

TITLE: ANTIBIOTIC RESISTANCE GENES IN SPECIES OF RUMINAL MICROBES

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ABSTRACT:

Antibiotic resistance represents a major threat to human and animal health. Food-producing animals, such as ruminants, are considered one of the potential sources of antimicrobial resistance to humans. These animals are raised in close contact with humans and are frequently exposed to therapeutic and sub-therapeutic concentrations of antibiotics. In this work, the objective was to evaluate the antibiotic resistance genes (ARGs) among ruminal microbial species. For this, three computational tools, Resfinder, Resfams and ARG-ANNOT, were used to detect antibiotic resistance genes in 435 microbial genomes available through the Hungate1000 Project. Phylogenetic analysis were carried out to analyze the distribution of these genes among the species of ruminal Bacteria and Archaea. The number and distribution of ARGs in ruminal microbial genomes varied according to the computational tool used for *in silico* screening with Resfams and ARG-ANNOT showing highest number of hits, respectively. The majority of the genes identified by Resfinder was associated with tetracycline resistance, while ARG-ANNOT detected mainly beta-lactam resistance genes and Resfams showed many hits to ABC efflux pumps. The phylogenetic analysis showed that the ARGs are widely distributed across the ruminal genomes, being frequently detected in the *Proteobacteria* phylum, in the families *Lachnospiraceae* and *Veillonelaceae* and in the genera *Bacteroides* and *Bifidobacterium*. Our results showed that 69.2% of the genomes harbored genes conferring resistance to one antibiotic class, mainly tetracycline resistance (66.6% of these genomes). The genome showing the highest number of resistance genes (n=5) was *E. coli* PA-3. Some ARGs were conserved across phylogenetically distant bacteria, suggesting that these genes may have spread by horizontal gene transfer. These results confirm the importance of using different computational approaches to screen for ARGs in microbial genomes and highlight the relevance of the rumen ecosystem as a reservoir of antibiotic resistance. Current studies are under way to investigate the potential of the genes identified in this study to be transferred across species of commensal gut bacteria.

Keywords: rumen, antibiotic resistance, Resfinder, ARG-ANNOT, Resfams

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