



**PHENOTYPIC, GENOTYPIC AND PROTEOMIC TYPING OF INVASIVE
GROUP B *STREPTOCOCCUS* ISOLATED FROM HUMANS AND TILAPIA
(*Oreochromis spp. PISCES*) IN MALAYSIA**

By

ABDULRAHMAN MANSOOR MOHAMMED MUTHANNA

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

March 2023

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March 2023

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Streptococcus agalactiae, also called Group B *Streptococcus* (GBS), is a major cause of several infectious diseases in humans and fish. However, the likelihood of GBS transmission between different host species leading to a potential zoonotic problem is less well studied. This study aims to determine the phenotype, antimicrobial susceptibility, serotype, virulence and pili gene profiles, sequence type (ST) and proteomic profiles of GBS isolated from humans and cultured fish (tilapia) in Malaysia for comparison between both hosts for understanding its zoonotic and virulence potential. Considering the sporadic pattern of invasive GBS cases, particularly in humans, a total of 227 invasive GBS isolated from humans ($n = 113$) and tilapia ($n = 114$) were subjected to phenotyping, serotyping, antimicrobial susceptibility testing and detection of GBS virulence and pilus genes to allow comparison between two origins. Multilocus sequence typing (MLST), phylogenetic analysis and proteomic analysis were also performed for selected GBS isolates. All GBS isolated from humans and fish showed grey to white colonies with β haemolysis on blood agar, pink colonies on CHROMAgar and GBS brilliance agar, a positive CAMP test, a catalase-negative, and a positive GBS latex agglutination test. The most common serotype among human GBS strains was V (23%), followed by Ia (19.5%), II (18.6%), VI (15.9%), III (10.6%), VII (4.4%), Ib and IV, (3.5% each) and IX (0.9%), while all the fish isolates have serotype III (100%). Human isolates had a higher frequency of resistance to erythromycin (15%), azithromycin (13.3%), clindamycin (8.8%), chloramphenicol (2.7%) and ofloxacin (0.9%). However, the tetracycline resistance rate was higher in fish (98.5%) than in human isolates (75.3%). In the evaluation of the virulence and pili gene profiles, there were significant differences between the human and fish isolates in the genes *rib*, *scpB*, *lmb*, *bac*, *PI -2a* and *PI -2b*, but there were similarities in the genes *cfb*, *cylE*, *hylB*, *fbsA*, *fbsB*, *spb1*, *bca* and *PI -1*. Nineteen different sequence types (ST) were found among human isolates, where ST1 was the most predominant; interestingly, three novel sequence types, ST1668, ST1669 and ST1670, were also found. In addition, an unusual finding of the fish-adapted serotype III/ST283 was found in human isolates. On the other

hand, all the randomly selected 15 fish isolates were ST283. In the phylogenetic analysis, there is a genetic linkage between both human and fish isolates sharing a similar lineage of CC283 in clade I. A total of 1405 proteins were identified by LCMS/MS in five human GBS and three fish strains belonging to ST283, ST1668, ST1669 and ST1670. A total of 1162 proteins were identified in the core proteome (with 82.5% similarity), 140 proteins were present in the human isolates, and 107 proteins were identified in the fish isolates. Proteins involved in stress response and gene expression regulation, metabolism, transcription and pathogenicity were also detected, reflecting the adaptability of GBS strains. This study suggests that human and fish GBS have similar phenotypic characteristics but differ in terms of virulence and pili gene profiles, antimicrobial susceptibility, serotype and sequence type. In addition, the proteomes of human and fish GBS isolates were found to be highly similar in this study.

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

**FENOTIP, GENOTIP DAN JENIS PROTEOMIK TERHADAP KUMPULAN
INVASIF *STREPTOCOCCUS* GROUP B YANG DIASINGKAN DARIPADA
MANUSIA DAN TILAPIA (*Oreochromis spp.* PISCES) DI MALAYSIA**

Oleh

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Streptococcus agalactiae, juga dikenali sebagai *Streptococcus* Kumpulan B (GBS), adalah merupakan penyebab utama kepada kebanyakkan penyakit berjangkit terhadap manusia dan ikan. Walau bagaimanapun, penghantaran GBS di antara spesies perumah berbeza, yang berkemungkinan telah menyebabkan masalah kepada potensi zoonosis kurang dikaji dengan baik. Tujuan kajian ini adalah untuk menentukan kerentanan antimikrob, serotype, virulens dan profil gen pili, jenis jujukan (ST) dan profil proteomik GBS yang diasingkan daripada manusia dan ikan ternakan (tilapia) di Malaysia bagi tujuan perbandangan di antara kedua-dua pencilan dalam memahami potensi zoonosis dan virulennya. Memandangkan corak kes terhadap GBS invasif yang sporadik, terutamanya pada manusia, sejumlah 227 isolat GBS invasif daripada manusia ($n = 113$) dan tilapia ($n = 114$) telah tertakluk kepada fenotaip, serotipe, ujian kerentanan antimikrob dan pengesan gen GBS virulensi dan pilus bagi tujuan perbandangan di antara kedua-dua asal usul. Penaipan jujukan multilocus (MLST), analisis filogenetik dan analisis proteomik juga telah dilakukan untuk pencilan GBS terpilih. Kesemua GBS yang diasingkan daripada manusia dan ikan telah menunjukkan koloni kelabu hingga putih dengan hemolis β pada agar darah, koloni merah jambu pada agar CHROMAgar dan agar GBS brilliance, ujian CAMP positif, catalase-negatif, dan ujian aglutinasi lateks GBS positif. Serotaip yang paling biasa di kalangan strain GBS manusia adalah V (23%), diikuti oleh Ia (19.5%), II (18.6%), VI (15.9%), III (10.6%), VII (4.4%), Ib dan IV, (3.5% setiap satu) dan IX (0.9%), manakala kesemua pencilan ikan mempunyai serotype III (100%). Pecilan manusia mempunyai frekuensi rintangan yang lebih tinggi terhadap eritromisin (15%), azitromisin (13.3%), klindamisin (8.8%), kloramfenikol (2.7%) dan ofloksasin (0.9%). Walau bagaimanapun, kadar rintangan tetrasiklin lebih tinggi di kalangan ikan (98.5%) berbanding di kalangan pencilan manusia (75.3%). Dalam penilaian virulensi dan profil gen pili, terdapat perbezaan yang ketara antara pengasingan manusia dan ikan dalam gen rusuk, *scpB*, *lmb*, *bac*, PI -2a dan PI -2b, tetapi terdapat persamaan dalam gen *cfb*, *cylE*, *hytB*, *fbsA*, *fbsB*, *spb1*, *bca* dan PI -1. Sembilan belas jenis jujukan (ST) berbeza ditemui di kalangan pencilan manusia, dimana ST1 adalah

yang paling dominan; menariknya, tiga jenis urutan novel, ST1668, ST1669 dan ST1670 telah turut ditemui. Di samping itu, penemuan luar biasa serotype III/ST283 yang disesuaikan dengan ikan telah ditemui dalam penciran manusia. Sebaliknya, kesemua 15 penciran ikan yang dipilih secara rawak adalah ST283. Dalam analisis filogenetik, terdapat kaitan genetik antara kedua-dua penciran manusia dan ikan yang berkongsi garis keturunan CC283 yang serupa dalam klad I. Sebanyak 1405 protein telah dikenal pasti oleh LCMS/MS dalam lima GBS manusia dan tiga strain ikan iaitu ST283, ST1668, ST1669 dan ST1670. Sejumlah 1162 protein telah dikenal pasti dalam proteom teras (dengan 82.5% persamaan), 140 protein terdapat dalam penciran manusia dan 107 protein telah dikenal pasti dalam penciran ikan. Protein yang terlibat dalam tindak balas tekanan dan peraturan ekspresi gen, metabolisme, transkripsi dan patogenik turut dikesan, mencerminkan kebolehsuaian strain GBS. Kajian ini mencadangkan bahawa GBS manusia dan ikan mempunyai ciri-ciri fenotip yang serupa tetapi berbeza dari segi profil gen virulens dan gen pili, kerentanan antimikrob, serotype dan jenis jujukan. Di samping itu, proteome GBS penciran manusia dan ikan di dapati sangat serupa dalam kajian ini.

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LIST OF ABBREVIATIONS

AMP	Ampicillin
AMR	Antimicrobial Resistance
AST	Antibiotic Susceptibility Test
ATCC	American Type Culture Collection
ATCC	American Type Culture Collection
AZM	Azithromycin
β H/C	β -hemolysin/Cytolysin
<i>bac</i>	Gene Encoding β -subunit of C Protein
<i>bca</i>	Gene Encoding α -subunit of C Protein
BGG	bovine Gamma Globulin
BHI	Brain Heart Infusion
BLAST	Basic Local Alignment Search Tool
BSA	Bovine Serum Albumin
C	Chloramphenicol
CAMP	Christie–Atkins–Munch–Petersen
CC	Clonal Complexes
CDC	Centers for Control Disease
<i>cfb</i>	Gene Encoding CAMP Factor
CFU	Colony-forming Unit
CLSI	Clinical and Laboratory Standards Institutes
CPS	capsular polysaccharide
CRO	Ceftriaxone
CSF	Cerebrospinal Fluid
CspA	Cell Surface-associated Protein

CTX	Cefotaxime
<i>cylE</i>	Gene encoding β -hemolysin/cytolysin toxin
DA	Clindamycin
DNA	Deoxyribonucleic Acid
DTT	Dithiothreitol
E	Erythromycin
EOD	Early Onset Disease
<i>fbsA</i>	Fibrinogen-binding Proteins A
<i>fbsB</i>	Fibrinogen-binding Proteins B
FDR	False Discovery Rate
FEP	Cefepime
GBS	Group B <i>streptococcus</i>
HM	Hospital Melaka
HS	Hospital Serdang
HSA	Hospital Sultanah Aminah
HSB	Hospital Sungai Buloh
HTJ	Hospital Tuanku Ja'afar
<i>hylB</i>	Hyaluronidase
IAP	Intrapartum Antibiotic Prophylaxis
IMR	IMR Institute for Medical Research
LC MS/MS	Liquid Chromatography–Mass Spectrometry
Lmb	laminin-binding Protein
LOD	Late Onset Disease
LZD	Linezolid
MDR	Multidrug-Resistant
MIC	Minimal Inhibitory Concentrations

MLST	Multilocus Sequence Typing
MS	Mass spectrometry
NC	Negative Control
NT	Non-typeable
OFX	Ofloxacin
P	Penicillin
PBS	Phosphate-buffered saline
PC	Positive Control
PFGE	Pulsed-Field Gel Electrophoresis
<i>rib</i>	Gene encoding Rib Protein
RNA	Ribonucleic Acid
S	Susceptible
SBA	Sheep Blood Agar
<i>scpB</i>	Gene encoding C5a Peptidase
SDS-PAGE	Sodium Dodecyl Sulphate–Polyacrylamide Gel Electrophoresis
ST	Sequence Type
TE	Tetracycline
TG-SDS	Tris-Glycine-Sodium Dodecyl Sulfate
TPP	Trans-Proteomic Pipeline
UKMMC	Universiti Kebangsaan Malaysia Medical Centre
UPM	Universiti Putra Malaysia
V	Vancomycin
WHO	World Health Organization

CHAPTER 1

INTRODUCTION

1.1 Background of the Study

Streptococcus agalactiae (also known as Group B *Streptococcus* or GBS) belongs to group B of the Rebecca Lancefield classification of β -haemolytic streptococci. GBS is an opportunistic commensal Gram-positive diplococci bacterium that occurs in 17-30% of healthy human adults without symptomatic disease worldwide (Shabayek & Spellerberg, 2018). Nonetheless, during pregnancy, GBS colonization in the genitourinary tract can be clinically significant as it is associated with certain illnesses such as urinary tract infection, chorioamnionitis, endometritis in the mother, and meningitis and septicemia in the neonate when it is transmitted vertically from the mother during labour. Moreover, GBS can induce labour and lead to premature delivery and miscarriage (Watkins et al., 2019). GBS contributes significantly to perinatal mortality, including stillbirths, with an estimated 147,000 fatal cases (0.41 cases per 1000 live births) annually worldwide and 127,000 fatal cases (0.32 cases per 1000 live births) in Asia (Madrid et al., 2017; Hasperhoven et al., 2020). An investigation in a teaching hospital in Malaysia reported that GBS vaginal rate was 9.7% among the pregnant women (Eskandarian et al., 2013). Recently, the incidence of invasive GBS infection has increased among immunocompromised individuals and those with underlying medical conditions such as diabetes, heart disease, malignancies, and ageing. GBS infections may result from hospital-acquired infection or, more likely, from preexisting colonization of the skin or mucous membrane, which causes numerous and varied clinical manifestations, including tissue and skin infections, septicemia, meningitis and others (Barshak, 2019).

Furthermore, GBS is an important pathogenic bacterium causing infections in cultured fishes worldwide, including economically important cultured fishes such as tilapia (*Oreochromis* species), channel catfish (*Ictalurus punctatus*) and rainbow trout (*Oncorhynchus mykiss*) (Zamri-Saad et al., 2014). The disease is commonly affecting various tilapia-producing countries in Southeast Asia, including Malaysia, Indonesia, Vietnam and Thailand, where the mortality can be as high as 70% that leading to significant economic losses (approximately 250 million USD annually) and posing a threat to the aquaculture industry's development in this region (Anshary et al., 2014; Kayansamruaj et al., 2019; Syuhada et al., 2020). Streptococcosis manifests in clinical manifestations in fish such as exophthalmia, erratic swimming, pale gills, the opaque cornea, external hemorrhages, enlarged spleens, ascites of the abdominal cavity, and yellowed liver (Syuhada et al., 2020).

To elucidate the GBS population structure in relation to disease outbreaks in humans and fish, several phenotypic and genotypic techniques have been developed (Shabayek & Spellerberg, 2018). GBS virulence is determined by the capsular polysaccharide (CPS), which promotes adherence to epithelial surfaces of the host and play role in the escape

from host defenses that determined by *cps* gene type. GBS can be subtyped into 10 different capsular serotypes, including Ia, Ib, and II to IX, and each serotype possesses a significant virulent capability (Imperi et al., 2010). Serotypes Ia, II, III and V have been characterized as the major strains associated with invasive disease in pregnant women, neonates and non-pregnant adults, while serotypes Ia, Ib and III are commonly associated with fish infection (Eskandarian et al., 2015; Suhaimi et al., 2017; Shabayek & Spellerberg, 2018; Syuhada et al., 2020) However, the distribution and predominance of certain serotypes varies over time and differ with a geographical area (Imperi et al., 2010). As a result of information about capsular serotypes, disease and vaccine-related surveillance can be conducted in human and fish isolates (Imperi et al., 2010).

Additionally, GBS, provided with a comprehensive virulence gene profiles, are determined by genotypic characterization based on virulence regiment, including capsular polysaccharides, surface proteins, toxins and pili that are found in human and fish isolates, which can play a role in immune evasion, adhesion and invade the host cells (Shabayek & Spellerberg, 2018; Bobadilla et al., 2021). The major GBS adhesins that facilitate adherence and contact between the bacterial cell and the host cells include the fibrinogen-binding proteins (Fbs), the laminin-binding protein (Lmb), the group B streptococcal C5a peptidase (ScpB) and pili, while β -hemolysin/cytolysin (β H/C), hyaluronidase (HylB), Rib protein (Rib), (α and β -subunit of C protein) and Christie–Atkins–Munch–Petersen (CAMP) plays a role in invasion the host cells, evasion from the immune system and transmission to invasive infections (Shabayek & Spellerberg, 2018). A variation of genetic profiles has been observed between human and fish GBS (Springman et al., 2009; Chen, 2019).

Multilocus sequence typing (MLST) is a genotypic method that provides GBS strains' genetic characterization of both the sequence type (ST) and the clonal complex (CC) based on a nucleotide sequence of seven housekeeping genes (Jones et al., 2003). MLST data revealed that certain GBS strains of certain clonal complexes are more likely to cause invasive disease, whereas others harbour primarily colonizing strains (Kayansamruaj et al., 2019). MLST revealed to GBS consists of at least 2,105 sequence types (ST) worldwide (Jones et al., 2003; Jolley et al., 2018). Most human GBS strains cluster into four clonal complexes (CCs), including CC1, CC17, CC19, and CC23, which are recognized as human-adapted lineages, while fish GBS strains cluster into CC7 and CC283 (Ezhumalai et al., 2020; Syuhada et al., 2020).

In 2015, a rare outbreak of invasive disease due to the GBS serotype III, ST283, occurred in Singapore due to consuming contaminated raw fish salad (yusheng) typically made from two freshwater fish species. The outbreak has infected 238 people and caused septic arthritis, meningitis, and septicemia among a very different group of non-pregnant adults. This was the first documented case of invasive GBS associated with foodborne transmission (Chau et al., 2017).

Penicillin or ampicillin is the first line of antibiotics recommended to treat GBS infection by international and local guidelines, where GBS isolates remain susceptible primarily to penicillin and ampicillin, as observed in some studies in the local setting (Eskandarian

et al., 2015; Suhaimi et al., 2017; Chen, 2019). Erythromycin or clindamycin are the alternatives if the patient is allergic to penicillin. Consequently, the increasing use of these drugs, consumed by around 20% of all GBS carriers, resulted in elevated clindamycin and erythromycin resistance rates. In addition, GBS is sensitive to cephalosporins, rifampin, vancomycin and resistant to tetracycline (Eskandarian et al., 2015; Suhaimi et al., 2017). In Malaysia, according to the Institute for Medical Research (IMR), the resistance of GBS isolates to erythromycin was 6.8% and clindamycin resistance (7.2%) is the same as in 2016 compared to 2015. The resistance to tetracycline has markedly increased to 70%, and the penicillin resistance rate was 0.2% among GBS isolates (Ministry of Health Malaysia, 2019). Among fish GBS isolates, the resistance rate to erythromycin, clindamycin, and azithromycin was less than in human isolates, while the resistance of tetracycline was around 85% (Nhung, et al., 2016).

Proteomics provides a systems perspective, viewing the protein synthesis, abundance, structure and post-translational modifications, as well as physical or functional interaction partners, to map the proteome all at once (Nesvizhskii, 2014). Proteomics is used for prevention, diagnosis and treatment of disease and precision medicine, creating treatment groups based on GBS proteomics profile or even designing drugs to act on a specific biomarker (Nesvizhskii, 2014).

Zoonoses comprise a large percentage of all newly identified infectious diseases as well as existing infectious diseases. Cross-sectoral collaboration is key to understanding and managing public health risks at the human-animal-environment interface and improving global health security (World Health Organization, 2019). The Malaysian Ministry of Health cooperates with WHO in fostering cross-sectoral collaboration at the human-animal-environment interface among the different relevant sectors at international, regional, and national levels and in developing capacity and promoting practical, evidence-based, and cost-effective tools and mechanisms for zoonoses prevention, surveillance and detection, reporting, epidemiological and laboratory investigation, risk assessment, and control, and assisting countries in their implementation to prevent and reduce risks and manage outbreaks (Ministry of Health Malaysia, 2016).

1.2 Problem Statement

GBS has recently been associated with invasive infections in humans and fish (Cho et al., 2019; Chen et al., 2019). Globally, GBS infections are a growing problem in older adults, pregnant women and those with chronic medical conditions, particularly immunocompromised patients such as diabetes mellitus (Shabayek & Spellerberg, 2018). In Malaysia, literary research on GBS infection in humans has identified a low number of articles since the 1980s (Eskandarian et al., 2015; Suhaimi et al., 2017). Available studies described GBS infection and associated risk factors only at a specific location and point in time (Eskandarian et al., 2013; Khalid et al., 2018). This may not represent the real incidence of GBS infection in Malaysia, where actual cases could not have been reported. Moreover, the GBS infection rate increased among farmed fish, including tilapia species, globally and in Southeast Asian countries, including Malaysia,

causing significant economic losses to the aquaculture industry (Amal & Zamri-Saad, 2011; Syuhada et al., 2020).

GBS has long been associated with transmission from mother to baby (human to human) rather than fish to human (or vice versa), although fish may be the reservoir for GBS as well, where GBS strains that cause disease in humans are usually biochemically, phenotypically, genetically or serologically different than those causing disease in animals (Botelho et al., 2018). However, the Singaporean GBS fish-borne outbreak has sparked its zoonotic potential. The Singapore GBS outbreak was associated with sequence type (ST) 283 and contaminated raw fish salad consumption. This outbreak was unique because it affected non-pregnant and younger adults with fewer comorbidities, suggesting more prominent virulence (Chau et al., 2017). Another study of genome analysis involving GBS isolates collected from six Southeast Asian countries hypothesized that the ST283 human infections could be possibly acquired from fish (Barkham et al., 2019). This is considering that GBS ST283 and its variants were primarily found in invasive GBS infection in fish. GBS ST283 has been rarely reported in human infection but is commonly found in diseased fish. This creates a new perspective on GBS potential as a newly emerging zoonotic threat rather than being confined to humans only (Chau et al., 2017).

GBS has been studied in multiple contexts, including human health, veterinary medicine, and agriculture, to determine the antimicrobial susceptibility pattern, serotypes, virulence genes and genotypes in Malaysia. However, GBS transmission from fish to humans is unknown. Beyond the proximal questions of how GBS colonizes and causes specific diseases in specific hosts, GBS is an intriguing case study for the larger questions of how a broad host range at the species level is maintained despite evidence of variation at the subspecies level. These larger evolutionary questions are again made more urgent by convincing evidence of ongoing adaptation and emergence of pathogenicity and resistance in GBS. A study suggested that genetic linkage is not a prerequisite for GBS to cross the host-specific barrier (Pereira et al., 2010). However, due to limited studies on GBS, wide surveillance is needed to understand the genetic linkage and the crossing of the host-specific barrier of GBS from different origins.

Current studies realized that the genome alone was not always enough to give useful information as genes can be translated into a myriad of proteins depending on the environment the organism experiences, among other factors (Tavares et al., 2018; Tavares et al., 2019; Abril et al., 2020;). Proteomic studies make it possible to identify and quantify sets of proteins that are expressed by microorganisms under specific culture conditions (Zhang et al., 2014). Proteomics can be used to compare the qualitative and quantitative proteome across strains, allowing interpretation of bacterial physiology and promoting knowledge of the genetic variation of each isolate (Tavares et al., 2019). Previous studies have been conducted on the expression of proteins using GBS strains, with a particular emphasis on the analysis of surface proteins (Hughes et al., 2002; Doro et al., 2009; Liu et al., 2013; Li et al., 2016), secretory proteins (Papasergi et al., 2013; Li et al., 2016) and the comparative proteome (Li et al., 2014). There is still a lack of studies that compare the whole proteomic properties of GBS involving different origins, particular in human and fish settings. Thus, a proteomic study of GBS strains that infect

humans and fish would permit the analysis of protein variability within the strains belonging to the genotypes among humans and fish, increase scientific knowledge about the adaptation and pathogenesis of the GBS infections in humans and fish, and insight on the potential interspecies transmission between human and fish hosts. Additionally, this approach could identify antigenic proteins that can be used as targets for vaccine development.

In view of the increasing incidence of treatment failure for GBS infection by antimicrobial therapy due to its concurrent emerging resistance, an understanding of the phenotypes and genotypes of GBS from human and fish settings is warranted. Furthermore, antimicrobial resistance leads to increased morbidity and mortality since resistance increases the risk of inappropriate therapy (Andersson et al., 2016). The risk is that the patients who do not receive appropriate therapy will have a longer period of disease or fatal effect; therefore, morbidity and transmission of the microorganism will increase due to the patients remaining infectious for an extended period (CDC, 2019). Also, the increasing trend of antimicrobial resistance is a serious challenge in countries at all economic levels (Ventola, 2015).

The findings of this study will improve health protection in Malaysia through productive partnerships for the preparedness, planning, prevention, prompt detection, characterization, and the containment and control of emerging diseases and to provide risk assessment data to support outbreak control and prevention measures. Comparative proteomics of GBS for understanding its zoonotic and virulent potential can expand knowledge on the genetic for future manipulation. Data will serve as reference for comparative analysis with other studies worldwide on the genetic properties and population. The shared knowledge will be useful for prospective risk, diagnostic and prevention strategy.

1.3 Research Objectives

1.3.1 General Objective

This study aims to compare the phenotype, antimicrobial susceptibility patterns, serotype, virulence and pili gene profiles, sequence type (ST) and proteomic of GBS isolated from humans and tilapia fish in Malaysia.

1.3.2 Specific Objectives

- a. To determine the antimicrobial susceptibility patterns of human and fish GBS isolates.
- b. To determine the serotypes distribution of human and fish GBS isolates.

- c. To determine the distribution of the virulence genes (*cfb*, *cylE*, *lmb*, *scpB*, *hybL*, *rib*, *fbsA*, *fbsB*, *spbI*, *bca* and *bac*) and pili genes (PI-1, PI-2a and PI-2b) of human and fish GBS isolates.
- d. To determine the sequence type (ST) and clonal complex (CC) of selected human and fish GBS isolates using the MLST technique.
- e. To describe and compare the proteomic profiles of selected representative human and fish GBS isolates using the LCMS/MS technique.

1.4 Research Hypothesis

There are variations with respect to phenotype, antimicrobial susceptibility pattern, serotype distribution, virulence and pili genes distribution, genotypes and proteomic profiling between GBS isolated from humans and tilapia fish in Malaysia.

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