

OCURRENCE AND DIVERSITY OF *ENTEROCOCCUS* ISOLATES RECOVERED FROM RECREATIONAL COASTAL WATERS IN RIO DE JANEIRO

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The enterococci are opportunistic pathogens with a remarkable ability to acquire and exchange mobile genetic elements associated with antimicrobial resistance. These microorganisms are components of the intestinal microbiota of humans and animals and can also be found in foods, plants and a variety of environments. Their presence in environmental sources may be indicative of human or animal contamination representing a risk to human health. The aim of the present study was to evaluate the occurrence and distribution of enterococcal species in recreational coastal waters and determine their susceptibility to antimicrobial agents. Coastal water sampling was carried out on five different beaches located in Rio de Janeiro, during 2013 and 2014. MALDI-TOF-MS was used for species identification. Conventional biochemical tests and multiplex PCR were also performed to confirm the identification of selected isolates. Among a total of 192 isolates, the following species were identified: *E. faecium* (115 isolates), *E. hirae* (58), *E. faecalis* (12), *E. gallinarum* (3), *E. casseliflavus* (2), *E. canintestini* (1) and *E. asini* (1). Antimicrobial susceptibility was evaluated by the disk diffusion method, using a panel of 17 antimicrobials. Thirty-seven distinct antibiotypes were observed, with 13 multidrug resistant (MDR) and 3 pandrug resistant (PDR) profiles. Only 7% of the strains were susceptible to all antimicrobials tested. The highest percentages of nonsusceptibility were found to erythromycin (71.3%), rifampicin (51.5%), nitrofurantoin (37%), and tetracycline (36%), followed by ciprofloxacin (26.0%), dalfopristin/quinupristin (13.0%), fosfomicin (8.3%), norfloxacin (5.7%), penicillin (4.1%), streptomycin (3.1%), chloramphenicol (2.6%), linezolid (2.0%), gentamicin (1.5%), levofloxacin (1.5%), vancomycin (1.0%), and tigecycline (0.5%). The presence of genes associated with high-level resistance to aminoglycosides (HLR-A) and resistance to glycopeptides was evaluated by multiplex PCR. The following genes were found alone or in association: *ant(6')Ia*, *ant(9')Ia*, *ant(3')IIa*, *ant(4')Ia*, *aac(6')-Ie-aph(2'')-Ia* and *aph(2'')-Ic*. The results indicate the occurrence of a variety of enterococcal species in the recreational waters investigated, with the predominance of *E. faecium*, a species frequently associated with antimicrobial resistance and outbreaks. These findings reinforce the need for monitoring marine environments as potential reservoirs of antimicrobial-resistant microorganisms.

Keywords: Enterococci, recreational waters, Public Health, MALDI-TOF MS, multidrug-resistance.