



UNIVERSITI PUTRA MALAYSIA

***COMPREHENSIVE METABOLITE PROFILE OF *Chlorella vulgaris*  
AND METABOLIC SIGNATURE OF ITS IMMUNOSTIMULATING  
EFFECT IN NILE TILAPIA [*Oreochromis niloticus* (Linnaeus, 1758)]***

HAMZA AHMED PANTAMI

FS 2020 41



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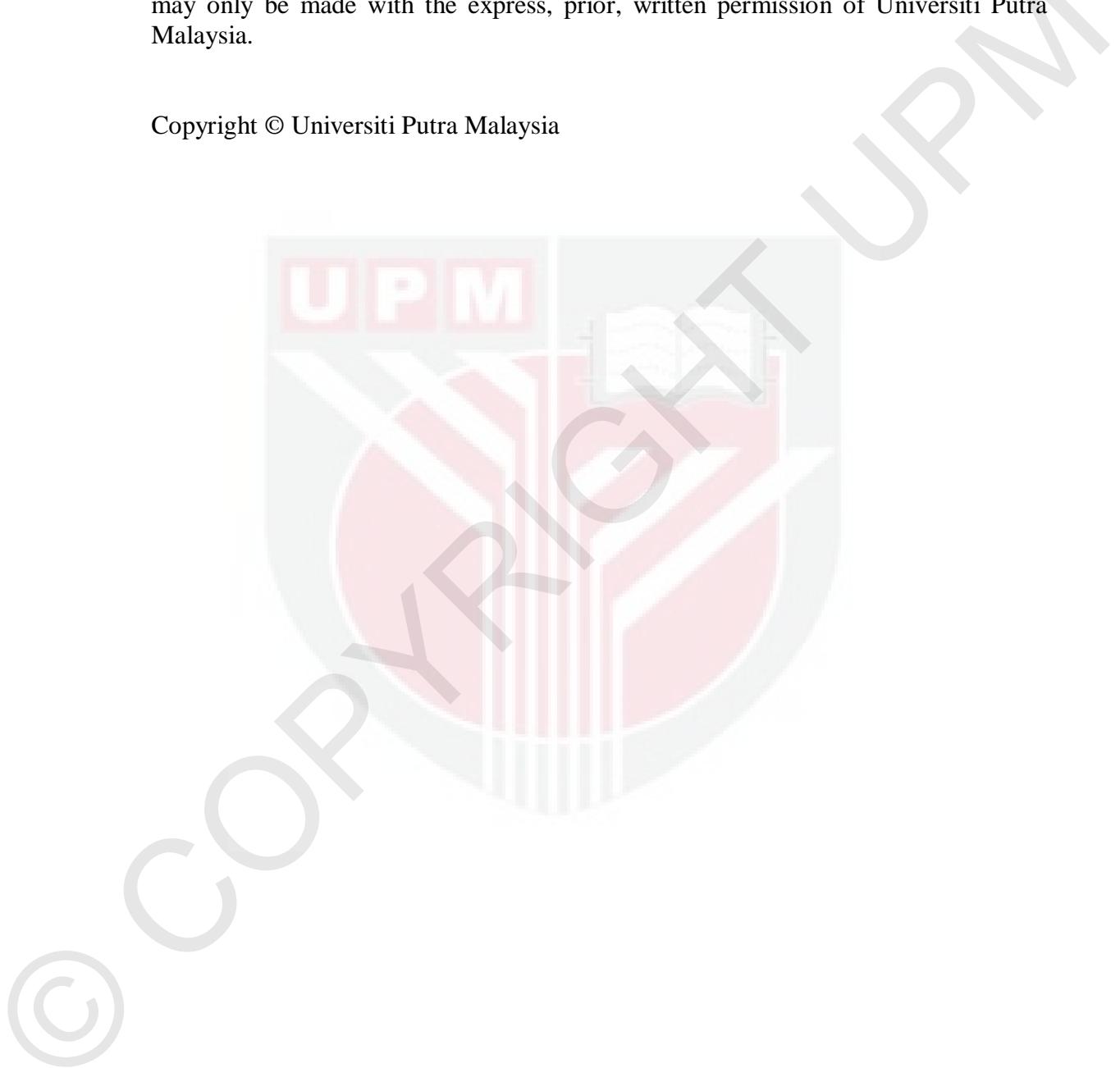
Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia,  
in Fulfilment of the Requirements for the Degree of Doctor of Philosophy

August 2020

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## **DEDICATION**

This thesis is dedicated to my late parents, my wife Habiba, my children; Ahmad, Nana Hafsat, Nana Aisha and the soon expected unborn child.



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

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**HAMZA AHMED PANTAMI**

**August 2020**

**Chairman : Professor Khozirah binti Shaari, PhD**  
**Faculty : Science**

*Chlorella vulgaris* is a green, single-celled, spherical freshwater microalga belonging to the family *Chlorellaceae* of the division *Chlorophyta*. *C. vulgaris* is currently used as food supplement and medicinal agent due to its carotenoids, chlorophylls and proteins content. *Chlorella vulgaris* is incorporated in fish feed as a growth and immune stimulant. Tilapia is one of the most important cultured fish species with numerous advantages, contributing more than USD 10 billion to the world's seafood market annually. Despite the important features of tilapia, disease outbreaks tend to cause massive mortalities in fish farms which impose serious negative impact to economies worldwide. Most tilapia mortalities were reported as a resultant stress due to overcrowding coupled with bacterial infection. *Streptococcus agalactiae* is one of the most virulent bacteria causing most of tilapia mortalities recently. The use of immunostimulants like microalgal supplementation in fish feed holds a promising future in mitigating tilapia fish disease. Nevertheless, the common amounts used ( $\geq 12\%$ ) in this practice is considered uneconomical by fish farmers, considering the high price of microalgal biomass procurement. In addition, scientific reports regarding the association of metabolites with pathways involved in the stimulation of immune system of tilapia fish (*Oreochromis niloticus*) exerted by consumption of *C. vulgaris* are still limited. Hence, the main aim of this study was to investigate the immune-stimulating role of bioactive metabolites from *C. vulgaris* on the tilapia fish at lower concentrations using proton nuclear magnetic resonance ( $^1\text{H-NMR}$ ) metabolomics approach. The first part of the study dealt with the characterization of the metabolite composition of the cultured samples of *C. vulgaris* via  $^1\text{H-NMR}$ , gas chromatography mass spectrometry (GCMS) lipid analysis and liquid chromatography mass spectrometry (LC-MS/MS) analysis.  $^1\text{H-NMR}$  data obtained from six different organic solvent extracts were used to establish the general metabolite profile and their variation was determined via multivariate data analysis (MVA) and complemented with mass spectrometric data. LC-MS/MS analysis led to the profiling of carotenoids

comprising of violaxanthin, neoxanthin, lutein,  $\beta$ -carotene, vulgaxanthin I, astaxanthin and antheraxanthin along with other metabolites such as amino acids, vitamins, and chlorophylls. The metabolite compositions indicated that *C. vulgaris* could serve as a good source of dietary nutrients. Fatty acid profile of *C. vulgaris* revealed that it was rich in omega-6,7,9 and 13 fatty acids, with dominance of omega-6 fatty acids (>60% of the total fatty acids). Besides, the main fatty acids were those of C<sub>16</sub>-C<sub>18</sub> (>92%), suggesting high potential for utilization of *C. vulgaris* in biodiesel production. In addition, 48 lipids were putatively identified via Molecular Networking of the LC-MS/MS data which include glycosphingolipids, phosphoethanolamines, phosphoserines and phosphocolines. The second part of the study determined the safety of *C. vulgaris* concentration as a fish feed at 500 mg/kg body weight (bw) by assessing several immune parameters. The immune parameters assessed were serum lysozyme activity (SLA), serum bactericidal activity (SBA), phagocytosis activity (PHA), respiratory burst activity (RBA) and lymphocyte proliferation (LP). There was no mortality recorded nor sign of organ lesion observed throughout the assessment period. The immune parameters assessed at 5%, 2.5%, 1.25% and 0.625% showed significant improvement in PHA, RBA and LP with 1.25% (125 mg/kg bw) been the best dose for future use economically. The third part of the present study correlated the immune parameters with the primary metabolite composition of the serum and spleen of the tilapia fish using <sup>1</sup>H-NMR metabolomics. Metabolites such as choline, glucose, riboflavin, stearic acid, linolenic acid, leucine, histamine, proline, glycine, and alanine levels in tilapia fish fed with *C. vulgaris* exhibited improvements compared to the control tilapia fish, with reduction in the level of glutamic acid. The linoleic acid metabolism had the highest impact factor, followed by riboflavin metabolism, D-glutamine and D-glutamate metabolism and starch and sucrose metabolism, with impact factors of 1.00, 0.50, 0.50 and 0.39, respectively. *Chlorella vulgaris* incorporation into fish diet at a concentration of 125 mg/kg bw showed to be considerably enough in improving tilapia immune parameters and was used for the prophylaxis studies in the last part of the research study for economic considerations. The last part of the study showed that the immune stimulation by *C. vulgaris* was sustained even after challenging of the tilapia fish with a virulent bacterium, *Streptococcus agalactiae* concentration of 10<sup>8</sup> CFU mL<sup>-1</sup> for 7 days. This finding agreed with the 90% survival rate of the fish fed with *C. vulgaris* (CVC) as compared to the 13% survival rate of the control fish (CF) and significantly higher metabolite fold changes in CVC in comparison with CF. This research provides scientific evidence for utilization of *C. vulgaris* as an immune stimulant for tilapia fish. On the other hand, <sup>1</sup>H-NMR metabolomics is a sound methodology for the identification of biomarkers in immune system-stimulated tilapia fish. To the best of our knowledge, the present study was the first investigation that proposed the biomarkers along with associated pathways involved in immune stimulation of tilapia fish consuming *C. vulgaris*. The findings could pave a way for development of efficient strategies in mitigating fish diseases in aquaculture practice.

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

**PROFIL METABOLITE KOMPREHENSIF *Chlorella vulgaris* DAN  
MAKLUMAT METABOLIK DENGAN KESAN IMMUNOSTIMULASI DI  
NILE TILAPIA [*Oreochromis niloticus* (Linnaeus, 1758)]**

Oleh

**HAMZA AHMED PANTAMI**

**Ogos 2020**

Pengerusi : Profesor Khozirah binti Shaari, PhD  
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*Chlorella vulgaris* ialah mikroalga air tawar berbentuk sfera, bersel tunggal dan berwarna hijau yang tergolong dalam keluarga Chlorellaceae di bahagian Chlorophyta. *C. vulgaris* kini digunakan sebagai makanan tambahan dan agen perubatan disebabkan kandungan karotenoid, klorofil dan proteinnya. *Chlorella vulgaris* digunakan sebagai satu bahan dalam makanan ikan untuk merangsang sistem tumbesaran dan imun. Tilapia adalah salah satu spesies ikan berbudaya yang paling penting dengan banyak kelebihan, menyumbang lebih dari USD 10 bilion untuk pasar makanan laut dunia setiap tahun. Walaupun terdapat ciri penting ikan nila, wabak penyakit cenderung menyebabkan kematian besar-besaran di ladang ikan yang memberikan kesan negatif yang serius kepada ekonomi di seluruh dunia. Sebilangan besar kematian tilapia dilaporkan sebagai tekanan yang disebabkan oleh kesesakan yang banyak ditambah dengan jangkitan bakteria. *Streptococcus agalactiae* adalah salah satu bakteria yang paling banyak menyebabkan kematian tilapia baru-baru ini. Penggunaan imunostimulan seperti suplemen mikroalga dalam makanan ikan memiliki masa depan yang menjanjikan dalam mengurangkan penyakit ikan nila. Walaubagaimanapun, jumlah *C. vulgaris* yang biasa digunakan dalam amalan ini ( $\geq 12\%$ ) dianggap tidak ekonomik oleh penternak ikan, memandangkan harga perolehan biojisimnya yang tinggi. Di samping itu, kajian saintifik mengenai hubungkait metabolit dengan laluan yang terlibat dalam rangsangan sistem imun ikan tilapia (*Oreochromis niloticus*) kesan daripada pengambilan *C. vulgaris* adalah masih kurang. Oleh yang demikian, matlamat utama kajian ini ialah untuk mengkaji sebatian bioaktif dalam *C. vulgaris* yang berperanan merangsang sistem imun ikan tilapia pada kepekatan yang lebih rendah menggunakan pendekatan metabolomik resonans magnet nuklear proton ( $^1\text{H-NMR}$ ). Bahagian pertama kajian mencirikan komposisi metabolit sampel kultur *C. vulgaris* melalui  $^1\text{H-NMR}$ , analisis asid lemak spektrometri jisim-kromatografi gas (GC-MS) dan analisis spektrometri jisim serentak-kromatografi cecair (LC-MS/MS). Data  $^1\text{H-NMR}$  enam ekstrak pelarut organik yang berbeza

digunakan untuk mengetahui profil metabolit umum *C. vulgaris* dan variasi ekstrak-ekstrak ini ditentukan melalui analisis data pelbagai pembolehubah (MVA) dan dilengkapi dengan data spektrometri jisim. Analisis LC-MS/MS menunjukkan profil karotenoid yang terdiri daripada violazantin, neozantin, lutein,  $\beta$ -karotena, vulgazantin I, astazantin dan antherazantin bersama-sama dengan sebatian lain seperti asid amino, vitamin dan klorofil. Komposisi metabolit menunjukkan bahawa *C. vulgaris* ialah sumber nutrisi yang baik. Profil asid lemak *C. vulgaris* mendedahkan bahawa ia kaya dengan asid lemak omega-6,7,9 dan 13, dengan dominasi asid lemak omega-6 ( $> 60\%$  daripada jumlah asid lemak). Selain itu, asid lemak utama ialah C<sub>16</sub>-C<sub>18</sub> ( $> 92\%$ ), justeru mencadangkan penggunaan *C. vulgaris* dalam penghasilan biodiesel. Di samping itu, 48 sebatian lemak telah dikenalpasti melalui Rangkaian Molekular data LC-MS/MS, yang merangkumi glycosphingolipids, phosphoethanolamines, phosphoserines dan phosphocolines. Bahagian kedua kajian menentukan keselamatan *C. vulgaris* sebagai makanan ikan pada kepekatan 500 mg/kg berat badan (bw) dengan penilaian beberapa parameter sistem imun. Parameter sistem imun yang dinilai ialah aktiviti serum lisozim (SLA), aktiviti bakterisida serum (SBA), aktiviti fagositosis (PHA), aktiviti pecah pernafasan (RBA) dan proliferasi limfosit (LP). Tiada kematian atau tanda luka organ direkodkan sepanjang tempoh penilaian. Parameter sistem imun yang dinilai pada 5%, 2.5%, 1.25% dan 0.625% menunjukkan peningkatan yang ketara dalam PHA, RBA dan LP dengan 1.25% (125 mg / kg bw) adalah dos terbaik untuk penggunaan masa depan secara ekonomi. Bahagian ketiga kajian ini mengaitkan parameter imun dengan komposisi metabolit serum dan limpa ikan tilapia menggunakan metabolomik <sup>1</sup>H-NMR. Metabolit seperti kolin, glukosa, riboflavin, asid stearik, asid linolenik, leusin, histamin, prolin, glisin, dan alanin dalam ikan tilapia yang diberi makan *C. vulgaris* menunjukkan peningkatan berbanding ikan tilapia kawalan, dengan pengurangan tahap asid glutamik. Metabolisma asid linoleik mempunyai faktor kesan tertinggi, diikuti dengan metabolisma riboflavin, D-glutamin dan metabolisma D-glutamat dan metabolisme kanji dan sukrosa, dengan faktor kesan masing-masing 1.00, 0.50, 0.50 dan 0.39. Penggabungan *Chlorella vulgaris* ke dalam diet ikan pada kepekatan 125 mg / kg bw terbukti cukup baik dalam meningkatkan parameter imun tilapia dan digunakan untuk kajian profilaksis di bahagian terakhir kajian penyelidikan untuk pertimbangan ekonomi. Bahagian terakhir kajian menunjukkan bahawa rangsangan imun oleh *C. vulgaris* telah dikekalkan walaupun selepas cabaran ikan tilapia dengan bakteria *Streptococcus agalactiae* kepekatan 10<sup>8</sup> CFU mL<sup>-1</sup> selama 7 hari. Dapatan ini bertepatan dengan 90% kadar survival ikan tilapia yang diberi makan *C. vulgaris* (CVC) berbanding kadar survival 13% ikan kawalan (CF) dan perubahan lipatan metabolit yang lebih tinggi dalam CVC berbanding CF. Penyelidikan ini memberikan bukti saintifik penggunaan *C. vulgaris* sebagai perangsang imun bagi ikan tilapia. Selain itu, metabolomik <sup>1</sup>H-NMR ialah satu kaedah yang baik untuk mengenalpasti biomarker dalam ikan tilapia yang dirangsang sistem imunnya. Dalam amatan kami, kajian ini merupakan penyiasatan pertama yang mencadangkan biomarker bersama-sama dengan laluan yang berkaitan dengan rangsangan imun ikan tilapia yang memakan *C. vulgaris*. Penemuan ini dapat membuka jalan bagi pembangunan strategi yang cekap dalam mengurangkan penyakit ikan dalam amalan akuakultur.

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This thesis was submitted to the Senate of the 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:

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## TABLE OF CONTENTS

	Page
<b>ABSTRACT</b>	i
<b>ABSTRAK</b>	iii
<b>ACKNOWLEDGEMENTS</b>	v
<b>APPROVAL</b>	vii
<b>DECLARATION</b>	ix
<b>LIST OF TABLES</b>	xvi
<b>LIST OF FIGURES</b>	xviii
<b>LIST OF ABBREVIATIONS</b>	xxii
 <b>CHAPTER</b>	
<b>1 INTRODUCTION</b>	<b>1</b>
1.1 Background	1
1.2 Statement of the problem	2
1.3 Justification of the study	2
1.4 Research objectives	2
<b>2 LITERATURE REVIEW</b>	<b>3</b>
2.1 Microalgae	3
2.2 <i>Chlorella vulgaris</i>	4
2.2.1 Applications of <i>Chlorella vulgaris</i>	5
2.2.2 <i>Chlorella vulgaris</i> in meal and its cell wall digestibility in tilapia	6
2.2.3 <i>Chlorella vulgaris</i> growth medium requirements	6
2.2.4 Metabolite profile of <i>Chlorella vulgaris</i>	9
2.2.5 Effect of <i>Chlorella vulgaris</i> inclusion in fish feed	11
2.3 Tilapia ( <i>Oreochromis niloticus</i> )	13
2.4 Common bacterial disease affecting tilapia	14
2.5 Metabolomics.	15
2.6 Metabolomic profiling via nuclear magnetic resonance (NMR) spectroscopy and mass spectrometry (MS)	16
2.6.1 NMR-based metabolomics	18
2.6.2 Biofluid sample preparation for NMR analysis	18
2.6.3 Animal tissue sample preparation for NMR analysis	19
2.6.4 NMR spectra acquisition	19
2.6.5 NMR spectra processing	19
2.6.6 Plant and microalgae sample preparation for NMR analysis	20
2.6.7 Chemometrics analysis	21
2.6.8 Principal component analysis (PCA)	21
2.6.9 Partial least squares (PLS)	22
2.6.10 Partial least square discriminate analysis (PLS-DA)	22
2.7 Biomarker	22

<b>3</b>	<b>CHARACTERIZATION OF <i>Chlorella vulgaris</i> VIA 1H NMR-BASED METABOLOMICS, GCMS FATTY ACID ANALYSIS AND LCMS/MS METABOLITE PROFILING</b>	24
3.1	Introduction	24
3.1.1	Specific objective	24
3.2	Materials and methods	25
3.2.1	Instruments	25
3.2.2	Chemicals and reagents	26
3.2.3	Microalgae biomass procurement	26
3.2.4	Microalgae solvent extraction for <sup>1</sup> H NMR-based metabolomics profiling	27
3.2.5	Sample preparation for NMR analysis	27
3.2.6	NMR analysis	27
3.2.7	NMR spectra processing (bucketing/binning) and multivariate data analysis	28
3.2.8	<i>Chlorella vulgaris</i> fatty acid extraction for GCMS analysis	28
3.2.9	Sample preparation for GCMS fatty acid analysis.	29
3.2.10	GCMS fatty acid analysis	29
3.2.11	<i>Chlorella vulgaris</i> solvent extraction for LCMS/MS analysis	29
3.2.12	Sample preparation for LCMS analysis	29
3.2.13	LCMS/MS analysis	30
3.3	Results and discussions	30
3.3.1	Assignment of metabolites by 1D NMR spectra of <i>Chlorella vulgaris</i> solvent extracts	30
3.3.2	Classification of different solvent extracts by (PCA) and PLS-DA	38
3.3.3	PLS-DA model validation	41
3.3.4	Relative quantification using <sup>1</sup> H NMR data	41
3.3.5	Identification of fatty acids as FAMEs using GC-MS	44
3.3.6	LCMS/MS metabolite profile of <i>Chlorella vulgaris</i>	48
3.3.6.1	Identification of carotenoids by LCMS/MS	48
3.3.6.2	Identification of chlorophyll pigments by LCMS/MS and ultraviolet visible photo diode array (UV.vis PDA)	54
3.3.6.3	Identification of amino acids, fatty acids, lipids, and fatty acyls by LC-MS	56
3.3.6.4	Identification of vitamins by LC-MS	59
3.3.6.5	Identification of other compounds by LC-MS	59
3.3.6.6	Identification of lipids via molecular networking	60
3.4	Conclusions	74

<b>4</b>	<b>ASSESSMENT OF SAFETY AND IMMUNE ASSAY OF <i>Chlorella vulgaris</i> In NILE TILAPIA <i>Oreochromis niloticus</i></b>	<b>75</b>
4.1	Introduction	75
4.1.1	Specific objective	76
4.2	Instruments	76
4.3	Chemicals	76
4.4	Methodology	76
4.4.1	Feed preparation	77
4.4.2	Safety concentration study	77
4.4.3	Immune assays	77
4.4.3.1	Fish grouping	77
4.4.3.2	Fish sacrifice and sampling	78
4.4.3.3	Preparation of freezing media	78
4.4.4	Lysozyme activity	79
4.4.5	Serum bactericidal activity	79
4.4.6	Phagocytosis activity	80
4.4.7	Respiratory burst activity (RBA)	81
4.4.8	Lymphoproliferation assay	81
4.4.9	Serum and spleen sample preparation for NMR analysis	82
4.4.10	<sup>1</sup> H NMR spectra processing and multivariate analysis	82
4.4.11	Statistical analysis	82
4.5	Results and discussions	83
4.5.1	Proximate analysis of fish feed incorporated with <i>Chlorella vulgaris</i> and its growth performance in experimental fish.	83
4.5.2	Serum biochemical analysis in safety concentration studies	83
4.5.3	Histopathology of fish organs in safety concentration studies	84
4.5.4	Lysozyme activity	86
4.5.5	Serum bactericidal activity	87
4.5.6	Phagocytosis activity	87
4.5.7	Respiratory burst activity (RBA)	89
4.5.8	Lymphoproliferation of T and B cells	89
4.5.9	Variation between treated and non-treated fish samples using PLS-DA and correlation between immune parameters and detected metabolites using PLS	91
4.5.9.1	Validation of PLS models	97
4.6	Conclusions	98
<b>5</b>	<b>IDENTIFICATION OF IMMUNOSTIMULANT SIGNATURES OF <i>Chlorella vulgaris</i> INCORPORATED FISH DIET USING <sup>1</sup>H NMR-BASED METABOLOMICS APPROACH</b>	<b>100</b>
5.1	Introduction	100
5.1.1	Specific objective	100

5.2	Instruments	100
5.3	Chemicals	101
5.4	Methodology	101
5.4.1	Serum and organ preparation for NMR analysis	101
5.4.2	$^1\text{H}$ NMR spectra processing and multivariate analysis	101
5.5	Results and discussions	101
5.5.1	Metabolite analysis of serum samples and immune improvement biomarkers of <i>Chlorella vulgaris</i> fed fish	101
5.5.2	Metabolite analysis of spleen samples and immune improvement biomarkers of <i>Chlorella vulgaris</i> fed fish.	107
5.5.3	PLS-DA, PLS model validation	112
5.5.4	Metabolite association and pathway analysis	114
5.5.5	2D-NMR verification of VIP metabolites with high hits and higher impact factors in the pathway analysis	118
5.6	Conclusions	123
<b>6</b>	<b>ASSESSMENT OF THE EFFECT OF PROPHYLACTIC TREATMENT WITH <i>Chlorella vulgaris</i> INCORPORATED DIET AGAINST <i>Streptococcus agalactiae</i> CHALLENGE</b>	<b>125</b>
6.1	Introduction	125
6.1.1	Specific objectives	125
6.2	Instruments	125
6.3	Chemicals	126
6.4	Methodology	126
6.4.1	Bacterial challenge LC <sub>50</sub>	126
6.4.1.1	Bacterial strain	126
6.4.1.2	Preparation of live bacteria inoculums and preparation of its different concentrations for challenge	126
6.4.2	Prophylactic treatment and bacterial challenge	127
6.4.3	Spleen preparation for NMR analysis	128
6.4.4	$^1\text{H}$ NMR spectra processing and multivariate analysis	128
6.5	Results and discussions	129
6.5.1	LC <sub>50</sub>	129
6.5.2	Bacterial challenge mortality and survival rate	131
6.5.3	Identification of compounds from spleen samples	132
6.5.4	Effect of environment on the experimental fish	134
6.5.5	Effect of <i>Chlorella vulgaris</i> on experimental fish	135
6.5.6	Effect of <i>Streptococcus agalactiae</i> bacteria on the experimental fish	138
6.5.7	Effect of <i>Streptococcus agalactiae</i> bacteria on <i>Chlorella vulgaris</i> fed fish	140
6.5.8	Model validation	143
6.6	Conclusions	145

<b>7</b>	<b>CONCLUSIONS AND RECOMMENDATIONS</b>	146
7.1	Conclusions	146
7.2	Recommendations	148
<b>BIBLIOGRAPHY</b>		149
<b>BIODATA OF STUDENT</b>		172
<b>LIST OF PUBLICATIONS</b>		173



## LIST OF TABLES

Table	Page
2.1 Botanical classification of <i>Chlorella vulgaris</i>	4
2.2 Carotenoids and chlorophylls from <i>C. vulgaris</i>	9
2.3 Amino acid profile of <i>C. vulgaris</i>	10
2.4 Effect of <i>C. vulgaris</i> inclusion in fish feed	12
3.1 Upscale parameters for culture medium of <i>C. vulgaris</i> sample procurement	27
3.2 Identified metabolites and its 500 MHz $^1\text{H}$ NMR chloroform-d4: methanol-d4(2:8) assignment of <i>C. vulgaris</i> in six different solvent extractions	34
3.3 Fatty acid composition of <i>Chlorella vulgaris</i> . The table shows the peak numbers, the corresponding systematic and trivial names of the fatty acid, designation and percentage composition	46
3.4 Carotenoids identified in <i>Chlorella vulgaris</i> .	50
3.5 Chlorophylic pigments identified in <i>Chlorella vulgaris</i>	55
3.6 Amino acids, fatty acids, lipids and fatty acyls composition of <i>Chlorella vulgaris</i>	57
3.7 Composition of vitamins in <i>Chlorella vulgaris</i>	59
3.8 Identified simple sugars and R-cryptone in <i>Chlorella vulgaris</i> . Underlined $m/z$ values indicate intense fragments	60
3.9 Putative annotation of the lipids from ethanol extract of <i>Chlorella vulgaris</i>	64
4.1 Fish grouping and amount of <i>C. vulgaris</i> biomass incorporated into fish feed for immune and metabolomics studies	78
4.2 Proximate analysis of the re-pelleted commercial fish feed supplemented with different concentration of <i>C. vulgaris</i>	83
4.3 PLS Variable importance projection metabolites in which the VIP values is greater than or equal to 1 and in which the error bar does not cross the X-axis	93

4.4	PLS Variable importance projection metabolites in which the VIP values is greater than or equal to 1 and in which the error bar does not cross the X-axis	96
6.1	Results of percentage mortality from bacterial challenge test	131
6.2	Identified metabolites from spleen samples of experimental fish and their corresponding 700 MHz $^1\text{H}$ NMR chemical shifts	133
6.3	OPLS-DA VIP analysis showing metabolites with $\text{VIP} \geq 1$ resulting from the separation of CV and CF by PC1	137
6.4	Metabolite fold changes as a result of <i>C. vulgaris</i> feeding (CV/CF)	138
6.5	Metabolite fold changes as a result of <i>S. agalactiae</i> challenge on control fish	140
6.6	Metabolite fold changes as a result of <i>S. agalactiae</i> challenge on <i>C. vulgaris</i> fed fish	142
6.7	Comparison between metabolite fold changes as a result of bacteria <i>S. agalactiae</i> challenge on control fish (CF) and on <i>C. vulgaris</i> fed fish (CFC)	143

## LIST OF FIGURES

<b>Figure</b>	
	<b>Page</b>
2.1 Schematic ultrastructure of <i>C. vulgaris</i> representing different organelles	5
2.2 Nile tilapia fish <i>Oreochromis niloticus</i> used for identification in present research	14
2.3 NMR-based and MS-based metabolomics publications in duration of 12 years, between 200-2012	16
3.1 Schematic representation of overall workflow of the chapter	25
3.2 Representative 500 MHz $^1\text{H}$ NMR spectra of different solvent extracts of <i>Chlorella vulgaris</i> for chemical shift regions 0 – 5 ppm	33
3.3 The A, PCA score plot; B, PLS-DA score plot for the discrimination between different solvent extracts of <i>C. vulgaris</i>	39
3.4 The PLS-DA loading plot for the discrimination between different solvent extracts of <i>C. vulgaris</i>	40
3.5 The VIP plot showing the major compounds responsible for the variation between different solvent extracts of <i>C. vulgaris</i>	40
3.6 The PLS-DA model validation with 100 permutations of identified metabolites	41
3.7 Relative quantification	44
3.8 A: Total ion chromatogram of extracted fatty acid methyl esters in <i>Chlorella vulgaris</i> obtained by GC–MS analysis (numbers correspond to peak numbers in Table 3.3) B: The percentage composition of saturated and unsaturated fatty acid methyl esters C: Percentage distribution of individual saturated fatty acids relative to the total saturated fatty acid content D: Percentage distribution of individual unsaturated fatty acids relative to the total unsaturated fatty acid content	47
3.9 A; UV.vis PDA of the representative pigments comprising of carotenoids and chlorophylls. B; MS base peaks of all the identified compounds of <i>C. vulgaris</i> by LCMS	49
3.10 Fragmentation pathway of vulgaxanthin I, showing the main detected MS/MS fragments used for its identification in <i>C. vulgaris</i>	51

3.11	<i>m/z</i> 221 MS/MS fragments from A: neoxanthin and B: violaxanthin used in their identification as isomers	52
3.12	Extraction ion chromatogram (EIC) (peak 26)	53
3.13	Fragmentation pattern of phenylalanine	58
3.14	Fragmentation pathway of Vitamin B-3	59
3.15	Different fragments of r-cryptone showing the MS/MS data	60
3.16	MN of ethanol extract of <i>C. vulgaris</i>	62
3.17	Diacylglycerophosphoserine cluster with MS1 showing the nodes	67
3.18	Diacylglycerophosphoserines cluster; MS2 and some of the common fragments within the cluster	68
3.19	Diacylglycerophosphocholine cluster with MS1 showing the nodes	70
3.20	Diacylglycerophosphocholines cluster (2); MS2 showing some common fragments within the cluster	71
3.21	Glycosphingolipid cluster with MS1 showing the nodes	72
3.22	Some common fragments within the glycosphingolipid cluster based on MS1 and MS2	73
4.1	Overall schematic diagram of the workflow of the chapter	75
4.2	Serum biochemical analysis from safety concentration studies	84
4.3	CG gills, CG liver, TG gills, TG liver	85
4.4	Effect of <i>C. vulgaris</i> incorporation in fish feed in different concentrations on serum lysozyme activity	86
4.5	Effect of <i>C. vulgaris</i> incorporation into fish diet in different concentrations on serum bactericidal activity	87
4.6	Phagocytosis immune assay: Left; arrow points to a phagocytic cell, right; arrow points to a non-phagocytic cell	88
4.7	Effect of incorporation of <i>C. vulgaris</i> in fish diet in different levels on the phagocytosis activity of the fish spleen	88
4.8	Effect of incorporation of <i>C. vulgaris</i> in fish diet in different levels on the respiratory burst activity of the fish spleen	89

4.9	A; Effect of incorporation of <i>C. vulgaris</i> in fish diet at different concentration on the mitogen induced proliferation of T-cells of the fish spleen, B; Spontaneous proliferation of T-cells	90
4.10	A; Effect of incorporation of <i>C. vulgaris</i> in fish diet in different levels on the proliferation of B-cells of the fish spleen, B; Spontaneous proliferation of B-cells	90
4.11	PLS-DA score plot of the samples from fish serum. srA is the control; srB, srC, srD and srE are serum samples from fish fed with different concentrations of <i>C. vulgaris</i> , (n=6)	92
4.12	PLS loading plots showing proximity of identified metabolites to the serum immune parameters; SLA and SBA	93
4.13	The biplot of the PLS model showing the correlation between the VIP metabolites and the serum immune parameters	94
4.14	PLS-DA score plot of the samples from fish spleen. SpA is the control; SpB, SpC, SpD and SpE were spleen samples from fish fed with different concentrations of <i>C. vulgaris</i> , (n=6)	95
4.15	PLS loading plots showing proximity of identified metabolites to the spleen immune parameters; SBA, PHG and LPA	95
4.16	The biplot of the PLS model showing the correlation between the VIP metabolites and the spleen immune parameters	96
4.17	The PLS models validation with 100 permutations of SBA (a), RBA (b)	98
5.1	A; PLS-DA score plot and B; PLS-DA loading plot of the samples from fish serum	102
5.2	The VIP plot obtained from the PLS-DA showing the most significant metabolites that contributed for the separation of <i>C. vulgaris</i> fed fish serum samples from the control	103
5.3	The heatmap showing the concentration of the VIP metabolites in each of the serum sample	104
5.4	The box plot showing the relative quantification of the VIP metabolites from serum analysis	107
5.5	A; PLS-DA score plot and B; PLS-DA loading plot of the samples from fish spleen	108
5.6	The VIP plot obtained from the PLS-DA showing the most significant metabolites that contributed for the separation of <i>C. vulgaris</i> fed fish spleen samples from the control	109

5.7	The heatmap showing the concentration of the VIP metabolites in each of the spleen sample	110
5.8	The box plot showing the relative quantification of the VIP metabolites from spleen analysis	112
5.9	The PLS-DA (a) and PLS (b) model validation with 100 permutations for serum analysis	113
5.10	The PLS-DA (a) and PLS (b) model validation with 100 permutations for spleen analysis	114
5.11	Summary of the pathway analysis	115
5.12	Schematic diagram that summarized the metabolites that were altered in the serum and spleen of <i>C. vulgaris</i> treated groups, possible pathways and aspect of metabolism involved	116
5.13	2D-NMR verification of VIP metabolites with higher impact factors in the pathway analysis	123
6.1	Overall schematic diagram of the chapter	128
6.2	Tilapia infected by <i>S. agalactiae</i> showing	130
6.3	Plot of bacterial concentration and mortality for determination of LC <sub>50</sub>	131
6.4	Survival percentage rate of challenged experimental fish with <i>S. agalactiae</i> concentration of 10 <sup>8</sup>	132
6.5	PCA score plot of the zero-day fish (0-D) and the control fish (CF) showing minimal effect of environment on the experimental fish	135
6.6	OPLS-DA score plot of <i>C. vulgaris</i> (CV) fish and the control fish (CF) showing their variability by PC1	136
6.7	A; OPLS-DA score plot of control fish challenged (CFC) and the control fish (CF) showing their variability by PC1, B; OPLS-DA S-plot showing metabolites which are greatly affected by the bacterial challenge and which contributed for the separation of CFC and CF by PC1	139
6.8	A; OPLS-DA score plot of <i>C. vulgaris</i> (CV) fed fish and the <i>C. vulgaris</i> challenged fish (CVC) showing their variability by PC1, B; OPLS-DA S-plot showing regulated metabolites which contributed for the separation of CV and CVC by PC1	141
6.9	The PLS-DA; CV and CF	144

## LIST OF ABBREVIATIONS

<sup>1</sup> H-NMR	Proton Nuclear Magnetic Resonance Spectroscopy
d	Doublet
dd	Doublet of doublet
m	Multiplet
DAD	Diode Array Detector
ESI	Electrospray Ionisation
g	Gram
mg	Milligram
mL	Millilitre
HMBC	Heteronuclear Multiple bond Correlation
HSQC	Heteronuclear Single bond Correlation
HCA	Hierarchical Cluster Analysis
HPLC	High Performance Liquid Chromatography
Hz	Hertz
LC <sub>50</sub>	Lethal Concentration at 50 Percent
L	Litre
LC-MS	Liquid Chromatography-Mass Spectrometry
GC-MS	Gas Chromatography-Mass Spectrometry
m	Multiplet
<i>m/z</i>	Mass to charge ratio
MeOH	Methanol
Et	Ethanol
Ea	Ethyl acetate
Ch	Chloroform
Hex	Hexane
50% Et	50% ethanol
Aq	Aqueous

MVDA	Multivariate Data Analysis
°C	Degrees Celsius
PC	Principal Component
PCA	Principal Component analysis
PLS	Partial Least Squares
PLS-DA	Partial Least Squares-Discriminate Analysis
OPLSD-DA	Orthogonal PLS-DA
ppm	Part per million
s	Singlet
SIMCA	Soft Independent Modelling of Class Analogy
UV	Ultraviolet
UV/VIS	Ultraviolet/visible
VIP	Variable Importance in the Projection
δ	Chemical shift in ppm
µL	Microlitre
WHO	World Health Organisation
ANOVA	Analysis of Variance
CID	Collision Induced Dissociation
NaOD	Sodium Deuterium Oxide
D <sub>2</sub> O	Deuterium Oxide
CD <sub>3</sub> OD	Methanol- <i>d</i> <sub>4</sub>
KH <sub>2</sub> PO <sub>4</sub>	Potassium Dihydrogen Phosphate
K <sub>2</sub> HPO <sub>4</sub>	Dipotassium Hydrogen Phosphate
2D	Two Dimensional
HMDB	Human Metabolome Database
KEGG	Kyoto Encyclopedia of Genes and Genomes

# CHAPTER 1

## INTRODUCTION

### 1.1 Background

Algae are the organisms that possess chlorophyll(s), having thallus that does not differentiate into roots, stem or leaves. They can use the light energy and carbon dioxide for the photosynthetic biomass production with higher efficiency compared to plants. There are over 300,000 species of microalgae, of which around 30,000 of them have been documented. They live in complex natural habitats, making them able to adapt rapidly in different extreme conditions like variable salinity, temperature, nutrients and UV-irradiation (Tomaselli, 2004).

*Chlorella vulgaris* is a freshwater microalga, green color, spherical and single-celled, belonging to the family *Chlorellaceae* of the division *Chlorophyta*. It is currently used as a healthy food supplement of valuable contents and for medicinal purposes due to its carotenoids, chlorophylls and proteins content (Sharma et al., 2011). In addition, growth performance and total fish protein were both observed by using fish feed supplemented with *Chlorella* (Maliwat et al., 2016). It was also reported that *C. vulgaris* is a potential source of fatty acids due to its high lipid content (Varfolomeev & Wasserman, 2011).

Metabolomics is the most recent emerging ‘omics’ discipline that emphasizes more on the identity and quantity of the endogenous metabolites and measures the dynamic responses of the metabolome to various stimuli (Hounoum et al., 2015). This is because small variation in the body system results into great changes in the metabolite levels. Metabolome referred to the amplification of these changes, and is the most real reflection of biological status of the overall system (Booth et al., 2011). Metabolomics is related to metabolome, which in turn represents the small existing molecules of the cells of organisms. The approach is highly competent in the study and evaluation of changes in the small molecular metabolites composition of a biological system under various circumstances. Furthermore, globally, metabolomics is a well-accepted profiling tool for the detection of metabolites and metabolic pathways (Kaddurah-Daouk et al., 2008). Its additional value is in the biological regulation including the control and management of diseases and sheds light on medicine with the help of technological advancements, hence its rapid growth in biological and biomedical research areas. Many new ideas and insights provided by metabolomics-based researches on metabolites and their mechanism of action validated the platform to be further regarded as a leading platform for the study of diseases. Proton nuclear magnetic resonance ( $^1\text{H}$  NMR) is emerging as a leading analytical tool in metabolomics studies due to its large usage and the bulk number of compounds identified. Thus,  $^1\text{H}$  NMR-based metabolomics can be used as a valid approach to assess the correlation between identified metabolites of an animal model and its biological parameters (Cevallos-Cevallos et al., 2009).

## **1.2 Statement of the problem**

Tilapia is one of the most important cultured fish species worldwide, due to their exceptional fast growth rate and high tolerances towards various harsh environmental conditions (Zahran & Risha, 2014). Despite these important features of tilapia, various diseases find their way to attack and destroy them during culturing as a result of expansion and advancement of human activities, especially industrial. Most farmers revert to use antibiotics in fish disease treatment, but this practice is not completely a safe alternative. Increase in antimicrobial resistance keeps rising consequently leading to more fish mortality and pose threat to fish consumer's health. This is a major setback in aquaculture practices and requires immediate scientific attention to resolve the problem; it is believed that the introduction of microalgae as immunostimulants will replace other modalities used in disease mitigation in fish.

## **1.3 Justification of the study**

Although *C. vulgaris* is one of the most studied microalga worldwide, nevertheless no research has been conducted to identify the correlation between the chemical biomarkers responsible for its immunostimulant property in tilapia sp. using metabolomics approach. Hence this research project reports for the first time the metabolic signatures of immunostimulant effects of *C. vulgaris* in tilapia *O. niloticus* via metabolomics approach.

## **1.4 Research objectives**

The focus of the study is to obtain a deeper insight into the beneficial effects of the microalgae *C. vulgaris* as an immunostimulant for tilapia fish (*O. niloticus*). Towards realizing this goal, the study sets out to achieve the following objectives:

1. To comprehensively characterize the metabolome of *C. vulgaris* via metabolite profiling using NMR metabolomics, GCMS fatty acid analysis and LCMS/MS spectrometry.
2. To determine the biological and health effects of *C. vulgaris* on tilapia fish in a safety concentration study and evaluate the immunostimulant properties of *C. vulgaris* in the same model via immune and challenge assays.
3. To correlate the biological activity of *C. vulgaris* in tilapia to the metabolite's regulation via biomarker identification, and identify the biochemical pathways involved via metabolites association and pathway analysis.

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