

Enterococci: Emerging Drug Resistant Bacteria In Hospital Acquired Infections At Hospital Kuala Lumpur, Malaysia

R Ibrahim, M Mohamad, M Rahman

Citation

R Ibrahim, M Mohamad, M Rahman. *Enterococci: Emerging Drug Resistant Bacteria In Hospital Acquired Infections At Hospital Kuala Lumpur, Malaysia*. The Internet Journal of Microbiology. 2010 Volume 9 Number 2.

Abstract

Enterococci are the most common pathogens in hospital acquired infections. Some of them are resistant to Vancomycin (VRE) and some are susceptible to Vancomycin (VSE). The present study was carried out to identify enterococci from clinical cases and to illustrate their clinical features and drug resistance characteristics. Antibiotics susceptibility of the identified bacteria was determined by disk diffusion method and E-test. Drug resistance properties were evaluated against ampicillin, gentamicin, vancomycin, teicoplanin and linezolid. Relating to clinical features, 244 cases of enterococci infected patients were identified at hospital Kuala Lumpur (HKL) Malaysia based on clinical information from the hospital. Of the patients 21% had history of urinary tract infections, 17.2% end stage renal disease, 12.2% sepsis, 8.4% malignancy, 12.2% had head injury and neurological problems, 4.2% diabetes mellitus and other clinical manifestations. In case of Vancomycin resistant enterococci infection, the clinical features of the patients were: end stage renal failure 3/6 (50%) and others with diabetes mellitus, interstitial lung disease and nephrotic syndrome. The patients of the enterococci infections were more prevalent in nephrology-urology unit (39%) and medical wards (including ICU, 23%). The findings would serve as an alert to the clinicians of the emergence of infections by enterococci and encourage implementation of appropriate infection control measures in order to curb further rise in prevalence.

INTRODUCTION

Enterococci normally present in the human intestines and in the female genital tract and are often found in the environment. Recent National Nosocomial Infections Surveillance¹ reveals that these enterococci remain in the top 3 most common pathogens that cause nosocomial infections. These are: urinary tract infections, bloodstream infections, and wound infections in hospitalized patients. Enterococci infections typically occur in very ill debilitated patients who have been exposed to broad-spectrum antibiotics. According to NNIS² data from January 2003 through December 2003, more than 28% of enterococci isolates were found to be associated infections in intensive care unit (ICU) of 300 participating hospitals.

The acquisition of vancomycin resistance by enterococci has seriously affects treatment and infection control program which leaves clinicians treating VRE infections with limited therapeutic options (Fraser, 2010)

NNIS² reported that more than 25% of health care-associated enterococcal infections were associated with organisms resistant to vancomycin. In Malaysia 2006, a confirmed case of vancomycin resistant Enterococci isolated from blood

culture of a young woman with chronic renal failure was first reported in Hospital Kuala Lumpur (HKL).³ However, later on, no systematic study was undertaken to determine the prevalence of enterococci infections from the hospitalized patients in Malaysia. Therefore, the present study was undertaken to determine the prevalence of enterococci infections in hospitalized patients and determination of their clinical features and drug resistance nature.

MATERIALS AND METHODS

STUDY AREA

The study was carried out during May 2007 to April 2008 at Hospital Kuala Lumpur (HKL), Malaysia. The hospital consists of 3000 beds and 90 wards and provides services and acts as a reference centre for the hospitals of other states, in Malaysia.

STUDY POPULATION AND SAMPLE COLLECTION

A total number of 244 samples obtained from the patients of different infections during the period. The samples included blood, urine, pus, tissue, body fluids and swabs from wound and placenta. The samples were sent to the Microbiology

Laboratory, Department of Medical Microbiology and Immunology, Faculty of Medicine, University Kebangsaan Malaysia for identification and characterization.

INFORMATION ON CLINICAL DATA

Information on patient's profiles :age, diagnosis, risk factors such as duration of hospitalization (prolonged >2 weeks), catheter use, usage of antibiotics like cephalosporin, carbapenem, vancomycin, recurrent admission and others such as malignancy, use of steroids were obtained from their medical records.

IDENTIFICATION OF ENTEROCOCCUS SPP

Enterococcal genus identification was based on Gram staining that showed gram positive cocci in pairs or short chains, growth and blackening of bile-esculin agar after overnight incubation , growth in the presence of 6.5% NaCl, absence of catalase (catalase negativity) and presence of pyrrolidonyl arylamidase (PYR). Streptococcal group antigens were also detected using group D antisera (Slidex Strepto-Kit; Bio Merieux, France). API 20Strep (BioMerieux, France) was used for species identification.

ANTIBIOTIC SUSCEPTIBILITY TEST

Antibiogram of the isolates was determined by disk diffusion method, testing for vancomycin (30µg), teicoplanin (30µg), ampicillin (10µg), high concentration of gentamicin (120µg) and linezolid (30µg). The tests were performed using the methodology recommended by the Clinical and Laboratory Standards Institute ⁴

DISK DIFFUSION METHOD

Susceptibility test of enterococci to ampicillin, high level gentamicin, vancomycin, teicoplanin and linezolid was determined by a Kirby-Bauer disk diffusion method as per CLSI criteria ⁴

E-TEST OF VANCOMYCIN

Minimum inhibitory concentration (MIC) for vancomycin was determined by E-test as per the procedure of CLSI⁴ An isolate is considered susceptible to vancomycin if the MIC is $\leq 4\mu\text{g/ml}$ and resistant if $\text{MIC} \geq 32 \mu\text{g/ml}$ ⁴

QUALITY CONTROL

Two QC strains *Enterococcus faecalis* ATCC 29212 and ATCC 51299 were used as sensitive and resistant controls, respectively. The MIC values of vancomycin for the control strains must be within the ranges provided by the Clinical

and Laboratory Standard Institute⁴ prior proceeding to test organisms.

MOLECULAR DETECTION OF VANCOMYCIN RESISTANCE GENES

Vancomycin-resistance genes were detected by PCR using specific primers as per the procedure of Boyd ⁵ et al. Briefly, PCR conditions consisted of a pre-denaturation step at 94°C for 5 min, followed by 30 cycles of 45 sec denaturation at 94°C, 45 sec annealing at 54°C and 45 sec extension at 72°C. A final extension step was performed at 72°C for 5 min. Amplified products were analyzed by electrophoresis on 1.5% agarose gel.

STATISTICAL ANALYSIS

All statistical analyses were carried out using SPSS version 12.0.

ETHICS COMMITTEE APPROVAL

The research work was approved by Ethics committee after finalization of the project proposal.

RESULTS

Enterococci of both vancomycin resistant and susceptible were isolated and identified from different clinical conditions (Table-1). It was observed that 21.5% enterococci were isolated from urinary tract infections, 18% from end stage renal failure, 12.2% from neurological problem, 12.3% from sepsis, 8.2% from malignancy, 7.4% from surgical problem, 4.1% from diabetes mellitus, 2.9% from motor vehicle accident with head injury, 2.5% from respiratory infections, 1.6% from neonatal infections, .8% from skin infections and .4% from nephritic syndrome

Figure 1

Table 1: The underlying clinical conditions for enterococci infections (VRE and VSE) at HKL, Malaysia

Clinical manifestations	Frequency		Percentage (%)
	VSE	VRE	
UTI	50		21.5
ESRF	41	3	18.0
Neurological problem	29		12.2
Sepsis (including urosepsis)	30		12.3
Malignancy	20		8.2
Others	20		8.2
Surgical problem	18		7.4
DM	10	1	4.1
MVA (with head injury)	7		2.9
Respiratory infections	5	1	2.5
Neonatal infection	4		1.6
Skin infections	2		0.8
Burn	2		0.8
Nephrotic syndrome	0	1	0.4
Total	238	6	100.0

ESRF=end stage renal failure

MVA= motorvehicle accident DM=Diabetes mellitus UTI= Urinary tract infection.

Enterococci identified from the patients of different wards and department at hospital KKL have been listed (Table-2). In the study 39% Enterococci were identified from the patients of nephrology ward, 23% from medical ward, 12% from surgical ward, 13% from neurology ward, 5% from pediatric, 3% from oncology/radiotherapy, 2% from maternity, 1% from burn and 2% from out patient department(OPD)

Figure 2

Table 2: Distribution of vancomycin-resistant and vancomycin-susceptible Enterococci in different ward and departments at HKL, Malaysia

Wards/ Departments	VRE	VSE	Percentages (%)
	N=6	N=238	
Urology/Nephrology	4	92	39%
Medical (including ICU)	2	55	23%
Surgical	0	29	12%
Neurology	0	31	13%
Pediatric	0	11	5%
Radiotherapy/Oncology	0	8	3%
Maternity(O&G)	0	6	2%
Burn	0	2	1%
Others(Clinics, OPD)	0	4	2%

OPD=out patient department

ICU=intensive care unit, O & G= Obstetric and Gynaecology

Clinical features that were recorded for the infections of vancomycin resistant and susceptible patients were analyzed.

Figure 3

Table 3: Clinical features of vancomycin resistant and susceptible Enterococci infected patients at HKL, Malaysia

Patients	Total number of patients	Total (%)	No. of VRE	% of VRE	No. of VSE	% of VSE
Prolonged hospitalization	54	22.1	3	50	51	21.4
Catheter usage	70	28.7	1	16.7	69	29
Vancomycin treatment before	17	7	4	66.7	13	5.5
Cephalosporin treatment before	22	9	2	33.3	20	8.4
Carbapenem treatment before	21	8.8	0	0	21	8.8
Recurrent hospitalization	73	30	4	66.7	69	29
Malignancy	20	8.4	0	0	20	8.4

Out of all enterococci isolated 6 were found to be resistant to

vancomycin.

PCR results revealed that all the 6 vancomycin resistant enterococci possess Van A gene(In press)

DISCUSSION

Enterococci have both an intrinsic and acquired resistance to antibiotics, which make them important nosocomial pathogens.

Of all the enterococci infections analyzed (Table-3), out of 244 patients, 50 (21%) presented with urinary tract infections, 41 (17.2%) end stage renal disease, 29 (12.2%) neurological problems, 20 (8.4%) malignancy, 18 (7.4%) had surgical intervention and 10 (4.2%) had diabetes mellitus. Amongst the factors that described in this study to favor the infections, majority of them (29%) had recurrent hospitalization and catheter usage, followed by prolonged hospitalization, 21.4%. Although recurrent hospitalization and catheter usage were more frequent risks described in the enterococci infections, these risk factors were not statistically significant. Other risk factors like carbapenem and cephalosporin usage were also not statistically significant. Enterococci are rated as the second leading cause of urinary tract infections (UTI) and comprised about 10% of nosocomial UTI⁶ and this study showed that UTI was the most common clinical manifestation of enterococci infections. Instrumentation like urinary catheter and urinary tract abnormality (urethral stricture, hydronephrosis) might have promoted infection with enterococci especially in elderly patients. In neurology units, most of the patients had limited mobility especially patients with cerebrovascular accidents and they usually used urinary and venous catheters that might have promoted enterococcal colonization and infections.

For patients with end stage renal disease, usually hospitalized frequently for dialysis. Some patients had dialysis via venous catheter (internal jugular catheter and/or femoral catheter) and this catheter was probably prone to be colonized with enterococci with the help of biofilm production. This group of patients had catheter related bloodstream infections and usually treated with intravenous antibiotics (cephalosporin, vancomycin, carbapenem) requiring prolonged hospitalization. The presence of an invasive device was identified previously as a strong clinical risk factor for VRE invasive infections⁷. It is unclear whether catheters served as the actual conduit through which VRE infection acquired, whether they were just markers of

debilitation, prolonged hospitalization and severe co-morbidities. Patients with prolonged hospital stay were more susceptible to cross-transmission of pathogens and to a greater use of antimicrobials with selective pressure; therefore they had a greater chance of acquiring resistant pathogens. A previous study found that the duration of hospitalization was considerably longer to pick up infections of the VRE groups (57.7 days) compared to VSE group (29 days)⁸

Among the 6 VRE cases, 4 (66%) isolates were identified as *E. faecium*, 1 (17%) *E. faecalis* and 1 (17%) *E. avium*, respectively. Three patients (50%) had underlying end stage renal disease and the VRE was isolated from blood specimens. Two of them were admitted to intensive care units for severe sepsis, however, patients already expired when we informed the positive culture for VRE. Another patient from whom enterococci was isolated from the blood taken via the femoral catheter, also had coagulase negative staphylococcus species (CONS) isolated from the peripheral blood. He was treated for catheter related bloodstream infection before with intravenous vancomycin, however repeated blood culture revealed no growth. This may suggest that this patient had been colonized with VRE. He was discharged well after 3 weeks in the ward and subsequent culture after that was negative for VRE.

The two remaining VRE isolates were obtained from urine specimens. The first urine specimen was taken from a 55 year old man with interstitial lung disease and respiratory failure and complicated with cardiac event. He had been hospitalized more than one month and also had recurrent admission to intensive care unit and prolonged intubation. He was put on piperacillin-tazobactam for more than 3 weeks because the tracheal aspirate and urine grew *Pseudomonas* sp. The urine culture was repeated twice after the initial VRE isolation. The patient was not treated for VRE in view of the negative blood culture. Repeated urine culture for the fourth time was negative for VRE but this patient died due to severe pneumonia with respiratory failure one month later. As highlighted by the case, the risk factors that were present such as prolonged hospitalization and exposure to antimicrobial agents could predict VRE colonization. Several studies used case control methods and multivariate analysis to examine the risk factors for VRE infection in hospitalized patients. Among the risk factors that emerged were longer duration of hospitalization and longer lengths of stay in ICU⁹ In our study, the use other antibiotics

(Carbapenem, Cephalosporin) was not statistically significant risk factor to predict the VRE. The other urine culture which isolated grew VRE was taken from a patient with nephrotic syndrome who also had recurrent hospitalization. However repeated urine culture 3 days after revealed no growth and patient was well. The 6th VRE isolate grew from a culture of tissue scrapings taken from sacral bed sores. The patient is a 68 year-old diabetic Chinese man with Parkinsonism who was admitted for severe pneumonia that required ventilation. He had been in ICU for more than 2 weeks and developed sacral sores. The patient expired on the day when the specimen was taken. The risk factor for this patient was vancomycin exposure for the treatment of Methicillin-Resistant *Staphylococcus aureus* (MRSA) in a previous admission and prolonged hospitalization. The exposure of patient's endogenous enterococcal flora to vancomycin is a known risk factor for the development of resistance. The patient might also be exposed to other antibiotics like cephalosporin group as he had history of recurrent hospitalization.

It has been shown that vancomycin use was a major risk factor for the VRE infection or colonization¹⁰. An increased risk of VRE infection and colonization had been associated with non-ambulatory status¹¹, receipt of antibiotics and hospitalization¹². In this study, the use of vancomycin was the significant risk factor for the development of VRE by statistical analysis. The RR (relative ratio) represents the effect of vancomycin use on promoting resistance to vancomycin in *Enterococcus* spp. In multivariate logistic regression analysis, prolonged hospitalization and use of vancomycin were statistically significant risk factors where the vancomycin usage gives the higher predictor for the development of VRE. Therefore, we can conclude that patients with the significant risk factors (prolonged hospitalization and vancomycin use) had 46% of getting the VRE.

In previous studies, VRE colonization was associated with prolonged length of hospital stay, previous admission to an intensive care unit (ICU), and severe underlying disease¹³. In addition, Huh et al.¹⁴ showed evidence that longer hospitalization and ICU stay are possible risk factors to get colonized with multiple clones of VRE. Extensive or multiple hospitalizations show a correlation between the subsequent development of VRE infections, prior antibiotic treatment, prolonged stay within intensive care units and, in some instances, even intrahospital transfers¹⁰.

Other investigators have shown that ongoing vancomycin use creates and maintains an intraluminal environment favorable to VRE growth, thus increasing the likelihood of VRE entry into bloodstream¹⁰. A study conducted from 2003 to 2004 showed that prior use of antimicrobial therapy, including vancomycin and cephalosporin, has been shown to be associated with acquisition of VRE¹⁵. Also, the presence of underlying disease was significantly associated with an increased risk for VRE colonization. Of note, impaired renal function and hemodialysis have been previously implicated as risk factors in VRE outbreaks¹². The use of vancomycin increased the risk of colonization 2.5-fold and third generation cephalosporins 2-fold^{10,11}. A study showed that vancomycin use is the major risk factor for VRE bacteremia. Since 1990s, vancomycin and ceftazidime have been used as first line empirical therapy for line related sepsis in the renal unit (HKL), however with the emergence of VRE, it has been changed to cloxacillin and ceftazidime.

Other risk factors that have described in this study like cephalosporin usage, use of carbapenem, malignancy, instrumentations like catheter and previous hospitalization were not statistically significant. Edmond et al¹⁶ studied VRE bacteremia on an oncology ward found that the use of antimicrobial agents with activity against anaerobes (metronidazoles, clindamycin and imipenem) determined a risk factor for the development of vancomycin-resistant bacteremia. In the present study, all the 6 confirmed VRE cases were further analysed by polymerase chain reaction (PCR) and all of them showed vanA phenotypes. Sixty seven percent (4/6) were identified as *E. faecium* and others were identified as *E. avium* and *E. faecalis*. Although *E. faecalis* was more common in human infections, vancomycin resistance was more frequently observed in *E. faecium* isolates. Most vancomycin-resistant *E. faecium* (VREF) strains isolated in Korea showed the VanA phenotype, which was defined as having high level resistance to vancomycin and teicoplanin⁶. There were reports of vancomycin-resistant enterococci with vanA genotype and vanB phenotype, detected in Japan, Korea and Taiwan^{17,18}. Van D-like phenotype associated with a vanA genotype, *E. faecium* was found in France¹⁹. In our study, we found vancomycin-resistant *E. avium*, that was isolated from a blood culture of an elderly man with end stage renal failure, exhibited lower MIC of vancomycin (84 µg/ml) compared to the other isolated VRE cases.

CONCLUSION

The findings of the study provided first Malaysian data on the prevalence of VRE and VSE in patients reported to HKL, Malaysia. Clinical features of the patients infected with enterococci infections were provided for the identification of the clinicians. The results would serve as an alert to the clinicians of the emergence of infections by VRE and VSE and encourages implementation of appropriate infection control measures in order to curb further rise in prevalence.

References

1. NNIS. www.vapaway.eu/.../national-nosocomial-infections-surveillance-nnis-system-report.html 2010.– Accessed on April, 8, 2011.
2. NNIS. National Nosocomial Infections Surveillance System Report, data summary from January 1992 through June 2004, issued October) *Am J Infect Control* 32(2004)470-485
3. Zubaidah A W. Ariza A. and Azmi S. Hospital-Acquired Vancomycin-Resistant Enterococci: Now Appearing in Kuala Lumpur Hospital *Med J Malaysia* : 61(4)(2006) 487
4. CLSI (Clinical and Laboratory Standards Institute) Performance Standards for Antimicrobial Susceptibility Testing; Sixteenth Informational Supplement. M7-A7-MIC Testing. CLSI document M100-S16. CLSI, Wayne, Pennsylvania (2006). USA.
5. Boyd DA. Willey BM. Fawcett D. Gillani N. and Mulvey MR. Molecular Characterization of *Enterococcus faecalis* N06-0364 with Low-Level Vancomycin Resistance Harboring a Novel D-Ala-D-Ser Gene Cluster, *vanL*, *Antimicrobial Agents and Chemotherapy*; 52(2008)2667-2672.
6. Cetinkaya Y. Falk P. and Mayhall CG. Vancomycin-resistant Enterococci, *Clin Microbiol Rev.* 13 (2000)686-707.
7. Lautenbach E. Bilker WB. Brennan PJ. Enterococcal bacteremia: risk factors for vancomycin resistance and predictors of mortality. *Infect Control Hosp Epidemiol*, 20 (1999) 318–323.
8. Lucas GM. Lechtzin N. Puryear DW. Yau LL. Flexner CW. and Moore RD. Vancomycin-resistant and vancomycin-susceptible enterococcal bacteremia: comparison of clinical features and outcomes. *Clin Infect Dis.* 26 (1998)1127-1133.
9. Tornieporth, NG. Roberts RB. John J. Hafnir A. and Riley LW. Risk factors associated with vancomycin-resistant Enterococci faecium infection or colonization in 145 matched case patients and control patients. *Clinical Infectious Disease*, 23(1996) 767-772.
10. Zaas AK. Song X. Tucker P. Perl TM. Risk factors for development of vancomycin-resistant enterococcal bloodstream infection in patients with cancer who are colonized with vancomycin-resistant enterococci. *Clin Infect Dis*, 35 (2002)1139-48.
11. D'Agata E M C. Green WK. Schulman G. Tang Li H. and Schaffner YW. Vancomycin-Resistant Enterococci among Chronic Hemodialysis Patients: A Prospective Study of Acquisition. *Clinical Infectious Diseases*. 32(2001) 23-29.
12. Barbosa DL. Lima S. Silbert H. Sader M. Cendoroglo S. Draibe L. Camargo L. Vianna A. Belasco R. Sesso. Evaluation of the prevalence and risk factors for colonization by vancomycin-resistant Enterococcus among patients on dialysis, *Am J Kidney Dis.* 44(2004)337–343.
13. Metallidis S. Chatzidimitriou M. Tsona A. Bisiklis A. Lazaraki G. Koumentaki E. Gikas A. Alexiou-Daniel S. and Nikolaidis P. Vancomycin-resistant enterococci, colonizing the intestinal tract of patients in a university hospital in Greece. *Braz. J. Infect. Dis.* 10(2006) 179–184.
14. Huh JY. Lee WG. Jin HY. Molecular characterization of vancomycin-resistant enterococci from clinical and surveillance specimens. *Infect. Control Hosp. Epidemiol* 27(2006)1076–1078.
15. Mehrad A.. Rahim A.. Ahmad M. Florian D. Ojan A. Risk factor for rectal colonization with vancomycin-resistant enterococci in Shiraz, Iran. *Int. Society for Infectious Diseases*, 12(2008)171-175.
16. Edmond MB. Ober JF. Weibbaum DL. Pfaller M A. Hwang T. Sanford MD. Wenzel RP. Vancomycin-resistant *Enterococcus faecium* bacteremia: Risk factors for infections. *Clin Infect Dis* 20(1995) 1126-1133.
17. Hashimoto YK. Tanimoto Y. Ozawa T. Murata. and Ike Y. Amino acid substitutions in the VanS sensor of the VanA-type vancomycin-resistant *Enterococcus* strains result in high level vancomycin resistance and low level teicoplanin resistance. *FEMS Microbiol. Lett.* 185(2000) 247-254.
18. Lauderdale TL.. McDonald LC. Shiao Y. Chen PC. Wang HY. Lai JF. and M. Ho.. Vancomycin-resistant enterococci from humans and retail chickens in Taiwan with unique VanB phenotype-vanA genotype incongruence. *Antimicrob. Agents Chemother*; 48(2002)1379-1381.
19. Thierry N. Nicolas F. Renaud S. Colette S. Antoine D. and Patrice N. First Nosocomial Outbreak of Vancomycin-Resistant *Enterococcus faecium* expressing a VanD-like Phenotype Associated with a vanA Genotype. *American Society for Microbiology. Journal of Clin Microbiology*, 43 (2005) 3642-3649.

Author Information

R.B. Ibrahim

Department of Medical Microbiology and Immunology, Faculty of Medicine, National University Malaysia

M. Mohamad

Department of Medical Microbiology and Immunology, Faculty of Medicine, National University Malaysia

M. M. Rahman

Department of Medical Microbiology and Immunology, Faculty of Medicine, National University Malaysia