TITLE: ANTIMICROBIAL RESISTANCE PROFILES AND CLONAL DIVERSITY AMONG *Enterococcus faecalis* ISOLATES FROM HOSPITALIZATED PATIENTS IN TWO INSTITUTIONS OF CACHOEIRO DE ITAPEMIRIM, ESPÍRITO SANTO, BRAZIL

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ABSTRACT Members of the genus Enterococcus are important agents of healthcareassociated infections due to their remarkable capacity of acquiring resistance to different antimicrobial agents. Among the different species, Enterococcus faecalis is responsible for the majority of enterococcal diseases, and it is commonly associated with increasing morbidity and mortality when resistant to vancomycin (VRE). This study aims to investigate the antibiotic resistance and genetic diversity among E. faecalis isolates from two hospitals [hospital A (129 beds) and hospital B (217 beds)] located in Cachoeiro de Itapemirim, Espírito Santo. A total of 78 E. faecalis isolates [42 (53.9%) isolates from hospital A and 36 (46.1%) from hospital B] were recovered from patients receiving assistance during the period from Sept 2016 to 2017. The isolates were identified by MALDI-TOF MS. Susceptibility to 18 antimicrobials was evaluated according to the CLSI guidelines. The isolates that were non-susceptible to ≥ 3 antimicrobial categories were defined as multidrug-resistant (MDR). Detection of antimicrobial resistance genes was accomplished by using PCR-based tests. Pulsed-Field Gel Electrophoresis (PFGE) was performed subsequently to DNA digestion with Smal. The most frequent clinical sources were urine [29 (37.2%) and blood [18 (23.1%)]; while 20.5% (16 isolates) were from surveillance cultures. The highest percentages of resistance were related to tetracycline (65 isolates; 83.3%), erythromycin (55 isolates; 70.5%), ciprofloxacin and gentamicin (45 isolates; 57.7% each) and vancomycin and teicoplanin (28 isolates; 35.9% each). Resistance to linezolid and tigecycline was not found. MDR was observed among 56 (71.8%) isolates, including all 28 VRE that carried the vanA gene. The 45 isolates with highlevel resistance to aminoglycosides presented the aac-(6')-le-aph(2")-la gene only (26 isolates), or in association with the aph-(2')-lc gene (13 isolates) or the aph-(3')-Illa gene (six other isolates). Analysis of genetic diversity by PFGE revealed 12 clonal groups and five unique pulsotypes among 76 isolates. The major clonal group included 27 isolates, being 26 (96.1%) resistant to vancomycin and carrying the vanA gene, and 25 (92.6%) resistant to gentamicin and carrying the aac(6')-le-aph(2")-la gene. A large genetic diversity was observed among vancomycin-sensitive isolates. These findings improve our understanding about characteristics of clinical and epidemiological importance exhibited by E. faecalis circulating in a region with limited data.

Keywords: *Enterococcus faecalis*, antimicrobial resistance, vancomycin-resistant enterococci, clonal diversity

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