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Emergence of multidrug-resistant enterococci isolated from a tertiary care teaching hospital, Vadodara.

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Abstract:

Enterococci, which are commonly found in human fecal flora, have undergone a significant shift in recent years. Once viewed as minor clinical concerns for intestinal commensals, enterococci are now one of the most prevalent nosocomial pathogens, causing substantial morbidity and mortality. **Aim:** The objective of this study was to ascertain the emergence of multidrug-resistant enterococci isolated from a tertiary care teaching hospital in Vadodara. **Materials & methods:** In a retrospective analytical cross-sectional study conducted at a tertiary care center, 81 non-repetitive clinical isolates of enterococci were collected from a range of clinical samples and subjected to traditional phenotypic techniques, such as colony morphology, catalase test, bile esculin test ,automated Vitek 2 compact use to identify the isolates at the species level & to performed further antimicrobial susceptibility testing. The susceptibility and resistance of enterococci to antibiotics were determined based on recent the Clinical and Laboratory Standards Institute guidelines. **Results:** Enterococci isolates distributed by sample. 40 urine (49%) samples were collected, followed by blood (19%), then by pus (16%), and the others constituted 7%. study shows the sorting of enterococci isolates from different wards. In this study, 27% (n=22) of the patients from whom enterococci were isolated were from the NICU, 26% (n=21) from the MICU, and 47% (n=38) from various wards. **Conclusion:** Enterococcal isolates showed multidrug resistance, with E. faecium having a higher prevalence (53.08%) than E. faecalis (34.5%). Some isolates were resistant to all antibiotics tested, indicating that multidrug-resistant enterococci have become more common and pose a significant challenge for treatment. To address this issue, routine monitoring of antimicrobial resistance and implementation of effective infection control programs are essential. With a judicious antibiotic policy, the management of enterococcal infections can be improved.

Key words: Enterococci, antibiotics, multi-drug resistance, aminoglycosides, nosocomial infections.

Introduction:

Enterococci, commonly present in the human fecal flora, has experienced a notable shift in recent years [1]. Previously perceived as minor clinical issues as intestinal commensals, enterococci are now among the most prevalent hospital-acquired pathogens, causing substantial illness and fatality [2]. This surge in enterococcal infections is largely due to their resistance to various antimicrobial medications. Urinary tract infections and surgical site infections are the most common types of nosocomial infections caused by enterococci [3,4]. The emergence of antimicrobial resistance in enterococci has presented significant challenges to healthcare professionals, resulting in increased death rates due to prolonged hospital stays, excessive use of antibiotics, and inadequate infection control measures to prevent the rapid spread of enterococci [2-5]. The aim of this research study was to determine the emergence of multidrug-resistant enterococci isolated from a tertiary care teaching hospital in Vadodara.

Materials & methods:

In a cross-sectional study conducted at a tertiary care center, 81 non-repetitive clinical isolates of enterococci were gathered from a range of clinical samples and subjected to traditional phenotypic techniques, such as colony morphology, catalase test, bile esculin test, automated Vitek 2 compact use to identify the isolates at the species level & to performed further antimicrobial susceptibility testing. The susceptibility and resistance of enterococci to antibiotics were determined based on recent the Clinical and Laboratory Standards Institute guidelines. To determine the antimicrobial susceptibility of the enterococcal isolates, the Kirby Bauer disc diffusion method was employed. High-level gentamicin (120 mg) and streptomycin (300 mg) discs were utilized to assess resistance to high-level amino glycosides. All results were analyzed according to the guidelines set forth by the Clinical and Laboratory Standards Institute (CLSI) [6].

Results:

Figure 1 shows the distribution of the Enterococcus isolates by sample. Forty urine samples (49 %) were collected, followed by blood (19%), pus (16%), and other samples (7%). Figure 2 shows the sorting of enterococci isolates from different wards. In this study, 27% (n=22) of the patients from whom enterococci were isolated were from the NICU, 26% (n=21) from the MICU, and 47% (n=38) from various wards.

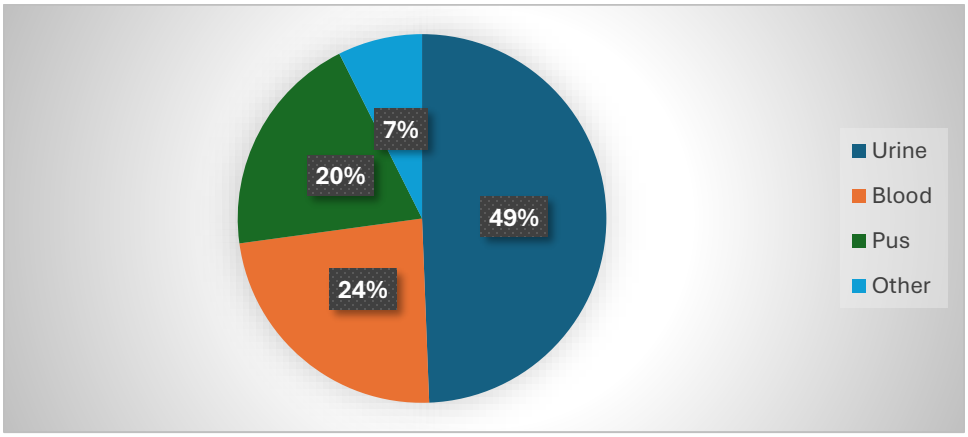

Figure 1: Enterococcus isolates distributed by sample.

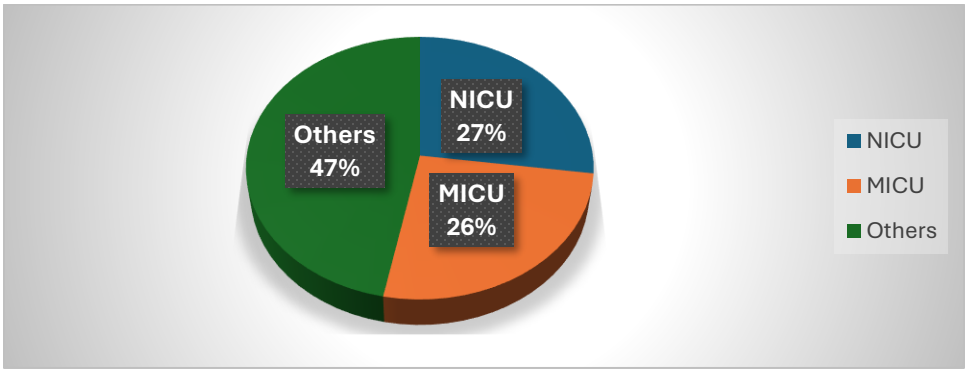

Figure 2: Sorting Enterococci isolates by ward.

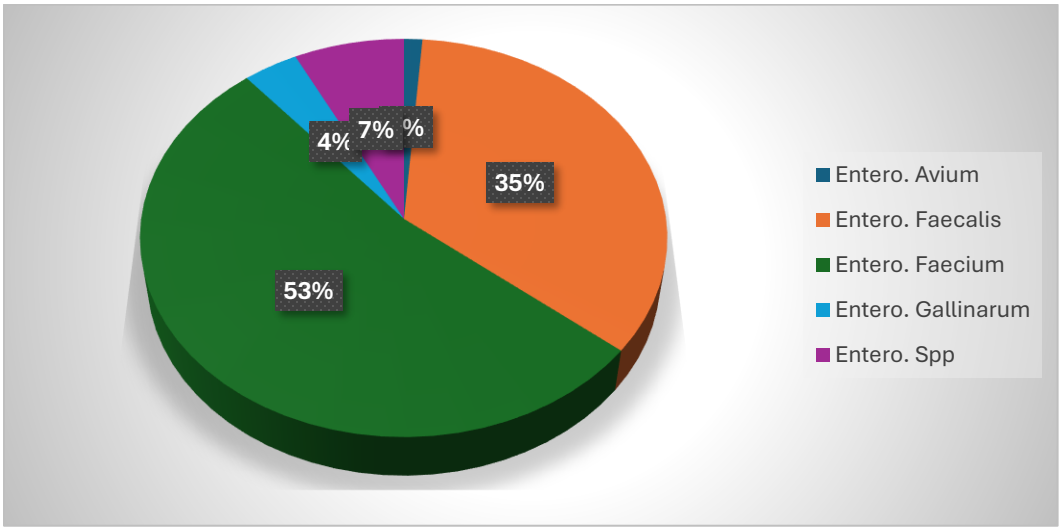

Figure 3: Number of species present in different samples

Enterococcus spp. accounted for 6, 43 (Enterococcus faecium), 28 (Enterococcus faecalis), 3 (Enterococcus Gallinarum), and 1 (Enterococcus avium) of the 81 identified isolates (Figure 3). No additional enterococcal species were found. Of all the clinical samples tested, enterococci were most frequently found in the urine (41 cases), blood (18 cases), pus (16 cases), and other fluids. Colonizers were defined as urine isolates that did not meet the requirements for substantial bacteriuria; only those isolates that met these criteria were included in the study and continued with processing.

Aminoglycoside resistance was observed in various Enterococcus species, including E. faecalis (n=28), E. faecium (n=36), E. gallinarum (n=4), and E. spp (n=4) for the Aminoglycosides-1 family. For the Aminoglycosides-2 family, resistance was observed in E. faecalis (n=5), E. gallinarum (n=1), and E. spp (n=2) isolates. Similarly, resistance to the Aminoglycosides-3 family was observed in E. faecalis (n=26), E. faecium (n=36), E. gallinarum (n=4), and E. spp (n=4) isolates. Resistance to the Aminoglycosides-4 family was observed in E. faecium (n=5), E.

gallinarum (n=1), and E. spp (n=2) isolates. Lastly, resistance to the Aminoglycosides-5 family was observed in E. faecium (n=5), E. gallinarum (n=1), and E. spp (n=2) isolates.

Resistance to the Lactams-1 family was observed in *E. faecalis* (n=6), *E. faecium* (n=34), *and E. spp* (n=4). Resistance (wild) to Furanes-1 family was seen in isolates *E.Faecalis* (n=3), *E.Faecium* (n=32), *E. Gallinarum* (n=1), *and E.Spp* (n=3). Resistance to the Furanes-2 family was observed in *E. faecalis* (n=25), *E. faecium* (n=14), *E. Gallinarum* (n=2), *and E. spp* (n=4).

Resistance to the Glycopeptides-2 family (*Van B-like*)was observed in *E. faecalis* (n=10) and *E. faecium* (n=7). Resistance (wild) to the Glycopeptides-3 family was observed in *E. faecalis* (n=17), *E. faecium* (n=31), *and E. Spp* (n=5). Resistance to the Glycopeptides-4 family was observed in the isolates *E. Gallinarum* (n=2) *and E. Spp* (n=1).

Resistance to Macrolides/Lincosamides/Streptogramins-1 family was observed in *E. Gallinarum* (n=34) *and E. Spp* (n=4). Resistance (MLSB) to Macrolides/Lincosamides/Streptogramins-2 family was seen in isolates *E.Faecalis* (n=17), *E.Faecium* (n=6), *E. Gallinarum* (n=2), *and E.Spp* (n=2). Resistance (wild) to Macrolides/Lincosamides/Streptogramins-3 family was seen in isolates *E.Faecalis* (n=7), *E.Faecium* (n=6), *E. Gallinarum* (n=2), *and E.Spp* (n=2).

Resistance to the Oxazolidinone-1 family was observed in *E. faecalis* (n=4), *E. faecium* (n=5), *and E. spp.* (n=1). Resistance (wild) to Oxazolidinone-2 family was observed in *E. faecalis* (n=22), *E. faecium* (n=36), *E. Gallinarum* (n=3), *and E. spp* (n=5).

Resistance to the Quinolones-1 family was observed in *E. faecalis* (n=14), *E. faecium* (n=39), *E. Gallinarum* (n=3), *and E. spp* (n=4). Resistance to Quinolones-2 family was seen in isolates *E.Faecalis* (n=12), *E.Faecium* (n=3), *E. Gallinarum* (n=1), *and E.Spp* (n=3).

Resistance to the Tetracyclines-1 family was observed in *E. faecalis* (n=19), *E. faecium* (n=33), *E. Gallinarum* (n=3), *and E. spp* (n=4). Resistance to the Tetracyclines-2 family was observed in *E. faecalis* (n=6), *E. faecium* (n=9), *and E. spp* (n=2).

Discussion:

The most frequent clinical sample from which enterococci were isolated was urine, accounting for 49% of cases, followed by blood at 19%, pus at 16%, and other samples at 16%. Previous research has also found urine to be the primary source of enterococci, and percentages of isolates from urine are like those observed in the current study. Studies [7], [8], and [9] have reported 49%, 50%, and 36.6% of enterococci, respectively, from urine samples.

The majority of enterococcal species, 80-85% of clinical isolates, are identified as *E. faecalis*, while *E. faecium* accounts for approximately 10-15% of clinical isolates, as reported by various studies [5]. The enterococcal isolates in this investigation were identified through a range of phenotypic testing methods, as accurate speciation is essential due to the varying levels of antibiotic resistance exhibited by different species. Among the 81 isolates tested, 43 (53%) were identified as *E. faecium*, and 28 (35%) were identified as *E. faecalis*.

In the present study, 68 (83.9%) isolates were found to be resistant to Aminoglycoside-1 and three family drugs, as enterococci exhibit intrinsic low-level cross-resistance to all aminoglycosides due to decreased uptake. Additionally, acquired resistance to high levels of aminoglycosides can also be present in enterococci due to genes encoding amino-glycoside-modifying enzymes.

A total of 44 (54.3%) of the isolates were resistant to beta-lactam drugs, with E. faecium showing higher resistance. However, a prior study [7] found that 66% of these isolates were resistant to ampicillin. No significant difference was observed between the resistance of *E. faecalis* and *E. faecium* to penicillin. In the present study, quinolone resistance was 74%, with resistance being higher in E. faecium. Another study [8] reported that 72% of strains were resistant to ciprofloxacin using the disk diffusion method. Resistance to fluoroquinolones is more common in *E. faecium* than in *E. faecalis*.

In the present study, 48 (59.2%) of the isolates were resistant to glycopeptide family drugs. All 48 isolates exhibited high-level resistance to glycopeptide drugs (VanB and Van C). Of the 81 isolates of *E. faecium*, 31 (38.2%) were resistant to glycopeptide drugs, while 17 of 48 isolates (35.4%) of *E. faecalis* were resistant. However, various studies have shown that *E. faecium* accounts for far fewer clinical enterococcal isolates than *E. faecalis* but is far more resistant to glycopeptides. In studies conducted by [9,10], less than 2% of *E. faecalis* isolates were resistant to vancomycin, whereas 52% of *E. faecium* isolates were resistant to vancomycin. The frequency and extent of glycopeptide resistance in this study were much higher compared to those of previous reports from India [11,12].

Conclusion:

Multidrug resistance was detected in enterococcal isolates, with *E. faecium* exhibiting a higher prevalence of 53.08% compared to *E. Faecalis* with a prevalence of 34.5%. A small number of isolates in this study were resistant to all the antibiotics tested, indicating that multidrug-resistant

enterococci have become increasingly prevalent and pose a significant therapeutic challenge. Antimicrobial resistance in enterococci warrants continuous monitoring, and an effective infection control program must be established to address this issue and formulate a judicious antibiotic policy to improve the management of enterococcal infections.

Conflict of interest:

The authors declare that they have no conflict of interest.

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