

## Genotypic Characterization of Gram-Positive Bacteria Isolated on Ornamental Animals Feed

**Authors :** C. Miranda, R. Soares, S. Cunha, L. Ferreira, G. Igrejas, P. Poeta

**Abstract :** Different animal species, including ornamental animals, are reported as potential reservoirs of antibiotic resistance genes. Consequently, these resistances can be disseminated in the environment and transferred to humans. Moreover, multidrug-resistant bacteria reduce the efficacy of antibiotics, as the case of vancomycin-resistant enterococci. *Enterococcus faecalis* and *E. faecium* are described as the main nosocomial pathogens. In this line, the aim of this study was to characterize resistance and virulence genes of enterococci species isolated from samples of food supplied to ornamental animals during 2020. The 29 enterococci isolates (10 *E. faecalis* and 19 *E. faecium*) were tested for the presence of the resistance genes for the following antibiotics: erythromycin (*ermA*, *ermB* and *ermC*), tetracycline (*tetL*, *tetM*, *tetK* and *tetO*), quinupristin/dalfopristin (*vatD* and *vatE*), gentamicin (*aac(6')*-*aph(2'')*-Ia), chloramphenicol (*catA*), streptomycin (*ant(6)*-Ia) and vancomycin (*vanA* and *vanB*). The same isolates were also tested for 10 virulence factors genes (*esp*, *ace*, *gelE*, *agg*, *fsr*, *cpd*, *cylA*, *cylB*, *cylM* and *cylLL*). The resistance and virulence genes were performed by PCR, using specific primers and conditions. Negative and positive controls were used in all PCR assays. The most prevalent resistance genes detected in both enterococci species were *ermB* (n=15, 52%), *ermC* (n=7, 24%), *tetK* (n=8, 28%) and *vatE* (n=4, 14%). Resistance genes for vancomycin were found in ten (34%) *E. faecalis* and ten (34%) *E. faecium* isolates. Only *E. faecium* isolates showed the presence of *ermA* (n=2, 7%), *tetL* (n=13, 45%) and *ant(6)*-Ia gene (n=4, 14%). A total of nine (31%) enterococci isolates were classified as multidrug-resistant bacteria (3 *E. faecalis* and 6 *E. faecium*). In three *E. faecalis* and one *E. faecium* were not detected resistance genes. The virulence genes detected in both species were *agg* (n=6, 21%) and *cylLL* (n=11, 38%). In general, each isolate showed only one of these virulence genes. Five *E. faecalis* and eleven *E. faecium* isolates were negative for all analyzed virulence genes. These preliminary results showed the presence of multidrug-resistant enterococci in food supplied to ornamental animals, in particular vancomycin-resistant enterococci. This genotypic characterization reinforces the relevance to public health in the control of antibiotic-resistant bacteria.

**Keywords :** antibiotic resistance, enterococci, feed, ornamental animals

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