Diversity of resistant-Enterococcus species in wild animals from Portuguese fauna

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Introduction
Enterococci are Gram-positive commensal bacteria present in animal enteric systems. However, they have pathogenic potential. The most prevalent species are Enterococcus faecalis and Enterococcus faecium, representing more than 90% of the isolates in humans [1].

Aim
➢ To evaluate the Enterococcus species diversity in wild animal intestinal flora;
➢ To evaluate the antibiotic resistance profile of the Enterococcus isolates.

Methodology
Isolates were obtained from 103 wild animal faecal samples, ungulates (wild boar, red deer and fallow deer) and carnivorous (fox) animals from continental Portugal. The selection of these isolates was performed in Slanetz and Bartley culture media, confirmation was conducted with chromogenic media and Bile Esculin agar. Previously, the samples were submitted to enrichment step in TSB. Antimicrobial susceptibility test was achieved by the disk-diffusion method, according to the EUCAST and CLSI. PCR standard protocol was used to identify isolates at species level.

Results

Bacterial species
- E. hirae
- E. faecalis
- E. faecium
- E. durans
- E. munditti

Resistance profile

Conclusion
Results show a diversified profile of 113 isolates of Enterococcus species in these animals, with Enterococcus hirae as the most prevalent species, which is a common species in cattle, followed by E. faecium, commonly described as human pathogen, including reporting with antibiotic resistance [1]. Once wild animals should not theoretically have contact with antibiotics, it might be inferred that, due to the anthropogenic action these animals can be indirectly exposed to antibiotics. That would generate selective pressure on commensal microorganisms in the animal ecosystem, allowing it to become a reservoir for resistant-bacteria relevant to human health.

References

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