



**UNIVERSITI PUTRA MALAYSIA**

**CHARACTERIZATION OF ANTIBIOTIC SUSCEPTIBILITY AND HIGH  
LEVEL AMINOGLYCOSIDE RESISTANT GENES IN *Enterococcus  
faecalis* AND *Enterococcus faecium* CLINICAL ISOLATES**

**AYAN ADEN MOUSSA**

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By

**AYAN ADEN MOUSSA**

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

**May 2018**

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**DEDICATION**

*To my parents*



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

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LEVEL AMINOGLYCOSIDE RESISTANT GENES IN *Enterococcus  
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**AYAN ADEN MOUSSA**

**May 2018**

**Chairman : Azmiza Syawani Jasni, PhD**  
**Faculty : Medicine and Health Sciences**

*Enterococcus faecium* and *Enterococcus faecalis* are among the predominant species causing hospital-acquired infections, with high mortality and morbidity rates. Enterococci which exhibit high level aminoglycoside (HLAR) and vancomycin resistance (VRE) possess a significant problem in therapeutic treatment. These resistance strains are becoming more widespread in Europe, USA and Asia. Studies have shown that the different distributions of aminoglycoside modifying enzymes (AMEs) among HLAR are based on the geographical regions. In Malaysia, however, data on the prevalence of HLAR and the distribution of AMEs are still limited. Hence, the aims of this study were to determine the antibiotic susceptibility patterns of the clinical isolates *E. faecalis* and *E. faecium* and the distribution of HLAR genes among the resistant isolates. Seventy-five clinical enterococci isolates used in this study were originally obtained from a tertiary centre, in the year 2009 and 2010. These isolates were isolated from different sources including pus (50%), blood (32%), urine (11%) and other sources such as CSF and HVS (7%). Re-identification of these isolates was carried out using several methods including sub-culturing on selective medium and Gram staining, followed by confirmatory tests using a commercial biochemical profiling (API20 strep) and 16s rRNA PCR amplification. Antimicrobial susceptibility tests were performed using disc diffusion, E-test and broth microdilution methods. The antibiotics used were aminoglycosides (gentamicin, streptomycin, kanamycin, amikacin, tobramycin) and other antibiotics which are commonly

used in the hospital to treat enterococcal infections such as ampicillin, vancomycin, erythromycin, tetracycline, chloramphenicol and linezolid. Detection of HLAR genes was performed on resistance isolates using single PCR amplifications. Out of 25 (33.3%) isolates of *E. faecium*, 84% and 68% showed high level gentamicin resistance (HLGR) and high level streptomycin resistance (HLSR), respectively. Resistance against erythromycin and tetracycline were 100%, while ampicillin and chloramphenicol showed 84% and 32% resistance rates, respectively. None of the *E. faecium* isolates showed resistance towards vancomycin and linezolid. On the other hand, all 50 (66.7%) *E. faecalis* isolates were resistance to all aminoglycosides tested with the following percentages; amikacin (100%), kanamycin (90%), tobramycin (70%), HLGR (36%) and HLSR (46%). These isolates were also resistance to tetracycline (98%), erythromycin (96%), chloramphenicol (46%), ampicillin (24%), linezolid (8%), and vancomycin (4%). Interestingly, the *E. faecalis* isolates that were resistant to vancomycin were previously reported as susceptible. In this study, *E. faecium* exhibited higher resistance rates to all antibiotics except vancomycin and linezolid compared to *E. faecalis*. Additionally, 46% of *E. faecalis* showed MIC of streptomycin up to 1042 µg/mL while another 36% showed MIC of gentamicin equal to 512 µg/mL. The MIC of aminoglycosides determined in this study showed similar level as observed in other countries, despite the variation of the methods used. The presence of aminoglycoside modifying enzyme (AME) genes [*aac(6)-Ie-aph(2)-Ia*, *aph(2)-Ib*, *aph(2)-Ic*, *aph(2)-Id*, *aph(3)-IIIa*] were detected using PCR amplification. The results demonstrated that the HLGR gene, *aac(6)-Ie-aph(2)-Ia* and the HLSR gene, *aph(3)-IIIa* were detected in 32% and 40% of *E. faecalis* and *E. faecium* resistance isolates, respectively. The spread of these genes were responsible for high level resistance to gentamicin and streptomycin among enterococci isolated in this study. As HLAR genes are highly transferable to not only among the enterococci species but also among various bacterial species, continuous antibiotic surveillance in Malaysian hospitals is warranted in future and preventive measures can be implemented accordingly.

**Keywords:** High level aminoglycosides resistance, Enterococci

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

**PEMPROFILAN KERENTANAN ANTIBIOTIK DAN PENYEBARAN  
GEN KETAHANAN AMINOGLIKOSIDA TAHAP TINGGI DI  
KALANGAN *Enterococcus faecalis* DAN *Enterococcus faecium***

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*Enterococcus faecium* dan *Enterococcus faecalis* merupakan antara spesies utama yang menyebabkan infeksi dapatan hospital, dengan kadar kematian dan morbiditi yang tinggi. Enterococci yang rintang terhadap aminoglikosida (HLAR) dan vankomisin (VRE) tahap tinggi merupakan masalah yang signifikan di dalam rawatan terapeutik. Strain tersebut semakin meluas di Eropah, USA dan Asia. Kajian telah menunjukkan bahawa perbezaan penyebaran bagi enzim pengubahsuaian aminoglikosida (AMEs) di kalangan HLAR adalah berdasarkan kawasan geografi. Di Malaysia, walau bagaimanapun, data mengenai kelaziman HLAR dan penyebaran AME masih lagi terhad. Oleh itu, kajian ini bertujuan untuk menentukan pola kerintangan antibiotik bagi pencilan klinikal *E. faecalis* dan *E. faecium* dan penyebaran gen HLAR di kalangan pencilan yang rintang ini. Tujuh puluh lima pencilan enterococci klinikal yang digunakan di dalam kajian ini telah diperolehi daripada pusat tertier, pada tahun 2009 dan 2010. Pencilan tersebut telah dipencilkan daripada sumber yang berbeza termasuk nanah (50%), darah (32%), air kencing (11%) dan sumber lain seperti CSF dan HVS (7%). Pengenalpastian semula pencilan tersebut telah dijalankan menggunakan pelbagai kaedah termasuk sub-kultur ke atas medium selektif dan pewarnaan Gram, diikuti dengan ujian pengesahan menggunakan pemprofilan biokimia komersial (API20 strep) dan amplifikasi 16s RNA PCR. Ujian kerintangan antimikrobial telah dijalankan menggunakan difusi disk cakram kertas, Ujian-E dan kaedah mikrodilusi pencairan kaldu. Antibiotik yang digunakan ialah

aminoglikosida (gentamisin, streptomisin, kanamisin, amikasin, tobramisin) dan antibiotik lain yang biasanya digunakan di hospital bagi merawat infeksi enterococcal, seperti ampisilin, vankomisin, eritromisin, tetrasiklina, kloramfenikol dan linezolid. Pengesanan gen HLAR telah dijalankan ke atas pencilan yang rintang dengan menggunakan kaedah amplifikasi PCR tunggal. Daripada 25 (33.3%) pencilan *E. faecium*, 84% dan 68% masing-masing menunjukkan tahap ketahanan gentamisin (HLGR) dan ketahanan streptomisin (HLSR) tahap tinggi. Kerintangan terhadap eritromisin dan tetrasiklina ialah 100%, manakala ampisilin dan kloramfenikol, masing-masing menunjukkan 84% dan 32% kadar kerintangan. Tiada pencilan *E. faecium* menunjukkan kerintangan terhadap vankomisin dan linezolid. Di samping itu, kesemua 50 (66.7%) pencilan *E. faecalis* adalah rintang terhadap semua aminoglikosida yang diuji dengan peratusan berikut; amikasin (100%), kanamisin (90%), tobramisin (70%), HLGR (36%) dan HLSR (46%). Pencilan-pencilan tersebut juga rintang terhadap tetrasiklina (98%), eritromisin (96%), kloramfenikol (46%), ampisilin (24%), linezolid (8%), dan vankomisin (4%). Yang menariknya, pencilan *E. faecalis* yang rintang pada vankomisin sebelum ini telah dilaporkan sebagai rentan. Dalam kajian ini, *E. faecium* memperlihatkan kadar kerintangan yang tinggi terhadap semua antibiotik kecuali vankomisin dan linezolid berbanding dengan *E. faecalis*. Tambahan lagi, 46% *E. faecalis* menunjukkan MIC streptomisin sehingga 1042 µg/mL manakala selainnya 36% menunjukkan MIC gentamisin bersamaan 512 µg/mL. MIC aminoglikosida yang ditentukan dalam kajian ini menunjukkan tahap yang sama seperti yang didapati di negara lain, meskipun kepelbagaian kaedah yang digunakan. Kewujudan gen enzim pengubahsuaian aminoglikosida (AME) [*aac(6)-Ie-aph(2)-Ia*, *aph(2)-Ib*, *aph(2)-Ic*, *aph(2)-Id*, *aph(3)-IIIa*] telah dikesan dengan menggunakan amplifikasi PCR. Keputusan menunjukkan bahawa gen HLGR, *aac(6)-Ie-aph(2)-Ia* dan gen HLSR, *aph(3)-IIIa* telah dikesan, masing-masing di dalam 32% dan 40% pencilan *E. faecalis* dan *E. faecium* yang rintang. Penyebaran gen tersebut bertanggungjawab terhadap kerintangan tahap tinggi pada gentamisin dan streptomisin di kalangan pencilan enterococci di dalam kajian ini. Disebabkan gen HLAR berkeupayaan untuk pindah bukan sahaja di kalangan spesies enterococci yang sama tetapi juga pelbagai spesies bakteria yang berlainan, pengawasan antibiotik yang berterusan di hospital di Malaysia adalah perlu agar langkah-langkah pencegahan dapat dilaksanakan dengan sewajarnya.

**Kata kunci:** Tahap kerintangan, aminoglikosida tahap tinggi, Enterococci



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I certify that a Thesis Examination Committee has met on 16 May 2018 to conduct the final examination of Ayan Adan Moussa on his thesis entitled "Characterization of Antibiotic Susceptibility and High Level Aminoglycoside Resistant Genes in *Enterococcus faecalis* and *Enterococcus faecium* Clinical Isolates" in accordance with the Universities and University Colleges Act 1971 and the Constitution of the Universiti Putra Malaysia [P.U.(A) 106] 15 March 1998. The Committee recommends that the student be awarded the Master of Science.

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## LIST OF ABBREVIATIONS

WHO	World Health Organization
CDC	Centers for Disease Control and Prevention
IMR	Institute for Medical Research
AAC	Aminoglycoside N-acetyltransferase
AME	Aminoglycosides modifying enzyme
ANT	Aminoglycoside O-adenyltransferase
APH	Aminoglycoside O-Phosphotransferase
AST	Antibiotic susceptibility testing
ATCC	American type culture collection
BHI	Brain heart infusion agar
Blast	Basic local alignment search tool
CFU	Colony forming unit
CLSI	Clinical Laboratory Standard Institute
DNA	Deoxyribonucleic acid
HLAR	High level aminoglycoside resistance
ICU	Intensive care unit
MDR	Multi drug resistance
MHA	Muller Hinton agar
MIC	Minimal inhibitory concentration
NCBI	National Centre for Biology Information
PBP	Penicillin binding protein
PCR	Polymerase chain reaction
SPSS	Statistical Package for the Social Sciences
TBE	Mixture of tris base, boric acid, EDTA and water
VRE	Vancomycin resistant enterococci

# CHAPTER 1

## INTRODUCTION

### 1.1 Background

Enterococcal infections are significant hospital and community acquired infections due to multidrug resistance as widely reported (Arias & Murray, 2012). They have potential capacity to persist under various environmental conditions such as extreme temperature and osmolality (Garrido et al., 2014). These organisms are able to persist on various surfaces in hospitals and on hands of healthcare workers (Kuch et al., 2011). The Centre for Disease Control and Prevention (CDC) and prevention have estimated about 4 million patients in USA have hospital acquired infections (HAIs) annually (Weng et al., 2013). Recent report indicated that enterococci were placed as a second most common cause of hospital acquired infection after *Staphylococcus aureus* (Arias et al., 2010). In Malaysia between 2006 and 2007 about 2263 and 2647 patients respectively, were reported with HAIs which were due to enterococcal infections (Weng et al., 2013).

Enterococci are Gram positive bacteria which are found mostly in the gastrointestinal tract as normal flora (McBride et al., 2007). Presently, 54 various species have been described (O'Driscoll & Crank, 2015). The enterococci infection which include *Enterococcus faecium* and *Enterococcus faecalis* are predominantly associated with human diseases such as urinary tract infection, bacteremia, endocarditis, wound infections such as surgical burns, intra-abdominal abscess, septicemia, pelvic infection, meningitis as well as skin and soft tissue infections that result in high morbidity and mortality (Wang et al., 2013; Vu & Carvalho 2011). It is estimated that about 60% of enterococcal infections are associated with *E. faecalis*. However, infections due to *E. faecium* have risen over the last few decades in Europe, USA as well as Asia. This leads to a growing burden of enterococcal infections in general, and to a decreased ratio of *E. faecalis* to *E. faecium* infections (down to 60:40). Although *E. faecalis* remains generally less resistant to antibiotics than *E. faecium*, antimicrobial resistance in the former poses an increasing challenge to therapy as earlier reported (Kuch et al., 2011).

Enterococci are able to withstand harsh environmental conditions and acquire antibiotic resistant determinants. Enterococci are subject to horizontal gene transfer (HGT) elements, a characteristic which empowers bacterial organisms to develop rapidly through rapid exchange and distribution of beneficial trait-

encoding components, including antibiotic resistance genes (Fisher & Phillips, 2009).

Recently, several resistance determinants were reported to lead to the development of resistance to the seven groups of antibiotics by enterococci. Other determinants are encoded genes substances such as insertion sequence, intergrons, transposon and plasmids (Li et al., 2015). Horizontal gene transfer has been reported to be the main route through which 25% of genomic determinants are acquired by the enterococcus species (García-Solache et al., 2016). According to Patel et al (2008), enterococci are a normal microbial flora of the gut which is responsible for the spread of antibiotic resistant determinants. However, management of infection due to *E. faecium* today is highly challenging to the clinician due to multidrug resistance (MDR) which is currently on the increase in the population (Miller et al., 2014). Presently, enterococci are one of the leading etiologies of HAIs which are reported by National Healthcare Safety Network from CDC.

Management of enterococcal infections involves the actual synergistic effect of aminoglycosides and cell wall active antibiotics such as glycopeptides (vancomycin) or beta-lactam (ampicillin). To date, enterococci have exhibited multidrug-resistance (MDR) with high level of aminoglycoside resistance (HLAR) and vancomycin resistance (VRE). This has caused significant problem in clinical anti-infective therapy (Lebreton et al., 2016; Li et al., 2015). The strains of enterococci are becoming more widely spread in Europe, USA and Asia (Lebreton et al., 2016). Several studies have documented different distribution of aminoglycoside modifying enzymes (AMEs) and encoding genes differently based on the geographical regions (Zarrilli et al., 2005; Padmasini et al. 2014; Udo et al., 2004). In Malaysia, the data regarding the prevalence of HLAR and the distribution of AMEs are still limited. Hence, this study is aimed to determine the distribution of AMEs genes among enterococci isolates from clinical sample.

## 1.2 Problem statement

The Centre for Disease Control and Prevention (CDC, 2014) has reported that approximately 4 million hospitalized patients had nosocomial infections which are caused by antimicrobial resistance organisms. Among the pathogens, enterococci have been reported as the second most common cause of hospital acquired infections due to their wide-range of antimicrobial resistance and synergistic effects with beta-lactams, glycopeptides and aminoglycosides, which are currently being used in clinical practices.

Enterococci are inherently resistant to aminoglycosides due to aminoglycoside modified enzymes. Nevertheless, the types and distribution of resistance genes are different and geographically dependent. In Malaysia, data on the prevalence of HLAR and distributions of the resistance genes are still limited.

### 1.3 Objectives

#### General Objective

The aims of this study are to determine the antibiotic susceptibility patterns of the clinical isolates *Enterococcus faecalis* and *Enterococcus faecium* and the distribution of HLAR genes among the resistant enterococci isolates.

#### Specific Objectives

1. To re-identify *E. faecalis* and *E. faecium* using phenotypic and genotypic approaches.
2. To determine the antibiotic susceptibility profiles of *E. faecalis* and *E. faecium* by using disc diffusion.
3. To determine the minimum inhibitory concentrations of the resistant enterococci isolates using microdilution method.
4. To determine the distribution of aminoglycoside resistance encoding genes in the resistance enterococci isolates using molecular biology approaches.

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