TITLE: MOLECULAR CHARACTERIZATION OF HIGH-LEVEL AMINOGLYCOSIDE RESISTANT *Enterococcus* spp RECOVERED FROM DOGS

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ABSTRACT:

Even though enterococci are human and animal gut microbiota members, species like *Enterococcus faecalis* (Efs) e *Enterococcus faecium* (Efm) are important healthcare associated infection (HAI) agents. Most of enterococcal infections are caused by multidrug- resistant (MDR) strains increasing the risks of treatment failure. These strains are very often aminoglycoside resistant that are important antimicrobials used to treat severe enterococcal infections. Dogs keep a close contact with their owners and may be MDR bacteria carrier what suggest they may be more one spread source of these bacteria. Data are not available about the circulation and genetical traits of enterococci strains recovered from dogs in our country. Therefore, the aims of this study were to survey the occurrence of dogs colonized by MDR enterococci and characterize them genotypically. Rectal swabs were sampled from 260 dogs from Rio de Janeiro state between 2015 and 2017. After isolation, the bacterial identification was made by MALDI-TOF. Antimicrobial susceptibility patterns were determined by disk diffusion and detection of high-level aminoglycoside resistance (HLAR) genes by PCR. PFGE was used to analyze the genetic diversity of the HLAR strains while MLST to identify the lineages that circulate in the canine population. Efs and Efc were recovered from 181 (69.6%) and 23 (8.8%) dogs, respectively. Non susceptible strains to tetracycline, quinolones, aminoglycosides and beta-lactams were observed in both species, being detected strains resistant to three or more antimicrobials in 4.2% of the studied animals. All strains were susceptible to vancomycin and nitrofurantoin. HLAR-Efs and HLAR-Efm were detected in 16.5% and 1.2% of the dogs, in addition to other enterococci species. Of four genes investigated, *ant(6)-Ia* was most frequently detected. HLAR-Efs were allocated in four PFGE clonal groups and belonged to ST19, ST21 e ST324 (CC21), and ST40 (CC40). Among HLAR-Efm strains were detected ST262 (CC17) and a new ST. Although high resistance rates have not been found, HLAR lineages that commonly are responsible for HAIs were found in the healthy dog gut in our geographic region and may represent a risk for human population.

Key words: *Enterococcus*, high-level aminoglycoside resistance, colonization, lineage, dog

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