

Title: ANTIMICROBIAL RESISTANCE OF ENTEROCOCCI ISOLATES FROM INTESTINAL COLONIZATION SAMPLES AND SEVERAL INFECTIOUS SITES OF PATIENTS TREATED AT UNIVERSITY HOSPITAL IN RIO DE JANEIRO

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Abstract:

E. faecalis and *E. faecium* being among the main causes of healthcare-associated infections (HAIs), principally related to the increasing resistance to antimicrobial, mainly to glycopeptides. This study aimed to evaluate clinical isolates of *Enterococcus* from infection and intestinal colonization samples of patients from HUAP, regarding the susceptibility profile to antimicrobial and the presence of the *vanA* gene. For this, 58 consecutive strains identified as *Enterococcus* by automated system Phoenix BD™ were collected. From infectious origin (39.7%), 16 strains (69.6%) were identified as *E. faecalis*, six (26.1%) as *E. faecium* and one (4.3%) as *E. gallinarum/casseliflavus*. From colonization (60.3%), 23 (65.7%) were identified as *E. faecalis* and 12 (34.3%) as *E. faecium*. All strains were submitted to MALDI-TOF MS and the results showed 100% compatibility for genus and 92% for species. *E. faecium* (infectious origin) showed high rates of resistance (100%) to ampicillin, ciprofloxacin, erythromycin, levofloxacin, penicillin and rifampicin, while *E. faecalis* showed higher resistance rates to erythromycin (53%) and tetracycline (82%). It is also worth mentioning that none of the strains were positive for *vanA* gene. On the other hand, *E. faecium* (colonization) showed high rates of resistance (100%) to ampicillin, ciprofloxacin, erythromycin, levofloxacin, penicillin and rifampicin, while *E. faecalis* showed higher rates of resistance to ciprofloxacin, erythromycin, levofloxacin and vancomycin (100%). Besides, only one strain was negative for the *vanA* gene and one, despite being positive, did not present the resistance phenotype in the agar disk-diffusion test. Finally, the minimum inhibitory concentration for vancomycin performed for the 27 strains, being two of infection origin and 25 of colonization, which presented the resistance phenotype, revealed resistance to high levels (MIC > 512 µg/mL) of this antimicrobial by the vast majority of the strains (85.2%). Thus, we can conclude that, so far, regarding the infection strains, the epidemiological surveillance system carried out by the Hospital Infection Control Commission has been effective, leaving the rates of resistance to glycopeptides at low levels in our Institution. However, considering the colonization strains, most showed resistance to high levels of vancomycin, associated with the presence of the *vanA* gene, requiring constant monitoring of the epidemiology of VRE in hospital institutions.

Keywords: VRE, *Enterococcus faecium*, *Enterococcus faecalis*, enterococcal infection, enterococcal colonization, antimicrobial resistance,