



***VIBRIOSIS IN FLOATING MARINE
CAGE-CULTURED FOOD FISHES***

NURLIYANA MOHAMAD

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CAGE-CULTURED FOOD FISHES**

By

NURLIYANA MOHAMAD

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

July 2019

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

VIBRIOSIS IN FLOATING MARINE CAGE-CULTURED FOOD FISHES

By

NURLIYANA MOHAMAD

July 2019

Supervisor : Assoc. Prof. Mohammad Noor Amal Azmai, PhD
Faculty : Science

Vibriosis is a bacterial disease that is caused by several species from the genus of *Vibrio*. It leads to economic losses among the cage-cultured marine fishes throughout the world, including Malaysia. The lack of epidemiological data on vibriosis in this country has hindered the development of efficient curative and preventive measures to combat the disease. This study aimed to determine the prevalence of *Vibrio* spp., to identify the risk factors, transmission, clinical signs and histopathological changes in infected fish, and to understand the antibiotic resistance profiles and distribution of virulence genes of *Vibrio* spp. isolated from cage-cultured marine food fishes.

A cross-sectional and longitudinal study was conducted from December 2016 to August 2017, at a commercial floating cage farm located at Pulau Ketam, Klang, Selangor, Malaysia. Monthly samplings of Asian seabass, red snapper and hybrid grouper (giant grouper × tiger grouper) were carried out to isolate and identify *Vibrio* spp. At the same time, various biotic factors and environmental parameters of the sampling area were also determined. While sampling the fish, clinical signs and histopathological changes of fish naturally infected with vibriosis were noted. Pathogenicity study was carried out to further confirm the causal agent of disease in cultured fish. In addition, the possible transmission routes of *Vibrio* spp. in cultured fish were analyzed. Lastly, the distributions of virulence genes among *Vibrio* spp. were determined using PCR identification, while the antibiotic resistance patterns of the isolates were determined using disc diffusion method.

The highest occurrence of *Vibrio* spp. was found in the hybrid grouper (59%), followed by Asian seabass (31%) and red snapper (28%). Nine species of *Vibrio* were recovered from cultured fish in this study, where 88.1% of the isolated *Vibrio* belonged to the *Harveyi* clade, followed by the *Vulnificus* (6.6%) and the *Cholera* (0.6%) clades. Fish

mortality and size showed strong associations with the presence of some *Vibrio* spp. The water parameters were inconsistently correlated with *Vibrio* spp. in each fish species; the water SO₄, salinity and rainfall exhibited strong correlation with certain *Vibrio* spp. in the cultured fishes. In addition, fluctuation of physico-chemical properties of water may also impose stress to the cultured fish, thus increase their susceptibility to *Vibrio* infection.

Hybrid groupers naturally infected by *Vibrio harveyi* and *V. alginolyticus* displayed lethargy, excessive mucus production, fins rot, enlargement of spleens and generalize congestion of the brains and internal organs. Experimentally infected Asian seabass demonstrated similar clinical signs and histopathological changes as naturally infected hybrid groupers. Asian seabass infected with single *V. alginolyticus* and co-infected with both *Vibrio* spp. resulted in 100% mortality. However, concurrently infected fish demonstrated severe clinical signs and histopathological changes compared to single infections, indicating bigger impact brought by concurrent infections to cultured fish.

In addition, *pyrH* gene sequences of 160 isolates of *V. alginolyticus*, *V. campbellii*, *V. parahaemolyticus* and *V. harveyi* recovered from cultured fish, wild fish, trash fish, fish fry, water and sediment were used to investigate the degree of relatedness and possible transmission existing between the isolated *Vibrio* spp. The population tree revealed the possible transmission from the newly introduced fish fry and wild fish into the cultured fish, while water also might possibly serve as a natural transmission medium of certain *Vibrio* spp. in this fish farm.

Typical virulence genes produced by pathogenic *V. harveyi* were widely distributed among the 63 *Vibrio* spp. isolated from fish in various geographical regions of Peninsular Malaysia. Multiple antibiotic resistance (MAR) was exhibited in all *Vibrio* strains, particularly against ampicillin, penicillin, polypeptides, cepheps, and streptomycin, where 75% of the isolates have MAR index of higher than 0.20. Host species and geographical origin showed no correlation with the presence of virulence genes and the antibiotic resistance pattern of the *Vibrio* spp.

In conclusion, this study demonstrated a yearlong presence of *Vibrio* spp. in cultured fishes, where fluctuating water physico-chemical properties influenced the presence of certain *Vibrio* spp. Exposure of cultured fish to different *Vibrio* spp. may also resulted in synergistic interactions between the pathogens, thus increasing the severity of the infection. In addition, wild and fry fish could transmit the *Vibrio* spp. to the cultured fish in cage farm. Lastly, the majority of *Vibrio* spp. isolated exhibited multiple antibiotic resistances, which represents a real concern and warrants on-going surveillance. The data presented in this thesis offer an updated information on vibriosis in cultured marine fishes in Malaysia, which could help in future effective control measures and contribute to the insights on methods to prevent the disease in cultured fish.

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

**PENYAKIT VIBRIOSIS PADA IKAN MARIN MAKANAN
DALAM KULTUR SANGKAR TERAPUNG**

Oleh

NURLIYANA MOHAMAD

Julai 2019

Penyelia : Prof. Madya Mohammad Noor Amal Azmai, PhD
Fakulti : Sains

Vibriosis adalah merupakan penyakit yang disebabkan oleh beberapa spesies bakteria dari genus *Vibrio*. Penyakit ini telah mendatangkan kerugian ekonomi di seluruh dunia, termasuk Malaysia. Kekurangan data epidemiologi mengenai vibriosis di negara ini telah menghalang perkembangan langkah-langkah kuratif dan pencegahan yang berkesan untuk memerangi vibriosis. Kajian ini dijalankan bertujuan untuk menentukan prevalens, faktor risiko, penyebaran, tanda klinikal dan perubahan histopatologi dalam ikan yang dijangkiti vibriosis, serta untuk memahami profil rintangan antibiotik dan pengagihan gen virulen dalam spesies *Vibrio* yang dipencil dari ikan sangkar.

Satu kajian rentas dan longitudinal telah dijalankan dari Disember 2016 sehingga Ogos 2017, di sangkar terapung berskala komersial yang terletak di Pulau Ketam, Klang, Selangor, Malaysia. Persampelan bulanan terhadap ikan siakap, ikan merah dan kerapu hibrid (kerapu kertang × kerapu harimau) telah dijalankan untuk memencilkan dan mengenal pasti spesies *Vibrio*. Pada masa yang sama, pelbagai faktor biotik dan parameter alam sekitar di kawasan itu juga ditentukan. Tanda-tanda klinikal dan perubahan histopatologi ikan yang dijangkiti vibriosis secara semulajadi telah direkodkan. Ujian patogenisiti dilaksanakan bagi mengesahkan agen penyebab penyakit dalam ikan sangkar. Selain itu, kemungkinan penyebaran spesies *Vibrio* dalam ikan sangkar juga dianalisis. Akhir sekali, pengagihan gen virulen di kalangan spesies *Vibrio* ditentukan dengan menggunakan teknik PCR, manakala profil rintangan antibiotik ditentukan dengan menggunakan kaedah resapan cakera.

Prevalens tertinggi spesies *Vibrio* direkodkan dalam kerapu hibrid (59%), di ikuti oleh siakap (31%) dan ikan merah (28%). Sembilan spesies *Vibrio* telah dipencil dari ikan sangkar dalam kajian ini, di mana 88.1% daripada *Vibrio* yang dipencilkan terdiri daripada kumpulan *Harveyi*, diikuti oleh *Vulnificus* (5.5%) dan *Cholera* (0.6%). Kadar

kematian dan saiz ikan menunjukkan hubungan yang kuat dengan kehadiran beberapa spesies *Vibrio*. Parameter air tidak mempunyai hubungan yang konsisten dengan spesies *Vibrio* dalam setiap spesies ikan. Bagaimanapun, sulfat, kemasinan dan kehadiran hujan menunjukkan hubungan yang kuat dengan kehadiran sesetengah spesies *Vibrio* dalam ikan sangkar. Di samping itu, ketidakseimbangan ciri fiziko-kimia air juga boleh menyebabkan tekanan kepada ikan sangkar, lantas meningkatkan kecenderungan mereka terhadap jangkitan oleh *Vibrio*.

Kerapu hibrid yang dijangkiti oleh *Vibrio harveyi* dan *V. alginolyticus* secara semulajadi telah menunjukkan kelesuan, pengeluaran lendir yang berlebihan, pereputan sirip, pembengkakan limpa dan kesebakan pada otak dan organ dalaman. Siakap yang dijangkiti secara eksperimen menunjukkan tanda-tanda klinikal dan perubahan histopatologi yang sama seperti kerapu hibrid yang dijangkiti secara semulajadi. Siakap yang dijangkiti oleh *V. alginolyticus* dan juga kedua-dua *Vibrio* telah mengakibatkan kematian sebanyak 100%. Walau bagaimanapun, ikan yang dijangkiti oleh dua spesies *Vibrio* serentak menunjukkan tanda-tanda klinikal dan perubahan histopatologi yang lebih teruk berbanding dengan jangkitan tunggal, menunjukkan kesan yang lebih besar yang dibawa oleh jangkitan serentak kepada ikan sangkar.

Selain itu, urutan gen *pyrH* daripada 160 *V. alginolyticus*, *V. campbellii*, *V. parahaemolyticus* dan *V. harveyi* yang dipencil dari ikan sangkar, ikan liar, ikan baja, anak ikan, sampel air dan tanah digunakan untuk menyiasat hubungan filogenetik dan kemungkinan penyebaran di antara *Vibrio* yang terpencil. Analisis filogenetik mendedahkan kemungkinan bahawa anak ikan yang baru dilepaskan dalam sangkar dan ikan liar boleh menyebarkan *Vibrio* kepada ikan sangkar, sementara air berkemungkinan memainkan peranan sebagai medium penghantaran semulajadi *Vibrio* di dalam sangkar ikan.

Gen tipikal yang dihasilkan oleh patogen *V. harveyi* teredar secara meluas di kalangan 63 *Vibrio* yang dipencil dari ikan sangkar dari pelbagai kawasan di Semenanjung Malaysia. Rintangan antibiotik yang tinggi telah dipamerkan oleh semua *Vibrio*, terutamanya terhadap ampisilin, penisilin, polipeptida, cefem, dan streptomisin. Indeks rintangan pelbagai antibiotik adalah di antara 0.06 dan 0.56, dan 75% daripada isolat mempunyai indeks rintangan pelbagai antibiotik yang lebih tinggi daripada 0.20. Spesies perumah dan asal geografi tidak menunjukkan perhubungan di antara kehadiran gen virulen dan corak rintangan antibiotik dalam *Vibrio*.

Kesimpulannya, kajian ini membuktikan kehadiran *Vibrio* sepanjang tahun di dalam ikan sangkar di mana sifat fiziko-kimia kimia air yang tidak stabil mempengaruhi kehadiran spesies *Vibrio*. Pendedahan ikan sangkar kepada pelbagai spesies *Vibrio* juga boleh menyebabkan interaksi sinergistik antara patogen, dan seterusnya meningkatkan impak jangkitan. Di samping itu, ikan liar dan anak ikan boleh menjadi pembawa *Vibrio* kepada ikan laut yang diternak di dalam sangkar. Terakhir, majoriti *Vibrio* menunjukkan pelbagai rintangan antibiotik yang membawa kepada kebimbangan dan memerlukan pengawasan yang berterusan. Data yang dikemukakan dalam tesis ini

menyumbang kepada maklumat terkini mengenai vibriosis di kalangan ikan sangkar di Malaysia, yang dapat membantu dalam langkah-langkah kawalan yang lebih berkesan dan menyumbang kepada pandangan mengenai kaedah pencegahan penyakit ini dalam ikan sangkar pada masa akan datang.



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The 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:

Mohammad Noor Amal Azmai, PhD

Associate Professor
Faculty of Science
Universiti Putra Malaysia
(Chairman)

Ina Salwany Md. Yasin, PhD

Associate Professor
Faculty of Agriculture
Universiti Putra Malaysia
(Member)

Mohd Zamri Saad, PhD

Professor
Faculty of Veterinary Medicine
Universiti Putra Malaysia
(Member)

Muskhazli Mustafa, PhD

Associate Professor
Faculty of Science
Universiti Putra Malaysia
(Member)

ROBIAH BINTI YUNUS, PhD

Professor and Dean School of
Graduate Studies Universiti Putra
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Name and Matric No.: Nurliyana Mohamad (GS48741)

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Signature : _____
Name of Chairman
of Supervisory Committee : Assoc. Prof. Dr. Mohammad Noor Amal Azmai

Signature : _____
Name of Member
of Supervisory Committee : Assoc. Prof. Dr. Ina Salwany Md. Yasin

Signature : _____
Name of Member of
of Supervisory Committee : Prof. Dr. Mohd Zamri Saad

Signature : _____
Name of Member of
of Supervisory Committee : Assoc. Prof. Dr. Muskhazli Mustafa

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LIST OF ABBREVIATIONS

AHPND	Acute Hepatopancreatic Necrosis Disease
AFS	Asian Fisheries Society
ARGs	Antibiotic Resistant Genes
CFU	Colony Forming Unit
DNA	Deoxyribonucleic Acid
EO	Essential oil
ERIC-PCR	Enterobacterial Repetitive Intergenic Consensus Polymerase Chain Reaction
FAO	Food and Agriculture Organization
IPNV	Infectious Pancreatic Necrosis Virus
MABV-F	Marine Birnavirus
MAR	Multiple Antibiotic Resistant
MEGA	Molecular Evolutionary Genetics Analysis
MLSA	Multilocus Sequence Analysis
MS 222	Tricane Methanesulfonate
NCBI	National Center for Biotechnology Information
RAPD	Random Amplification of Polymorphic DNA
TCBS	Thiosulfate-Citrate-Bile Salts-Sucrose
TSA	Tryptone Soya Agar
TSB	Tryptone Soy Broth
VNN	Viral Nervous Necrosis

LIST OF FISH SPECIES

Accepted name	Scientific name
African sharptooth catfish	<i>Clarias gariepinus</i> (Burchell, 1822)
Arabian surgeon fish	<i>Acanthurus sohal</i> (Forsskål, 1775)
Asian seabass	<i>Lates calcarifer</i> (Bloch, 1790)
Atlantic cod	<i>Gadus morhua</i> Linnaeus, 1758
Atlantic halibut	<i>Hippoglossus hippoglossus</i> (Linnaeus, 1758)
Atlantic salmon	<i>Salmo salar</i> Linnaeus, 1758
Ayu	<i>Plecoglossus altivelis</i> (Temminck & Schlegel, 1846)
Bighead carp	<i>Hypophthalmichthys nobilis</i> (Richardson, 1845)
Black seabream	<i>Acanthopagrus schlegelii</i> (Bleeker, 1854)
Black rockfish	<i>Sebastes schlegeli</i> (Valenciennes, 1828)
Blackspot seabream	<i>Pagellus bogaraveo</i> (Brünnich, 1768)
Bluefin tuna	<i>Thunnus</i> sp.
Brown spotted grouper	<i>Epinephelus tauvina</i> (Forsskål, 1775)
Brown shark	<i>Carcharhinus plumbeus</i> (Nardo, 1827)
Camouflage grouper	<i>Epinephelus polyphemadion</i> (Bleeker, 1849)
Chinook salmon	<i>Oncorhynchus tshawytscha</i> (Walbaum, 1792)
Cobia	<i>Rachycentron canadum</i> (Linnaeus, 1766)
Coho salmon	<i>Oncorhynchus kisutch</i> (Walbaum, 1792)
Common snook	<i>Centropomus undecimalis</i> (Bloch, 1792)
Common sole	<i>Solea solea</i> (Linnaeus, 1758)
Crimson snapper	<i>Lutjanus erythropterus</i> Bloch, 1790
European eels	<i>Anguilla anguilla</i> (Linnaeus, 1758)
European seabass	<i>Dicentrarchus labrax</i> (Linnaeus, 1758)
Flounder	<i>Paralichthys</i> sp.
Giant grouper	<i>Epinephelus lanceolatus</i> (Bloch, 1790)
Gilthead seabream	<i>Sparus aurata</i> Linnaeus, 1758
Golden pompano	<i>Trachinotus ovatus</i> (Linnaeus, 1758)
Golden trevally	<i>Gnathanodon speciosus</i> (Forsskål, 1775)
Grass carp	<i>Ctenopharyngodon idella</i> (Valenciennes, 1844)
Green grouper	<i>Epinephelus coioides</i> (Hamilton, 1822)
Groupers	<i>Epinephelus</i> sp.
Half-smooth tongue sole	<i>Cynoglossus semilaevis</i> Günther, 1873
Horse mackerel	<i>Carangoides malabaricus</i> (Bloch & Schneider, 1801)

Hybrid striped bass	<i>Morone saxatilis</i> × <i>M. chrysops</i>
Iberian toothcarp	<i>Aphanius iberus</i> (Valenciennes, 1846)
Indian threadfin	<i>Alectis indica</i> (Rüppell, 1830)
Jack crevalle	<i>Caranx hippos</i> (Linnaeus, 1766)
Japanese horse mackerel	<i>Trachurus japonicus</i> (Temminck & Schlegel, 1844)
Japanese parrotfish	<i>Oplegnathus fasciatus</i> (Temminck & Schlegel, 1844)
John's snapper	<i>Lutjanus johnii</i> (Bloch, 1792)
Lemon sharks	<i>Negaprion brevirostris</i> (Poey, 1868)
Malabar grouper	<i>Epinephelus malabaricus</i> (Bloch & Schneider, 1801)
Malabar snapper	<i>Lutjanus inermis</i> (Peters, 1869)
Mangrove snapper	<i>Lutjanus griseus</i> (Linnaeus, 1758)
Mangrove red snapper	<i>Lutjanus argentimaculatus</i> (Forsskål, 1775)
Marine sunfish	<i>Mola mola</i> (Linnaeus, 1758)
Meagre	<i>Argyrosomus regius</i> (Asso, 1801)
Milkfish	<i>Chanos chanos</i> (Forsskål, 1775)
Humpback grouper	<i>Cromileptes altivelis</i> (Valenciennes, 1828)
Mullet	<i>Mugilidae</i> sp.
Nile tilapia	<i>Oreochromis niloticus</i> (Linnaeus, 1758)
Olive flounder	<i>Paralichthys olivaceus</i> (Temminck & Schlegel, 1846)
Orange-spotted grouper	<i>Epinephelus coioides</i> (Hamilton, 1822)
Pacific salmon	<i>Oncorhynchus</i> sp.
Pompano	<i>Trachinotus blochii</i> (Lacepède, 1801)
Rainbow trout	<i>Oncorhynchus mykiss</i> (Walbaum, 1792)
Redbanded seabream	<i>Pagrus auriga</i> Valenciennes, 1843
Red drum	<i>Sciaenops ocellatus</i> (Linnaeus, 1766)
Red seabream	<i>Pagrus major</i> (Temminck & Schlegel, 1843)
Red snapper	<i>Lutjanus</i> sp.
Sagor catfish	<i>Hexanematichthys sagor</i> (Hamilton, 1822)
Saithe	<i>Pollachius virens</i> (Linnaeus, 1758)
Sea mullet	<i>Mugil cephalus</i> Linnaeus, 1758
Sebae clownfish	<i>Amphiprion sebae</i> Bleeker, 1853
Senegalese sole	<i>Solea senegalensis</i> Kaup, 1858
Silver carp	<i>Hypophthalmichthys molitrix</i> (Valenciennes, 1844)
Silver seabream	<i>Pagrus auratus</i> (Forster, 1801)
Silver pomfret	<i>Pampus argenteus</i> (Euphrasen, 1788)
Silvery black porgy	<i>Sparidentex hasta</i> (Valenciennes, 1830)
Southern catfish	<i>Silurus soldatovi meridionalis</i> Chen, 1977

Spotted grouper	<i>Epinephelus analogus</i> Gill, 1863
Spotted sicklefish	<i>Drepane punctata</i> (Linnaeus, 1758)
Striped bass	<i>Morone saxatilis</i> (Walbaum, 1792)
Striped jack	<i>Pseudocaranx dentex</i> (Bloch & Schneider, 1801)
Summer flounder	<i>Paralichthys dentatus</i> (Linnaeus, 1766)
Tiger grouper/Brown-marbled grouper	<i>Epinephelus fuscoguttatus</i> (Forsskål, 1775)
Tilapia	<i>Oreochromis aureus</i> (Steindachner, 1864)
Turbot	<i>Scophthalmus maximus</i> (Linnaeus, 1758)
White perch	<i>Morone americana</i> (Gmelin, 1789)
White spotted spinefoot	<i>Siganus canaliculatus</i> (Park, 1797)
Yellow catfish	<i>Tachysurus fulvidraco</i> (Richardson, 1846)
Yellow croaker	<i>Larimichthys crocea</i> (Richardson, 1846)
Yellow grouper	<i>Epinephelus awoara</i> (Temminck & Schlegel, 1842)
Yellowtail	<i>Seriola quinqueradiata</i> Temminck & Schlegel, 1845
Yellowstreaked snapper	<i>Lutjanus lemniscatus</i> (Valenciennes, 1828)
Zhengchuan catfish	<i>Silurus soldatovi meridionalis</i> × <i>S. asotus</i>

CHAPTER 1

INTRODUCTION

1.1 General introduction

Vibrio takes its name from the Latin word *Vibrare*, meaning ‘to wave’ (Nishiguchi and Jones, 2004). *Vibrio*, which belongs to the family *Vibrionaceae*, is motile Gram-negative bacteria widely distributed in marine and estuarine environment. *Vibrio* can be found in various vertebrate and invertebrate marine animals, aquatic plants and sediments or freely living in the water column (Chase *et al.*, 2015). This bacterium is highly adaptable, robust and able to persist in aquatic environment even during harsh conditions (Vezzulli *et al.*, 2015). Some species of *Vibrio* are important for natural systems such as the nutrient cycle (Thompson *et al.*, 2004). However, *Vibrio* received the attention of many as the causative agent of a disease in aquatic animals.

Vibriosis is a disease that develops following infection by several species of pathogenic *Vibrio* (Haenen *et al.*, 2014). Vibriosis has been recognised since 1718. However, the first confirmed *Vibrio* infection in fish was reported in 1893, where it causes massive mortality among migrating wild eels (Canestrini, 1893). The diseases that develop following infection by *Vibrio* had started to receive serious attention when it became a threat to the economically important farmed fish such as salmonids in America and Europe (Sinderman *et al.*, 1990; Kashulin *et al.*, 2017). Since then, vibriosis is recognised as one of the notable diseases with huge economic impact on aquaculture worldwide (Abdel-Aziz *et al.*, 2013; Marudhupandi *et al.*, 2017). Previously, this disease has severely affected the shrimp aquaculture industry causing a significant economic loss of more than USD 1 billion (Zorriehzahra and Banaederakhshan, 2015). In recent years, losses due to vibriosis among cage-cultured fish have been reported in Asian country including Japan, India, Thailand, Vietnam and China (Mohi *et al.*, 2010; Khouadja *et al.*, 2013; Haenen *et al.*, 2014; Dong *et al.*, 2017; Rameshkumar *et al.*, 2017; Zhu *et al.*, 2017).

1.2 Problem statements

Epidemiology of vibriosis in Malaysian aquaculture sector remains poorly understood. To date, no comprehensive study has been conducted on the epidemiology of vibriosis in cage-cultured marine fish in Malaysia. Predominant species of *Vibrio* among cage-cultured marine food fish are not clearly known, especially when large number of *Vibrio* species can be present in marine environment (You *et al.*, 2016). Given that many *Vibrio* species shared high similarity in biochemical characteristic, biochemical identification-based methods used in previous studies may lead to misidentifying

and/or underestimating the prevalence of certain species of *Vibrio* in cultured fish (Crocini *et al.*, 2007).

Besides, the influence of various biotic and abiotic factors on the occurrence and abundance of *Vibrio* spp. in cage-cultured marine food fish are not completely understood. The distribution, composition and abundance of *Vibrio* spp. in aquatic environment are known to be dependant on the geographical location and the environmental conditions (Takemura *et al.*, 2014). However, the correlation between the environmental factors and the occurrence of individual *Vibrio* spp. in cage-cultured marine fish were not extensively discussed.

The presence of *Vibrio* spp. in cultured fish does not always cause a disease problem to the fish. Depending on the various factors such as environmental stressors and host health status, *Vibrio* manifestation in fish may result in either acute or chronic infections, producing various clinical signs, gross lesions and pathological changes (Bellos *et al.*, 2015; Liu *et al.*, 2016). Clinical signs and gross lesions particularly are very important as they serve as an indicator for *Vibrio* infection, ensuring rapid recognition of the disease (Noga *et al.*, 2010). However, clinical signs demonstrated by fish suffered from vibriosis are often non-distinguishable from other bacterial and viral infection. In addition, the presence of multiple infections by *Vibrio* spp. in cultured fishes are often negligible. Since cultured fishes are always exposed to various pathogens, it is important to understand the consequences of concurrent infection in cultured fish.

Horizontal transmission was reported as the most probable route in vibriosis (Leong and Colomi, 2002; Takemura *et al.*, 2014). However, the role of water, sediment, fry fish, wild fish and feed in transmission of vibriosis had not been studied. Assessing the possible routes of infection is important for the biosecurity of the farm, to prevent the introduction of potentially pathogenic *Vibrio* into grow-out cages and control the spread of the infection when it occurs.

Lastly, the virulence factors associated with the pathogenicity of *Vibrio* spp. in Malaysian cage-cultured marine fish were yet clarified. With the emerging concern on the multiple antibiotic resistant (MAR) bacterial populations, which threatens both aquaculture sectors and public health, it is essential to monitor the MAR among *Vibrio* species as well as preventing their widespread. On the other hand, expression of the virulence genes by the *Vibrio* spp. is important to assist the bacteria to enter and colonize the host, avoiding host defences and causing damage to the host (Ruwandepika *et al.*, 2010). Thus, information on the distribution and expression of virulence genes in *Vibrio* spp. may contribute invaluable insights to a more environmentally friendly approaches to treat *Vibrio* infection in cage-cultured fish. Better understanding of the epidemiology of vibriosis will facilitate further development of efficient curative and preventive measures to combat this disease.

1.3 Hypotheses

1. Objective 1:
H₀: The presence of *Vibrio* spp. in cultured fishes will not be influenced by different host species, host size and host health condition.
H_a: The presence of *Vibrio* spp. in cultured fishes will be influenced by different host species, host size and host health condition.
2. Objective 2:
H₀: Water physico-chemical parameters have no influence on the presence of *Vibrio* spp. in cultured fishes.
H_a: Water physico-chemical parameters will influence on the presence of *Vibrio* spp. in cultured fishes.
3. Objective 3:
H₀: Cultured fishes affected with vibriosis will not demonstrate certain clinical signs, gross lesions and pathological changes.
H_a: Cultured fishes affected with vibriosis will demonstrate certain clinical signs, gross lesions and pathological changes.
4. Objective 4:
H₀: No possible transmission of *Vibrio* spp. from other sources such as newly introduced fry, wild fish, feed and from surrounding environments including water and sediments.
H_a: *Vibrio* spp. may be transmitted or spread from other sources such as newly introduced fry, wild fish, feed and from surrounding environments including water and sediments.
5. Objective 5:
H₀: *Vibrio* spp. in cultured fishes does not possess virulence genes associated with fish and human disease. In addition, antibiotic resistant *Vibrio* strains are not detected in cultured fishes.
H_a: *Vibrio* spp. in cultured fishes posses virulence genes associated with fish and human disease. In addition, antibiotic resistant *Vibrio* strains will be detected in cultured fishes.

1.4 Objectives

1. To determine the prevalence of *Vibrio* spp. in floating cage-cultured Asian seabass, red snapper, hybrid grouper (giant grouper × tiger grouper) and its culturing environment.
2. To identify the risk factors that influences the presence of *Vibrio* spp. in the floating marine cage-cultured food fishes.
3. To describe the associated clinical signs and histopathological changes of the fish naturally and experimentally infected with vibriosis.
4. To determine the possible transmission routes of *Vibrio* spp. in the floating marine cage-cultured food fishes.
5. To analyse the distribution of virulence genes and the antibiotic resistance patterns of *Vibrio* spp. isolated from floating marine cage-cultured food fishes.

The objectives in this thesis could be integrated as described below:

1. Objective 1: This objective determined the prevalence of *Vibrio* spp. in Asian seabass, red snapper and hybrid grouper that were cultured in a farm between December 2016 and August 2017. The correlation between the presence of *Vibrio* spp. in cultured fishes with biotic factors such as the host species, clinical signs, gross lesions, mortality and size were also investigated. Data of Objectives 1 and 2 had been published in Journal of Aquatic Animal Health, 31: 154-167, 2019. DOI: 10.1002/aah.10062.
2. Objective 2: For this objective, the risk factors that influence the presence of *Vibrio* spp. in cultured Asian seabass, red snapper and hybrid grouper in Objective 1 were identified. Environmental parameters including temperature, pH, salinity, turbidity, dissolved oxygen, micronutrients and rainfall were recorded throughout the sampling period and analysed by using statistical analysis. Data of Objectives 1 and 2 had been published in Journal of Aquatic Animal Health, 31: 154-167, 2019. DOI: 10.1002/aah.10062.
3. Objective 3: This objective described the clinical signs, gross lesions and histopathological changes of fish naturally and experimentally infected with *Vibrio* spp. An outbreak of vibriosis had occurred during the data collection for Objectives 1 and 2. The pathogens were isolated and identified, while the pathogenicity test was carried out in the laboratory to confirm the etiological agent of the outbreak and to reproduce the observed clinical signs, gross lesions and histopathological changes in model fish. Data of Objective 3 had been published in Journal of Aquatic Animal Health, 31(1): 88-96, 2019. DOI: 10.1002/aah.10055.
4. Objective 4: This study determined the possible transmission routes of *Vibrio* spp. in floating cage-cultured marine food fishes. Representative

Vibrio spp. that were isolated from various biological and environmental sources including cultured fish, fry and wild fish, water and sediment in Objectives 1 and 2 were used in this study. Their genetic sequences were compared by using phylogenetic analyses in order to determine the relatedness between the *Vibrio* strains of the same species. Data of Objective 4 had been published in Letters in Applied Microbiology, 68(66): 485-496, 2019. DOI: 10.1111/lam.13146.

5. Objective 5: For this objective, the distribution of virulence genes and the antibiotic resistance patterns of *Vibrio* spp. isolated from Objectives 1 and 2, together with *Vibrio* isolates that were collected from previous studies were analysed. Firstly, the presence of selected virulence associated genes in the representative *Vibrio* spp. were investigated. Then, the extent of antibiotic resistance of *Vibrio* spp. isolated from marine fishes cultured in various farms in Peninsular Malaysia were discussed. Data of Objectives 5 had been published in BMC Veterinary Research, 15:176, 2019. DOI: 10.1186/s12917-019-1907-8.

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