

TITLE: ISOLATION AND CHARACTERIZATION OF *Enterococcus* STRAINS IN INFECTIOUS SAMPLES OF DOMESTIC DOGS IN RIO DE JANEIRO, BRAZIL.

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Enterococci are part of the normal flora of the gastrointestinal tract of humans and animals, and the main species of enterococci are *E. faecalis*, *E. faecium* and *E. durans*. Currently resistance to many antimicrobials such as the aminoglycosides and β -lactams, has increased its pathogenic potential. Despite the prevalence and vast clinical information published on enterococci in human health, the prevalence, clinical significance and proper management control strategies for enterococcal infections in veterinary patients are not fully elucidated. Thus, the aim of this study was to characterize *Enterococcus* spp. isolated from dogs affected by infectious cases of dogs from Rio de Janeiro for their antimicrobial resistance profile and presence of virulence and antimicrobial resistant genes. A total of 20 enterococci isolates obtained from canine infections (urinary tract or skin infections) were identified by MALDI-TOF and evaluated for their in vitro antimicrobial susceptibility by disk diffusion method. Genetic resistant determinants for macrolides and virulence factors were determined by PCR. From the 20 isolates, 15 were *E. faecalis* and five *E. faecium*. Antimicrobial resistance was a common finding, and resistance to fluoroquinolones and tetracycline classes were the most frequent. Tetracycline (14/20 – 70%), enrofloxacin and ciprofloxacin (10/20 – 50%) were the least effective antimicrobials. Some alarming finding was the high prevalence of resistance to ampicillin (9/20 – 45%). Although no isolate presented resistance to vancomycin, four isolates demonstrated intermediate results. High levels of resistant to aminoglycosides could also be found, with five and six isolates being resistant to high levels of gentamycin and streptomycin. Regarding macrolides the genes *ermA* and *ermB* were found in four isolates each, with one isolate harbouring both. *MefA/E* could be identified in only one isolate. Genetic determinants for virulence factors could be identified in 13 isolates, with *gelE* and *asa1* being the most frequently identified with eight and seven isolates harbouring them respectively. Still, the hyaluronidase gene *hyl* could not be identified in any sample. Although the present study is limited in the number of samples some alarming finding, suggesting that more attention should be directed to *Enterococcus* when it comes to canine infections. Also highlight the possible carrier state of domestic animals, specifically dogs, that could serve as reservoir for possible zoonotic transmission. Successful strategies to combat *Enterococcus* need strong and coordinated efforts from both, the human and the veterinary field according to the "One Health" concept.

Keywords: *Enterococcus*, Antimicrobial Resistance, virulence factors, dog.

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