal of Zoological Research*, 3(3): 67-74.

Simpson, S. D., Harrison, H. B., Claereboudt, M. R. and Planes, S. (2014). Long-distance dispersal via ocean currents connects Omani clownfish populations throughout entire species range. *PLoS One*, 9(9): e107610.

Slatkin, M. and Hudson, R. R. (1991). Pairwise comparisons of mitochondrial DNA sequences in stable and exponentially growing populations. *Genetics*, 129(2): 555-562.

Slatkin, M. (1995). A measure of population subdivision based on microsatellite allele frequencies. *Genetics*, 139(1): 457-462.

Smith, R. L. and Cameron, J. A. (1977). Acute Effects-Pacific herring roe in the Gulf of Alaska. *Environmental Assessment of the Alaskan Continental Shelf. Principal Investigators' Reports for the Year Ending March 1977*, *12*.

Steinke, D., Connell, A.D. and Hebert, P.D.N. (2016) .Linking adults and immatures of South African marine fishes. *Genome*, 59: 959–967.

Studier, J. A. and Keppler, K. J. (1988). A note on the neighbor-joining algorithm of Saitou and Nei. *Molecular biology and evolution*, 5(6): 729-731.

Song, W., Jiang, K., Zhang, F., Lin, Y. and Ma, L. (2015). Transcriptome sequencing, De Novo assembly and differential gene expression analysis of the early development of Acipenser baeri. *PloS one*, 10(9): e0137450.

Su, T. L. and Lim, S. S. (2016). Niche partitioning in two syntopic mudskipper species (Teleostei: Gobiidae: Oxudercinae) in a Singapore mangrove. *Raffles Bulletin of Zoology*, *64*.

Sukardjo, S. (2004). Fisheries associated with mangrove ecosystem in Indonesia: a view from a mangrove ecologist. *BIOTROPIA-The Southeast Asian Journal of Tropical Biology*, 23: 13-39

Sukumaran, S. and Gopalakrishnan, A. (2015). Molecular taxonomy – Applications, Limitations and future. Summer School on Recent Advances in Marine Biodiversity Conservation and Management. Pp157-161.

Sun, Q. B., Li, L. F., Li, Y., Wu, G. J. and Ge, X. J. (2008). SSR and AFLP markers reveal low genetic diversity in the biofuel plant in China. *Crop Science*, 48(5): 1865-1871.

Tan, K. H. (2007). Protection and Management of Mangroves in Malaysia: Challenges and Strategies. In: Proceedings of National Conference on Coastal and Marine Biodiversity Kuala Lumpur

Termvidchakorn, A. and Hortle, K.G. (2013). A guide to larvae and juveniles of some common fish species from the Mekong River Basin. MRC Technical Paper No. 38. Mekong River Commission, Phnom Penh. 234pp. ISSN: 1683-1489.

Tang, S. J., Liu, Z. Z., Tang, W. Q. and Yang, J. Q. (2009). A simple method for isolation of microsatellites from the mudskipper (*Boleophthalmus pectinirostris*), without constructing a genomic library. *Conservation genetics*, 10(6):1957.

Tautz, D., Arctander, P., Minelli, A., Thomas, R. H. and Vogler, A. P. (2003). A plea for DNA taxonomy. *Trends in Ecology & Evolution*, 18(2): 70-74.

Taylor, B. and Hayes, D. E. (1983). Origin and history of the South China Sea basin. *The Tectonic and Geologic Evolution of Southeast Asian Seas and Islands: Part 2*, 23-56.

Taylor, H.R. and Harris, W.E. (2012). An emergent science on the brink of irrelevance: a review of the past 8 years of DNA barcoding. *Molecular Ecology Resources*, 12: 377–388.

Temnykh, S., Park, W. D., Ayres, N., Cartinhour, S., Hauck, N., Lipovich, L., Cho, Y. G., Ishii, T. and McCouch, S. R. (2000). Mapping and genome organization of microsatellite sequences in rice (*Oryza sativa* L.). *TAG Theoretical and Applied Genetics*, 100(5): 697-712.

Thacker, C. E. (2004). Population structure in two species of the reef goby Gnatholepis (Teleostei: Perciformes) among four South Pacific island groups. *Coral Reefs*, 23(3) 357-366.

Thacker, C. E., Thompson, A. R., Roje, D. M. and Emily, Y. Shaw. (2008). New expansions in old clades: Population genetics and phylogeny

of *Gnatholepis* species (Teleostei: Gobioidei) in the Pacific. *Marine Biology*. 153: 375.

Thacker, C. E. (2011a). Systematics of Gobiidae. *The Biology of Gobies. Science Publisher Inc., Enfield*, 129-136.

Thacker, C. E. and Roje, D. M. (2011b). Phylogeny of Gobiidae and identification of gobiid lineages systematic and biodiversity, 9(4): 329-347.

Teh, L. and Teh, L. (2014). Reconstructing the marine fisheries catch of Peninsular Malaysia, Sarawak and Sabah, 1950-2010. Fisheries Centre The University of British Columbia. Working Paper #2014 – 16.

Thorrold, S. R., Zacherl, D. C. and Levin, L. A. (2007). Population connectivity and larval dispersal: using geochemical signatures in calcified structures. *Oceanography*, *20*(3): 80-89.

Thresher, R. E. (1984). *Reproduction in reef fishes.* T.F.H. Publications, Inc. Ltd., Neptune City, New Jersey. p 399.

Tito de Morais, A. and Tito de Morais, L. (1994). The abundance and diversity of larval and juvenile fish in a Tropical estuary. *Estuaries,* 17(18): 216-225.

Tong, J., Wang, D. and Cheng, L. (2009). Development of microsatellite markers by data mining from DNA sequences. In *Data Mining and Knowledge Discovery in Real Life Applications*. InTech.

Tóth, G., Gáspári, Z. and Jurka, J. (2000). Microsatellites in different eukaryotic genomes: survey and analysis. *Genome Research*, 10(7): 967-981.

Trivedi, S. (2004). Microsatellites (SSRs): puzzles within puzzle. Indian Journal of Biotechnology, 3: 331-47.

Trivedi, S., Aloufi, A. A., Ansari, A. A. and Ghosh, S. K. (2016). Role of DNA barcoding in marine biodiversity assessment and conservation: an update. *Saudi journal of biological sciences*, *23*(2): 161-171.

Tsang, Y. Y. (2007). Tetrodotoxin poisoning. Food safety focus: incident in focus. Retrieved from http://www.cfs.gov.hk/english/multimedia/multimedia_pub/multimedia_pub_fsf_09_01.html

Turan, C. (2004). Stock identification of Mediterranean horse mackerel (*Trachurus mediterraneus*) using morphometric and meristic characters. *ICES Journal of Marine Science*. 61(5):774-781.

Tzeng, W. N. and Wang, Y. T. (1992). Structure, composition and seasonal dynamics of the larval and juvenile fish community in the mangrove estuary of Tanshui River, Taiwan. *Marine Biology,* 113: 481-490.

Tzeng, W. N., Wang, Y. T. and Yarng, T. C. (1997). Species composition and distribution of fish larvae in Yenliao Bay, Northeastern Taiwan. *Zoological Studies*, 36(2): 146-158.

Valdez-Moreno, M., Va´squez-Yeomans, L., Elı´as-Gutie´rrez, M., Ivanova, N.V. and Hebert, P.D.N. (2010). Using DNA barcodes to connect adults and early life stages of marine fishes from the Yucatan Peninsula, Mexico: potential in fisheries management. *Marine and Freshwater Research*, 61: 665–671.

Varshney, R. K., Graner, A., and Sorrells, M. E. (2005). Genic microsatellite markers in plants: features and applications. *Trends Biotechnology,* 23: 48–55.

Velasco-Ramírez, A.P., Torres-Morán, M.I., Molina-Moret, S., Sánchez-González, J.J., and Santacruz-Ruvalcaba, F. (2014). Efficiency of RAPD, ISSR, AFLP and ISTR markers for the detection of polymorphisms and genetic relationships in camote de cerro (*Dioscorea* spp.). *Electronic Journal of Biotechnology*, 17(2): 65–71.

Vergnaud G. and Denoeud, F. (2000). Minisatellites: Mutability and genome architecture. *Genome Research*, 10**:** 899-907

Vieira, M. L. C., Santini, L., Diniz, A. L. and Munhoz, C. D. F. (2016). Microsatellite markers: what they mean and why they are so useful. *Genetics and molecular biology*, (AHEAD), 0-0.

Wan, Q-H., Wu, H., Fujihara, T. and Fang, S-G.(2004). Which genetic marker for which conservation genetics issue? *Electrophoresis,* 25: 2165–2176.

Wang, M., Huang, Z., Shi, F. and Wang, W. (2009). Are vegetated areas of mangrove attractive to juvenile and small fish? The case of Dongzhaigang Bay, Hainan Island, China. *Estuarine, Coastal and Shelf Science.* 85: 208-216.

Wang, X. L., Yang, R. H. and Yao, Y. J. (2011). Development of microsatellite markers for Ophiocordyceps sinensis (Ophiocordycipitaceae) using an

ISSR-TAIL-PCR method. *American journal of botany*, 98(12): e391-e394.

Wang, A., Ding, Y., Hu, Z., Lin, C., Wang, S., Wang, B., Zhang, H. and Zhou, G. (2012). Isolation and characterization of 13 new polymorphic microsatellite markers in the *Phaseolus vulgaris* L. (Common Bean) genome. *International journal of molecular sciences*, 13(9): 11188-11193.

Waples, R. S. (2014). Testing for Hardy–Weinberg proportions: have we lost the plot. *Journal of Heredity*, 106(1): 1-19.

Ward, R.D. and Elliott, N.G. (2001). Genetic population structure of species in the South East fishery of Australia. *Marine and Freshwater Research*, 52: 563–573.

Ward, R. D., Zemlak, T. S., Innes, B. H., Last, P. R. and Hebert, P. D. (2005). DNA barcoding Australia's fish species. *Philosophical Transactions of the Royal Society of London B: Biological Sciences*, *360*(1462): 1847-1857.

Ward, R. D., Costa, F. O., Holmes, B. H. and Steinke, D. (2008). DNA barcoding of shared fish species from the North Atlantic and Australasia: minimal divergence for most taxa, but Zeus faber and Lepidopus caudatus each probably constitute two species. *Aquatic Biology*, 3(1): 71-78.

Ward, R. D. (2012). FISH-BOL, *A case study for DNA barcodes. In:DNA Barcodes: Methods and Protocols, Methods in Molecular Biology* (eds Kress WJ, Erickson DL), 858: 423 – 439. Springer Science+Business Media, LLC, New York.

Webb, J.F. (1999). Larvae in fish development and evolution. In:Hall BK, Wake MH (eds) The origin and evolution of larval forms. Academic Press, San Diego, CA, p 109−158.

Weir, B.S. and Cockerham, C.C. (1996). *Genetic data analysis II: Methods for discrete population genetic data*. Sinauer Assoc. Inc, Sunderland, MA, USA.

Wibowo, A., Wahlberg, N. and Vasemägi, A. (2017). DNA barcoding of fish larvae reveals uncharacterised biodiversity in tropical peat swamps of New Guinea, Indonesia. *Marine and Freshwater Research*, 68(6): 1079-1087.

Williams, L. M., Ma, X., Boyko, A. R., Bustamante, C. D. and Oleksiak, M. F. (2010). SNP identification, verification, and utility for population genetics in a non-model genus *BMC Genetics* 11: 32.

Williamson, V. M., Ho, J. Y., Wu, F. F., Miller, N. and Kaloshian, I. (1994). A PCR-based marker tightly linked to the nematode resistance gene, Mi, in tomato. *TAG Theoretical and Applied Genetics*, 87(7): 757-763.

Wilk, R.J. and Horth, L. (2016). A genetically distinct hybrid zone occurs for two globally invasive mosquito fish species with striking phenotypic resemblance. *Ecol Evol.* 2016 Dec; 6(23): 8375–8388.

Wilson, A. F. and Sorant, A. J. (2000). Equivalence of single-and multilocus markers: power to detect linkage with composite markers derived from biallelic loci. *The American Journal of Human Genetics*, 66(5): 1610-1615.

Winterbottom, R. (1993). Search for the gobi old sister group (Actinopterygii: Percomorpha). *Bulletin of Marine Science*, 52(1): 395-414.

Wright, S. (1951). The genetical structure of populations. *Annals of Eugenics* 15: 323–354.

Wright, J. M. (1993). DNA fingerprinting of fishes. *Biochemistry and molecular biology of fishes*, 2: 57-91.

Wright, J. M. and Bentzen, P. (1994). Microsatellites: genetic markers for the future. *Reviews in Fish Biology and Fisheries*, 4(3): 384–388.

WWF (World Wide Fund for Nature), 2017. Project: Sustainable Management of Setiu Wetlands. Retrieved 1st June 2017, http://www.wwf.org.my/about_wwf/what_we_do/freshwater_main/freshwater_conserving_freshwater_habitats/projects_sustainable_management_of_setiu_wetlands/

Xia, X. (2013). DAMBE5: a comprehensive software package for data analysis in molecular biology and evolution. *Molecular biology and evolution*, 30(7): 1720-1728.

Ya, N. A., Harinder, R. S., Ramli, N. H., Makhtar, N., Mohd Rashid, H. N., Dzakaria, N. and Samat, A. (2014). Fish diversity in Sepang Besar estuary–a preliminary analysis. *Int'l Journal of Advances in Agricultural & Environmental Engg*, 1(2): 229-233.

Yang, Z. and Rannala, B. (1997). Bayesian phylogenetic inference using DNA sequences: a Markov Chain Monte Carlo method. *Molecular biology and evolution*, 14(7): 717-724.

Ye, Y. Y., Wu, C. W. and Li, J. J. (2015). Genetic population structure of *Macridiscus multifarius* (Mollusca: Bivalvia) on the basis of mitochondrial markers: strong population structure in a species with a short planktonic larval stage. *PloS one*, *10*(12): e0146260.

Yi, G., Lee, J. M., Lee, S., Choi, D. and Kim, B. D. (2006). Exploitation of pepper EST–SSRs and an SSR-based linkage map. *Theoretical and Applied Genetics*, 114(1): 113-130.

You, X., Bian, C., Zan3, Q., Xu, X., Liu, X., Chen, J., Wang, J., Qiu, Y., Li, W., Zhang, X., Sun, Y., Chen, S., Hong, W., Li, Y., Cheng, S. and Fan, G., Shi, C., Liang, J., Tang, Y.T., Yang, C., Ruan, Z., Bai, J., Peng, C., Mu, Q., Lu, J., Fan, M., Yang, S., Huang, Z., Jiang, X., Fang, X., Zhang, G., Zhang, Y., Polgar, G., Yu, H., Li, J., Liu, Y., Zhang, G., Ravi, V., Coon, S.L., Wang, J., Yang, H., Venkatesh, B., Wang, J. and Shi, Q. (2014). Mudskipper genomes provide insights into the terrestrial adaptation of amphibious fishes. *Nature communications*, *5*.

Yu, Z., Wang, Y. and Fu, D. (2010). Development of fifty-one novel EST-SSR loci in the Pacific oyster, *Crassostrea gigas* by data mining from the public EST database. *Conservation Genetics Resources*, 2(1): 13-18.

Yu, Z., Teng, X. and Bonini, N. M. (2011). Triplet Repeat–Derived siRNAs Enhance RNA–Mediated Toxicity in a Drosophila Model for Myotonic Dystrophy. *PLoS genetics*, 7(3): e1001340.

Yue, G. H., Zhu, Z. Y., Wang, C. M. and Xia, J. H. (2009). A simple and efficient method for isolating polymorphic microsatellites from cDNA. *BMC genomics*, 10(1): 125.

Vassarstat.net (2018). Two-way ANOVA calculator. Assessed on 1st February 2018. http://vassarstats.net/anova2u.html.

Zane, L., Bargelloni, L. and Patarnello, T. (2002). Strategies for microsatellite isolation: a review. *Molecular ecology*, 11(1): 1-16.

Zhang, Y., He, J., Zhao, P. X., Bouton, J. H. and Monteros, M. J. (2008). Genome-wide identification of microsatellites in white clover (*Trifolium repens* L.) using FIASCO and phpSSRMiner. *Plant Methods*, 4(1): 19.

Zhang, J. (2011). Species identification of marine fishes in China with DNA barcoding. *Evidence-Based Complementary and Alternative Medicine*, *2011*.

Zhao, L., Zhang, J., Liu, Z., Funk, S. M., Wei, F., Xu, M. and Li, M. (2008). Complex population genetic and demographic history of the Salangid, *Neosalanx taihuensis*, based on cytochrome b sequences. *BMC evolutionary biology*, 8(1): 201.

Zhivotovsky, L. A. and Feldman, M. W. (1995). Microsatellite variability and genetic distances. *Proceedings of the National Academy of Sciences*, 92(25): 11549-11552.

Zhu, Y., Queller, D. C. and Strassmann, J. E. (2000). A phylogenetic perspective on sequence evolution in microsatellite loci. *Journal of Molecular Evolution*, 50(4): 324-338.

Zietkiewicz, E., Rafalski, A. and Labuda, D. (1994). Genome fingerprinting by simple sequence repeat (SSR)-anchored polymerase chain reaction amplification. *Genomics*, 20(2): 176-183.

Zulkifli, T., Abd Haris Hilmi, A.A. and Rosdi M.N. (2001). Distribution of fish larvae in the coastal area of the East Coast of Peninsular Malaysia. In Rosdi Mohd Nor , Zulkifli Talib and Raja Mohammad Noordin Raja Omar 1998. Kind, Abundance and Distribution of Fish Larvae in the Malaysian Exclusive Economic Zone. In Status of fish larvae study in Malaysia. Retrieved June 1, 2016 from http://www.unepscs.org/Advanced_Larval_Fish_Training/Country%20Reports %20on%20Larval%20Fish%20Sampling%202008/30-Status-Fish-LarvaeStudy-Malaysia.pdf

Zulkifli. T. (2002). Fish juveniles and larvae identification and distribution. *SEAFDEC Newsletter*, 25(3): 8-9

LIST OF PUBLICATIONS

Journal Paper

Azmir, I. A., Esa, Y., Nurul Amin, S.M., Md Yasin, I.S., Md Yusuf, F.Z. (2017). Identification of Larval Fish in Mangrove Areas of Malaysia Using Morphology and DNA Barcoding Methods. *Journal of Applied Ichthyology*., 33:998-1006.

Conferences and Workshop participation

1. Participated in a Larval Fish Identification Workshop at Marine Science Center (COMAS), Universti Putra Malaysia, Teluk Kemang Port Dickson Negeri Sembilan on April 2015.
2. Participated in a poster presentation International Agricultural Congress 2016 (IAC) on 4^{th} – 6^{th} October 2016 in Bangi, Selangor. Poster title: Larval Fish: Identified Through Morphology and DNA Barcoding Methods.

UNIVERSITI PUTRA MALAYSIA

STATUS CONFIRMATION FOR THESIS / PROJECT REPORT AND COPYRIGHT

ACADEMIC SESSION : _____

TITLE OF THESIS / PROJECT REPORT :

FISH LARVAE SPECIES IDENTIFICATION AND POPULATION GENETIC STRUCTURE OF *Boleophthalmus boddarti* (PALLAS, 1770) FROM SELECTED MANGROVE SITES IN PENINSULAR MALAYSIA

NAME OF STUDENT: IZZATI ADILAH BINTI AZMIR

I acknowledge that the copyright and other intellectual property in the thesis/project report belonged to Universiti Putra Malaysia and I agree to allow this thesis/project report to be placed at the library under the following terms:

1. This thesis/project report is the property of Universiti Putra Malaysia.
2. The library of Universiti Putra Malaysia has the right to make copies for educational purposes only.
3. The library of Universiti Putra Malaysia is allowed to make copies of this thesis for academic exchange.

I declare that this thesis is classified as :

*Please tick (√)

☐	**CONFIDENTIAL**	(Contain confidential information under Official Secret Act 1972).
☐	**RESTRICTED**	(Contains restricted information as specified by the organization/institution where research was done).
☐	**OPEN ACCESS**	I agree that my thesis/project report to be published as hard copy or online open access.

This thesis is submitted for :

☐	**PATENT**	Embargo from_____ until _____ (date) (date)

Approved by:

_____ _____

(Signature of Student) (Signature of Chairman of Supervisory Committee)
New IC No/ Passport No.: Name:

Date : Date :

[Note : If the thesis is CONFIDENTIAL or RESTRICTED, please attach with the letter from the organization/institution with period and reasons for confidentially or restricted.]