The phenotypic and genotypic characterization of vancomycin-resistant enterococci in outpatients' urine culture

Snežana Brkić¹, Predrag Bugarić¹, Drina Topalov¹, Ivana Ćirković²
¹Konzilijum Institute for Laboratory Diagnostics, Belgrade, Serbia; ²University of Belgrade, School of Medicine, Institute of Microbiology and Immunology, Belgrade, Serbia

SUMMARY
Introduction/Objective In the era of emerging antibacterial resistance, the major burden of resistant strains is on hospitalized patients. Although community factors are also important in the spread of resistance, less attention has been paid to non-healthcare settings. The aim of the study is to determine the prevalence of vancomycin-resistant enterococci (VRE) in the outpatient’s urine culture and to perform phenotypic and genotypic characterization of VRE strains.

Methods During an 18-month period, a total of 5,164 Enterococcus spp. strains were isolated from urine and identified by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. Antimicrobial susceptibility testing was performed by disk diffusion method and by gradient test for glycopeptide-resistant strains. Genotypic characterization of VRE strains was done by multiplex polymerase chain reaction for the detection of the vancomycin resistance genes.

Results Among the isolated enterococci, 5,060 (98%) were E. faecalis and 104 (2%) were E. faecium. E. faecalis strains were susceptible to all tested antibiotics except norfloxacin (33% of strains were resistant), while E. faecium showed high level of resistance to most of the tested agents (91.3% to ampicillin, 77% to norfloxacin, and 75% to nitrofurantoin), and 26% of strains were resistant to vancomycin and teicoplanin. VanA gene was detected in all vancomycin resistant E. faecium (VREfm) strains.

Conclusion A high proportion of VREfm was noticed among outpatients in our country. All analyzed VREfm strains belonged to vanA genotype. Future surveillance studies of VRE are needed to follow up on this baseline study to monitor any possible changes in abundance and genotype of VRE in this population group.

Keywords: VRE; urine; outpatients

INTRODUCTION

Enterococcus spp. are not generally regarded as highly virulent bacterial pathogens. These bacteria are part of normal intestinal flora of both humans and animals, and can cause vast majority of human infections, such as: urinary tract infections, bacteremia, endocarditis and, less frequently, infections of other sites (wounds, bones, meninges, etc.). Enterococcus faecalis is the most common isolated species of Enterococcus spp., but in the last couple of decades, Enterococcus faecium has caused a substantial proportion of enterococcal infections, especially in hospital settings [1, 2].

Enterococci have emerged as important nosocomial pathogens. The major reason for this is the trend of increasing antimicrobial resistance seen in these organisms [2]. One of the main reasons why these organisms have survived in the hospital environment is their intrinsic resistance to commonly used antibiotics and, perhaps more importantly, their ability to acquire resistance to all currently available antibiotics, either by mutation or by receipt of foreign genetic material through the transfer of plasmids and transposons [3]. In the past decade, antibiotic resistance has been increas-ingly identified in the community. Although community factors are also important in the spread of resistance, less attention has been paid to non-healthcare settings [4]. Community-acquired infections account for the majority of prescribed antibiotics, very often wide-spectrum antibiotic therapy, which increases the rate of multidrug-resistant bacteria, e.g. multidrug-resistant enterococci strains isolated from urine culture [5, 6, 7]. The emergence of vancomycin-resistant enterococci (VRE) in the community has emphasized the non-existence of boundaries between hospitals, between people and animals, between countries, and probably between continents [8].

The aim of the study is to determine the prevalence of vancomycin-resistant enterococci (VRE) in outpatients’ urine culture and to perform phenotypic and genotypic characterization of VRE strains.

METHODS

Bacterial strains

From February 2014 to July 2015, a total of 53,348 urine samples were analyzed in our
laboratory. In accordance with European guideline recom-
mendations [9], 5,164 clinically significant enterococci
strains were included in this study. If there was more than
one sample per patient, only the first isolated strain was
included. Identification was performed by matrix-assisted
laser desorption/ionization time-of-flight mass spectrom-
etry (MALDI-TOF MS) (Vitek MS®, bioMerieux, Marcy-
l’Étoile, France).

Antimicrobial susceptibility testing

The antimicrobial susceptibility testing was done by Kir-
by–Bauer disk diffusion method using the following disks
(Bio-Rad Laboratories, Inc., Hercules, CA, USA): ampicil-
lin (2 μg), norfloxacin (10 μg), nitrofurantoin (100 μg),
vancymycin (5 μg), and teicoplanin (30 μg). Minimum
inhibitory concentration (MIC) in glycopeptides resistant
strains was determined by gradient test (E-test, bioM-
erieux) for vancomycin and teicoplanin. The results were
interpreted and quality control was done in accordance
with the European Committee on Antimicrobial Suscep-
tibility Testing (EUCAST) recommendations from 2015
[10, 11].

Multiplex polymerase chain reaction

Genotypic identification and determination of glycopep-
tide resistance genotype was done by multiplex polymerase
chain reaction (PCR). For identification, the genes encoding D-alanine–D-alanine ligases specific for
_E. faecium_ (ddlE. faecium) and for _E. faecalis_ (ddlE. faecalis) was
performed. For detection of the vancomycin resistance
genes, the attempt was made to identify the commonest
ones, i.e., _vanA_, _vanB_, and _vanC_ genotypes (_vanC1_ gene or
_vanC2/C3_ gene) [12, 13]. _E. faecium_ BM4147 (_vanA_ posi-
tive strain) was used as a positive control strain.

The PCR conditions and the primers used for the geno-
typic characterization of vancomycin resistant strains were
as previously described [14–17]. The following pairs of
primers were used: for _ddlE. faecium_ F (5’-GCAAGGCTTCT-
TAGAGA-3’), _ddlE. faecium_ R (5’-CATCGTGAAGC-
TAACCTC-3’), _ddlE. faecalis_ F (5’-ATCAAGTACAGT-
TAGTCTT-3’), _ddlE. faecalis_ R (5’-ACGATTCAAAGC-
TATT-3’), _vanAF_ (5’-GGAAACGACAATTGC-
TATT-3’), _vanAR_ (5’-GTACAATGCGCCGTATA-3’),
_VanB_ (5’-ACTGGCCTACATTCTTACA-3’), _VanBR_ (5’-AGCGTATTCTTCCGT-3’), _vanC1F_ (5’-TCTCA-
CAGAATCTCAGTGT-3’), _vanC1R_ (5’-ACATGGCACA-
CAACATAAG-3’), _vanC2/C3F_ (5’-CTCTCAAAAAGGTAT-
CCTAAG-3’), _vanC2/C3R_ (5’-TCTTGATAGGATAAGGC-
GA-3’).

Statistical analysis

The data obtained in this study were analyzed in the SPSS
statistical program (PASW statistics for Windows, Ver-
sion 18.0, SPSS Inc., Chicago, IL, USA) using methods of
descriptive statistics and χ² test.

RESULTS

Among isolated enterococci, 5,060 (98%) strains were
_E. faecalis_ and 104 (2%) strains were _E. faecium_.

_E. faecalis_ strains were susceptible to all tested antibac-
terial agents, except 33% of strains that were resistant
to norfloxacin, which is used for fluoroquinolones resistance
screening according to EUCAST recommendations (Table
1). Among tested _E. faecium_ strains, 91.3% were resistant
to ampicillin, 77% to norfloxacin, 75% to nitrofurantoin and
26% to vancomycin and teicoplanin, respectively (Table 1).

MIC for vancomycin among all detected vancomycin re-
sistant _E. faecium_ (VREfm) strains was higher than 256 µg/ml
and for teicoplanin it was in the 8–256 µg/ml range (Figure 1).

Out of 27 strains of VREfm subjected to multiplex PCR
for detecting vancomycin resistance genes, all strains were
found to possess the _vanA_ gene (Figure 2).

<table>
<thead>
<tr>
<th>Antibiotics</th>
<th>Enterococcus faecalis (n = 5,060)</th>
<th>Enterococcus faecium (n = 104)</th>
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</thead>
<tbody>
<tr>
<td></td>
<td>Susceptible</td>
<td>Resistant</td>
</tr>
<tr>
<td>Ampicillin</td>
<td>5,060 (100%)</td>
<td>0 (0%)</td>
</tr>
<tr>
<td>Nitrofurantoin</td>
<td>5,060 (100%)</td>
<td>0 (0%)</td>
</tr>
<tr>
<td>Norfloxacin</td>
<td>3,390 (67%)</td>
<td>1,670 (33%)</td>
</tr>
<tr>
<td>Vancomycin</td>
<td>5,060 (100%)</td>
<td>0 (0%)</td>
</tr>
<tr>
<td>Teicoplanin</td>
<td>5,060 (100%)</td>
<td>0 (0%)</td>
</tr>
</tbody>
</table>

Figure 1. Glycopeptides MIC Distribution for VREfm strains

Figure 2. Gel electrophoresis of amplified products by PCR for van-
comycin resistance genes; M – Gene Ruler Low range DNA Ladder
(Thermo Scientific); PC – positive control for _vanA_ gene; NC – negative
control _VanA_ gene; lines 1–4 positive for _vanA_ gene (731 bp), _ddlE. faecium/
D-alanine–D-alanine ligases _E. faecium_ (550 bp)
Incidence of vanA gene was significantly higher in all strains of VREFm compared to vanB and vanC genotypes (p < 0.001).

DISCUSSION

For accurate interpretation of antimicrobial resistance data, especially for glycopeptides, precise species identification is necessary. When interpreting the MIC/disk diffusion results, it is important to ensure that isolate is not E. casseliflavus or E. gallinarum, species that possess intrinsic resistance to glycopeptides. Furthermore, despite the number of studies on antibiotic-resistance in enterococci from Serbian clinical settings, there were no data about prevalence of VRE in the outpatients' settings in our country [18, 19, 20]. The results of the Central Asian and Eastern European Surveillance of Antimicrobial Resistance (CAESAR network) [7] showed high level of resistance to aminopenicillins among E. faecalis and E. faecium (41% and 94%, respectively). This result may reflect problems with species identification (comprising E. faecium, which is commonly resistant to aminopenicillins), rather than true high resistance in E. faecalis. On the other hand, high level of VREfm among invasive isolates in Serbia (75%) may indicate difficulty in distinguishing E. faecium from E. casseliflavus and E. gallinarum. The application of the latest methods for identification such as MALDI-TOF MS or molecular methods, overcomes this problem [21]. Therefore, MALDI-TOF MS, as the most reliable phenotypic method for bacterial identification, was used in this study.

Antimicrobial resistance data in our study indicates overall significant level of multidrug-resistant E. faecium among enterococci in outpatients’ urine culture, with 26% of VREfm strains. Comparing the results with other studies [22, 23], where no VREfm was detected, it can be concluded that increasing antibiotics resistance in community settings is a current trend.

Two principal phenotypes of acquired inducible vancomycin resistance have been described, VanA and VanB, encoded by two distinct gene clusters, the vanA and vanB clusters, respectively, which are carried on transposons Tn1546 and Tn1547, respectively. The VanA phenotype confers high-level resistance to both vancomycin and teicoplanin, while the VanB phenotype confers only moderate to high-level resistance to vancomycin. A third type of vancomycin resistance, termed VanC, has been known for many years to be natural (intrinsic) vancomycin resistance found in the motile enterococci (E. casseliflavus, E. gallinarum, and E. flavescens). VanC confers only low-level resistance to vancomycin [24, 25]. Compared to other phenotypes, the VanA is the most common in European countries [26, 27]. Our results confirmed this fact: 100% of VREfm strains belong to VanA phenotype.

To the best of our knowledge, this is the first molecular study on VRE strains among outpatients in our country. In accordance with phenotyping results, all strains were positive for vanA and negative for vanB, vanC1, and vanC2/C3 genes as evidenced by PCR. Genotypic results in various studies show similar results. Libisch et al. [18] reported that the vanA gene was the dominant gene among invasive isolates in Serbia. Similar results were obtained for hospitalized patients in Turkey [27]. As per Werner et al. [28], the vanA and vanB resistance genotypes are by far the most prevalent in Europe. The reservoir for vanA and vanB type resistance in humans is E. faecium, which shows an enhanced capacity to disseminate in the nosocomial setting and are thus called epidemic or hospital-acquired. These clones of E. faecium are mostly ampicillin-resistant, partly high-level ciprofloxacin-resistant. In our study, E. faecium strains were 91.3% resistant to ampicillin and 77% resistant to quinolones. This may suggest that probably majority of our strains originated from nosocomial settings, but this requires further investigations.

CONCLUSION

A high proportion of VRE was noted among outpatients. All analyzed VRE strains belonged to Enterococcus faecium species associated with vanA genotype. Future surveillance studies of VRE are needed to follow up on this baseline study to monitor any possible changes in abundance and genotype of VRE in this population group.

REFERENCES

Увод/Циљ
Савремена ентерококција је водичано антимикробно резистентна штампа, која је у Европи у рециклисаној верзији (VRE) у оквиру антимикробно резистентности." 

САЖЕТАК

Увод/Циљ
У ери антимикробне резистенције највећи број резистентних сојева потиче од хоспитализованих болесника. Јаки су антимикробни фактори важни у ширењу резистенције, али је у вировитим антимикробним сојевима изузетак. Циљ рада је проучавање антимикробне резистенције у ентерококовим штамама изолованим из урина ванболничких болесника.

Резултати

Извошћи изолованих ентерококова, E. faecalis чини 98% сојева, осетљивих на већину испитиваних антибиотика изузев норфлоксацина (33% сојева је било резистентно), док је E. faecium чини 2% сојева, који показују висок ниво резистенције на већину тестираних антибиотика (91.3% сојева је било резистентно на ампицилин, 77% на норфлоксацин и 75% на нитрофуранотион). Док је 26% сојева резистентног E. faecium чини 2% сојева, који показују висок ниво резистенције на већину тестираних антибиотика (91.3% сојева је било резистентно на ампицилин, 77% на норфлоксацин и 75% на нитрофуранотион). Док је 26% сојева резистентног E. faecium чини 2% сојева, који показују висок ниво резистенције на већину тестираних антибиотика (91.3% сојева је било резистентно на ампицилин, 77% на норфлоксацин и 75% на нитрофуранотион).

Закључак

У целине болничких болесница у нашој земљи утврдено је висок степен антимикробне резистенције и у овој популационој групи. Кључне речи: VRE, урина, антимикробне резистенције.