



DETECTION OF *Vibrio parahaemolyticus* INFECTION-RESISTANT BIOMARKERS IN TIGER GROUPER *Epinephelus fuscoguttatus* (Forsskål) USING QUANTITATIVE REAL-TIME PCR METHOD

By

NUR LIYANA BINTI IBRAHIM

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

September 2019

IB 2021 26

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

DETECTION OF *Vibrio parahaemolyticus* INFECTION-RESISTANT BIOMARKERS IN TIGER GROUPER *Epinephelus fuscoguttatus* (Forsskål) USING QUANTITATIVE REAL-TIME PCR METHOD

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September 2019

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Grouper species which includes *Epinephelus fuscoguttatus* also known as tiger grouper is one of the valuable species with great economic value in Southeast Asian countries. Various infectious diseases occur in grouper aquaculture and often create severe problems leading to economic losses. Causative agents of vibriosis in aquaculture include *Vibrio parahaemolyticus*. *Vibrio parahaemolyticus* is a major foodborne pathogen and classified as a Gram-negative halophilic bacterium which commonly inhabits estuarine and marine environments and causes worldwide health problems on consumption. Therapeutic options with antibiotics and vaccines have disadvantages such as resistance and contamination from overuse. For centuries farmers have been aware of specific phenotypic attributes in plants and animals that provided a production advantage of one species over another. The advances in technology have permitted researchers to examine these features at the genetic and molecular levels. Selective breeding is a viable option to improve health of fish in culture. Feasible and rapid methods for identification of relevant biomarkers in groupers are factors that aid in management of its produce. Real time qPCR-based methods are convenient, easy to screen for epidemiological, genetic studies and applicable to routine high-throughput detection of large numbers of samples and can be used for quantitative gene expression of biomarkers in grouper organs and tissues. The purpose of this study is to confirm usefulness of previously identified biomarkers in selection of fish with disease resistance. Herein the potential biomarkers, the alpha-2-Macroglobulin ($\alpha 2M$), Parvalbumin Beta-2 Subunit 1 (*PVALB*) and Nattectin genes were selected. Primers were designed using Primer-BLAST from the NCBI website and synthesized by a local company. β -actin (*ACTB*), acted as the reference gene. Experimental infections of grouper with *V. parahaemolyticus* were conducted to assess expression levels of these genes in infected fish compared to controls. Healthy juveniles' grouper fish infected with *V. parahaemolyticus* were monitored for skin lesions in tissues and samples collected after 2 weeks. *Vibrio parahaemolyticus* infected grouper displayed significantly increased expression of alpha-2-Macroglobulin ($\alpha 2M$), Parvalbumin Beta-2 Subunit 1 (*PVALB*), and Nattectin

in blood, liver and spleen compared to before infection. Infection susceptible fish was based on the development of skin lesion more than five millimeter (>5mm) in diameter while none was observed on infection resistant fish. When infection-resistant fish was compared to fish infection-susceptible for these three genes *NatTECTin*, *PVALB*, and *α 2M*, q-PCR analysis showed two-fold, two-fold, and four-fold significant under-expressions in the liver tissue, respectively. Similarly, significantly down-regulation ($p < 0.05$) was observed for *NatTECTin* and *PVALB* by three-fold and two-fold, except for *α 2M* with no significant difference in expression in spleen sample. Again, in blood samples *NatTECTin* was significantly decreased by four-fold, *PVALB* by two-fold, and *α 2M* by three-fold in infection-resistant samples. However, these results did not replicate data obtained from an earlier study which used proteomic method. Nevertheless, this study demonstrated that *NatTECTin*, *PVALB*, and *α 2M* were over-expressed in infection-susceptible fish providing evidence on the involvement of these gene during *V. parahaemolyticus* infection. These data will provide the foundation for use of biomarkers in identification of disease resistant groupers and selective breeding.

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

**PENGESANAN BIOPENANDA RENTAN JANGKITAN DARIPADA
Vibrio parahaemolyticus TERHADAP KERAPU HARIMAU
(*Epinephelus fuscoguttatus*) MENGGUNAKAN KAEDAH PCR KUANTITATIF
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Spesis kerapu termasuk *Epinephelus fuscoguttatus* yang dikenali sebagai kerapu harimau merupakan salah satu spesis bernilai ekonomi yang besar di negara-negara Asia Tenggara. Pelbagai jenis penyakit berjangkit berlaku dalam akuakultur kerapu dan sering mencetuskan masalah dan membawa kepada kerugian ekonomi. Agen penyebab vibriosis dalam akuakultur termasuklah *Vibrio parahaemolyticus*. *V. parahaemolyticus* adalah patogen penyakit bawaan makanan utama dan diklasifikasikan sebagai bakteria gram-negatif halofilik yang biasanya hidup di persekitaran marin dan lautan dan menyebabkan konsumsi masalah kesihatan di seluruh dunia. Selama berabad-abad para petani telah menyedari ciri-ciri fenotip tertentu dalam tumbuh-tumbuhan dan haiwan yang memberikan kelebihan penghasilan mutu satu spesis berbanding yang lain. Kemajuan dalam teknologi telah membolehkan para penyelidik memeriksa ciri-ciri ini di peringkat genetik dan molekul. Pembiakan selektif adalah salah satu pilihan untuk meningkatkan kesihatan ikan dalam kultur. Kaedah yang pantas dan sesuai untuk pengenalpastian biopenanda yang relevan dalam kumpulan kerapu adalah faktor yang akan membantu dalam pengurusan hasilnya. Kaedah berasaskan qPCR adalah mudah, sesuai digunakan dalam pemeriksaan epidemiologi, genetik dan pengesanan rutin sampel yang banyak dan juga pengekspresan gen biopenanda secara kuantitatif dalam organ-organ dan tisu kerapu. Tujuan kajian ini adalah untuk mengesan biopenanda yang telah dikenal pasti dalam kajian sebelum ini dalam pemilihan ikan dengan kelebihan dalam pertahanan penyakit. Di sini biopenanda berpotensi, alpha-2-Macroglobulin ($\alpha 2M$), Parvalbumin Beta-2 Subunit 1 (*PVALB*) dan gen Nattetin telah dipilih. Primer direka bentuk menggunakan Primer-BLAST dari laman web NCBI dan disintesis oleh syarikat tempatan. β -actin (*ACTB*), bertindak sebagai gen rujukan. Jangkitan eksperimental kerapu dengan *V. parahaemolyticus* dijalankan dan tahap pengekspresan gen-gen ini dinilai dalam ikan yang dijangkiti berbanding ikan yang tidak dijangkiti. Ikan kerapu juvenil yang dijangkiti *V. parahaemolyticus* telah dipantau untuk dianalisis rangsangan gen pada tisu sampel yang dikumpulkan selepas 2 minggu. Kerapu yang dijangkiti *Vibrio parahaemolyticus*

menunjukkan kesan peningkatan yang nyata untuk alpha-2-Macroglobulin ($\alpha 2M$), Parvalbumin Beta-2 Subunit 1 (*PVALB*), dan Nattectin dalam darah, hati dan limpa berbanding sebelum jangkitan. Pembezaan jangkitan ikan yang mudah-dijangkiti adalah berdasarkan perkembangan saiz lesi kulit lebih daripada lima milimeter ($> 5\text{mm}$) diameter manakala ikan yang tiada sebarang lesi dikenal pasti sebagai ikan rentan jangkitan. Dalam ikan rentan-infeksi, analisa q-PCR mendapati ketiga-tiga gen ini, Nattectin, *PVALB*, dan $\alpha 2M$, menunjukkan penurunan dua kali ganda, dua kali ganda dan empat kali ganda ekspresi dalam tisu hati, masing-masing berbanding ikan yang diinfeksi. Begitu juga penurunan tahap yang berkesan ($p < 0.05$) diperhatikan dalam Nattectin dan *PVALB* sebanyak tiga kali ganda dan dua kali ganda, masing-masing kecuali $\alpha 2M$ dimana dalam sampel limpa. Dalam sampel darah pula, Nattectin berkurangan dengan ketara sebanyak empat kali ganda, *PVALB* dua kali ganda, dan $\alpha 2M$ sebanyak tiga kali ganda dalam sampel dari ikan yang tahan terhadap jangkitan. Tetapi, keputusan ini tidak bersamaan dengan hasil yang diperoleh daripada kajian awal yang sama yang menggunakan kaedah proteomik. Walau bagaimanapun, kajian ini telah mendemonstrasikan kemampuan Nattectin, *PVALB*, dan $\alpha 2M$ untuk digunakan sebagai biopenanda dalam membezakan ikan yang mudah dijangkiti *V. parahaemolyticus*. Data-data ini akan menyediakan asas untuk penggunaan biopenanda dalam mengenal pasti kumpulan kerapu yang rentan-infeksi dan pembiakan selektif.

ACKNOWLEDGEMENT

To my parents and family and My deepest gratitude to the best supervisor, Assc.Prof.Dr.Maha Abdullah for her encouragement and advices. I would like to include a special note thanks to my co-supervisors Prof. Dato. Dr. Mohd Shariff B Mohd Din and Dr.Chong Chou Min for their valuable support and guidance.



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TABLE OF CONTENTS

	Page
ABSTRACT	i
ABSTRAK	iii
ACKNOWLEDGEMENT	v
APPROVAL	vi
DECLARATION	viii
LIST OF TABLES	xii
LIST OF FIGURES	xiii
CHAPTER	
1 INTRODUCTION	1
1.1 Introduction	1
1.2 General objective	2
1.2.1 Specific objectives	2
1.3 Problem Statement	2
1.4 Research Question	3
1.5 Hypothesis	3
2 LITERATURE REVIEW	4
2.1 Groupers Culture Status and its Economic Importance	4
2.2 <i>Epinephelus fuscoguttatus</i> sp taxonomy and distribution	5
2.3 Vibriosis and <i>Vibrio parahaemolyticus</i> infection	6
2.4 Role of immune defence systems in fish	7
2.5 Immune response in fish	8
2.5.1 Immunologically-active organ in fish	9
2.5.1.1 Skin of fish	9
2.5.1.2 Spleen in fish	10
2.5.1.3 Liver in fish	11
2.6 External factor influenced the immune system and fish response	12
2.7 Biomarkers involved in diseases-resistance in fish	12
2.7.1 Infection resistant genes in groupers used in the study	13
2.7.1.1 Alpha-2-Macroglobulin ($\alpha 2M$)	13
2.7.1.2 Parvalbumin Beta-2 Subunit 1 (PVALB)	14
2.7.1.3 Nattectin	14
2.8 Diagnostic Features in grouper culture and Fish Health improvements	15
2.9 Quantitative polymerase chain reaction (Real-time PCR)	15
3 MATERIALS AND METHODS	17
3.1 Introduction	17
3.2 Fish sources, husbandry and culture conditions	17
3.3 <i>Vibrio parahaemolyticus</i> (ATCC®17803™) inoculum	17

3.4	Bacteria culture preparation	18
3.5	Standard curve for bacterial enumeration	18
3.6	Determination of median lethal dose (LD50)	19
3.7	Experimental infection of tiger grouper with <i>Vibrio parahaemolyticus</i>	19
3.8	Establishment of qRT-PCR method to determine gene expression in untreated grouper	20
3.8.1	RNA Extraction	20
3.8.2	RNA Qualification and Quantification	21
3.8.3	DNase Treatment	21
3.8.4	cDNA Synthesis	21
3.8.5	Primer design for RT-PCR amplification	21
3.8.6	Quantitative PCR with SYBR green	22
3.9	Statistical analysis	22
4	RESULT	25
4.1	Standard Curve Graph for Bacterial Count	25
4.2	LD ₅₀ of <i>Vibrio parahaemolyticus</i> infected <i>Epinephelus fuscoguttatus</i>	26
4.3	Experimental Infection of Fish with <i>Vibrio</i>	27
4.4	Analysis of Total RNA extraction	31
4.5	Gene expression using quantitative real-time polymerase chain reaction (qPCR)	32
4.5.1	Standard Curve for Genes of Interest	35
4.6	Expression of Selected Genes in Untreated Tiger Grouper Fish.	37
4.7	Expression Profile of Selected Genes in <i>Vibrio</i> -Infected Grouper.	39
5	DISCUSSION	41
6	CONCLUSION	48
6.1	Conclusion	48
6.2	Recommendations for Future Research	48
	REFERENCES	49
	APPENDICES	62
	BIODATA OF STUDENT	63

LIST OF TABLES

Table	Page
2.7.1.1 Species used in studies showing <i>a2M</i> gene over-expression by real-time PCR	14
3.3.1 Confirmation of live attenuated <i>Vibrio parahaemolyticus</i> strain by PCR method	18
1 Gene accession numbers and primer sequences used for qRT-PCR analysis. Beta-actin (<i>ACTB</i>), acted as the reference gene and Alpha-2-macroglobulin (<i>a2M</i>), Parvalbumin (<i>PVALB</i>) and Nattectin were genes of interest	22
4.7.1 qPCR analyses of the <i>a2m</i> , <i>PVALB</i> , and <i>Nattectin</i> transcripts at mean expression levels+SD in blood, liver and spleen of the tiger grouper <i>Epinephelus fuscoguttatus</i> in untreated, resistant and susceptible value prior to seven days infected	39

LIST OF FIGURES

Figure	Page
2.2.1 <i>Epinephelus fuscoguttatus</i> (Tiger Grouper)	5
2.3.1 Hemorrhagic skin lesions on the dorsal part of <i>Epinephelus coioides</i> broodstock	7
2.3.2 Severe hemorrhagic pectoral fin indicating fin rot on the grouper broodstock (<i>Epinephelus coioides</i>)	7
2.5.1 The external anatomy of tiger grouper fish	9
2.5.2 The internal anatomy of tiger grouper fish	9
2.5.1.1 A close up for tiger grouper (<i>Epinephelus fuscoguttatus</i>) fish skin	10
2.5.1.2 The normal condition of spleen of tiger grouper (<i>Epinephelus fuscoguttatus</i>)	11
2.5.1.3 The dissection internal organ (liver) shown with an arrow of tiger grouper (<i>Epinephelus fuscoguttatus</i>)	12
4.1.1 Standard linear curve for <i>V. parahaemolyticus</i> count generated through plotting the mean absorbance values read at 600-nm wavelength from 0.202 to 1.62 against calculated colony forming unit per millilitre (CFU/mL) for 6 dilutions from (5×10^8 CFU/mL) to (2.5×10^8 CFU/mL)	25
4.1.2 Subculture of <i>Vibrio parahaemolyticus</i> using streak method to obtain pure colonies	26
4.2.1 Lethal doses of <i>V. parahaemolyticus</i> for the determination of LD ₅₀ after intramuscularly injection in fishes	26
4.2.2 A fitting curve was then generated by plotting cumulative percent mortality against a number of bacteria	27
4.3.1 The normal condition of Tiger grouper (<i>Epinephelus fuscoguttatus</i>)	28
4.3.2 (A) and (B) Tiger grouper fish infected with <i>V. parahaemolyticus</i> via intramuscularly showing lesion on the skin which is more than 5 mm	29
4.3.3 (C) Hemorrhagic skin lesions on the dorsal part (D) red skin lesion with a diameter less than 5 mm and hemorrhagic pectoral fin indicating fin rot	30

4.3.4	The spleen (left) and liver (right) become pale greenish colour after infected with <i>V. parahaemolyticus</i> .	30
4.4.1	Gel image of RNA extracted from blood, liver and spleen of grouper without infection	31
4.4.2	Gel image of RNA extracted from liver and spleen after infection with <i>Vibrio parahaemolyticus</i> .	32
4.5.1	Representative SYBR Green fluorescence image from real-time PCR amplification curves obtained from serial dilutions of the reference gene, <i>ACTB</i>	33
4.5.2	Melting curve analysis of PCR products from <i>ACTB</i> gene amplification revealed single melting peak indicative of single-specific size products	33
4.5.3	Amplification curves of $\alpha 2M$ obtained from serial dilutions	34
4.5.4	Melting curve analysis of the products revealed single melting peaks indicative of single-specific size products of $\alpha 2M$.	34
4.5.5	Real-time PCR standard curve for <i>ACTB</i>	35
4.5.6	Standard curve for Alpha- 2- macroglobulin ($\alpha 2M$), log of two-fold serial dilution factor of cDNA from fish liver sample was plotted against average Ct value obtained after real-time PCR amplification of the gene	35
4.5.7	Standard curve of Parvalbumin (<i>PVALB</i>)	36
4.5.8	Standard curve of Nattectin Log of two-fold serial dilution factor of cDNA from fish liver sample was plotted against average Ct value obtained after real-time PCR amplification of the gene	36
4.6.1	Expression levels of $\alpha 2M$, <i>PVALB</i> and <i>Nattectin</i> in blood, liver and spleen tissue of <i>Epinephelus Fuscoguttatus</i> (<i>Tiger Grouper</i>) in ten individual fish,(n=10) Specific gene expression were presented relative to the corresponding <i>ACTB</i> expression	38
4.8	Expression level of $\alpha 2M$, <i>PVALB</i> and <i>Nattectin</i> in blood, liver and spleen tissues of <i>Epinephelus fuscoguttatus</i> (<i>Tiger Grouper</i>) infected with <i>V. parahaemolyticus</i> in resistant and susceptible fish compared to the earlier uninfected group	40

CHAPTER 1

INTRODUCTION

1.1 Introduction

Groupers are one of the highly desirable species that have high market demand from the family Serranidae. Groupers have superior market value compared to other marine fish (Nurdalila et al., 2015). Due to its economic value, the grouper is commonly cultured by the farming community as well as caught by the fishers from the ocean (Chen et al., 2012).

However, tiger grouper cultivation is plagued with increased prevalence of diseases associated with intensive farming systems and has hampered the development of its culture (Tahir et al., 2018) and become a major constraint to sustainable growth production (Kevin et al., 2015). The decline in growth production is also due to the increasing number of diseases triggered by stress conditions associated with improper intensification systems of farming (Terceti et al., 2016 and Haenen et al., 2014). Poor farming conditions increases the fish susceptibility to opportunistic pathogen across all developmental stages of grouper (Abdullah et al., 2017). A major constraint in grouper hatchery production and farming is vibriosis with approximately 66.7% disease incidence reported and is responsible for up to 50% economic loss globally (Galil et al., 2012 and Chong et al., 2017). *Vibrio parahaemolyticus*, is the most important pathogen that affects aquafarming species (Amalina et al., 2017) due to its pathogenicity and the ability to produce hemolysins that causes severe hemorrhagic septicemia leading to mortality in fish (Noriea et al., 2010) and gastroenteritis syndrome (Harikrishnan et al., 2011). Manifestation of *V. parahaemolyticus* infection is often marked with presence of visible red spots on the fish skin, prior its progression towards circular- and/or oval-shaped hemorrhagic ulcer (Hazeri et al., 2016).

This study aimed to continue the work on the selected biomarkers of tiger grouper (*Epinephelus fuscoguttatus sp*) for their response to the bacterial pathogen. Earlier work presented preliminary results on serum proteins that showed a significant increase in *Epinephelus fuscoguttatus sp* disease resistance against *V. parahaemolyticus* (Low et al., 2015). A key research needs to continue the earlier work by Low to identify disease resistant biomarkers and its detection in line with the need to advance mariculture technology and to provide services to farmers in disease management and enhancement of their fish production. Thus, the present study will focus on quantitative PCR-based detection method, which has the capacity for rapid detection and quantitation of gene expressions in association with the identification of disease resistance biomarkers.

1.2 General objective

To identify biomarkers to select infection-resistant grouper.

1.2.1 Specific objectives

- 1.2.1 To establish real time-PCR-based method to detect gene expressions of selected biomarkers in grouper (*Epinephelus fuscoguttatus*) tissues (blood, spleen, and liver).
- 1.2.2 To determine the level of expressions of Alpha-2-macroglobulin ($\alpha 2M$), Parvalbumin (*PVALB*) and Nattectin genes in tissues of experimental *Vibrio parahaemolyticus* infected grouper.

1.3 Problem Statement

The rapid development of intensive culture of grouper has resulted in the frequent outbreak of the infectious diseases. The diseases in the grouper contribute to severe economic losses. To overcome these issues, most of the farmers have been using antibiotics and pesticides frequently in their farms to control the diseases and kills the insects or weeds. However, these lead to antibiotic resistant bacteria, which are becoming more and more difficult to treat as we run out of new antibiotics. Furthermore, the use of antibiotics and pesticides in fish farming may affect immune suppression and result in a negative impact to the environment by contaminating the water sediments. In addition, the use of antibiotics and pesticides can be toxic to a host of other organisms and consumers may be ingesting harmful levels of antibiotic residues.

Selection for natural traits with agricultural advantage has been done since humans started farming. With advances in molecular technology, the use of biomarkers to identify disease resistant candidates will be more specific and reproducible and may provide a safer alternative. Study of Low et al, (2014) has revealed the finding of several potential biomarkers in disease resistant Tiger grouper infected with *Vibrio parahaemolyticus* and the results were achieved from comparison of the serum proteome profiles between resistant and susceptible candidates' fish via two- dimensional gel electrophoresis (2-DE) LC/MS/MS. Further analysis is needed to confirm these potential biomarkers as diseases resistant for tiger grouper fish. The Real -time Polymerase Chain Reaction (qPCR) was selected to identify those genes as it is relatively cheaper, rapid, convenient, easy to screen for epidemiological, genetic studies and applicable to routine high- throughput detection of large numbers of sample (Chen et al., 2017). The precise confirmation can be obtained via real-time PCR by specifically identify the genes and differentiate experiment within those susceptible and resistant.

1.4 Research Question

- 1.4.1 What are the potential biomarkers useful to select for infection-resistant grouper?
- 1.4.2 Is quantitative-PCR a suitable method to detect these biomarkers?

1.5 Hypothesis

- 1.5.1 The selected biomarkers are differentially expressed in infection-resistant and infection-susceptible grouper.
- 1.5.2 The biomarkers are detectable in tissues of grouper using quantitative polymerase chain method (qPCR).

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