

# ECM 2023 – Abstract

## Isolation and characterization of *Enterococcus* spp. from animal settings: surveillance for antimicrobial resistance

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*Enterococcus* spp. are ubiquitous bacteria that inhabit the normal intestinal microbiota of most animals and are widespread in the environment. Enterococci have emerged as opportunistic pathogens, due to rapid adaptation features and ability to acquire virulence and antibiotic resistance genes. Considering the low numbers of investigations on the characterization of enterococcal isolates from animals and animal-related samples, the goal of the present study was to isolate enterococci from those settings and evaluate the associated antibiotic susceptibility.

Briefly, enterococci were isolated from faecal samples of stabled animals (horses, cows, and goats), healthy domestic cats and dogs, and from surface swabs and dogs' anal exudates at a veterinary teaching hospital. Each sample was spread-plated in enterococcal selective media, Slanetz and Bartley agar, with/without vancomycin supplementation. Subsequently, 20% of the characteristic colonies were selected, submitted to DNA extraction and genetic comparison using RAPD-PCR. RAPD-pattern analysis and dendrogram construction allowed the selection of 110 genomically distinct representative isolates, further characterized for antibiotic susceptibility.

Regarding the results, around 3% were found to be vancomycin-resistant (two from goat and one from a domestic cat), while 10% were considered multidrug-resistant (isolates from one goat, one dogs' scale, 1 tickets' machine and 8 dogs' anal exudates). Most enterococci recovered from stabled animals, and some from domestic dogs/cats, were classified as susceptible to all tested antibiotics.

Overall, relevant antibiotic resistances were detected, and resistance phenotypes were found to be disseminated among distinct sample sources.

**Keywords:** *Enterococcus*, animals, environment, antibiotic resistance, genetic lineages

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