

TITLE: THE MICROBIOTA FROM DIFFERENT SOURCES OF BOVINES' GASTROINTESTINAL TRACT AND ITS RELATIONSHIP WITH GAIN OF WEIGHT

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ABSTRACT:

Microbes are key drivers for cattle nutrition. Along the whole gastrointestinal tract of bovines, many microbial taxa conduct carbohydrate degradation and nutrient absorption. However, the relationships among different parts of the animal body and how microbial communities affect aspects like the average daily gain of weight (ADG) remain unclear. Here, we used next-generation sequencing to evaluate bacteria and archaea communities from 110 microbial samples of saliva, ruminal fluid, and feces from heifers raised in natural grasslands from the Pampa biome. Our target was to establish how similar these communities are and how they are correlated with the gain of weight in cattle. We conducted the 16S rRNA sequencing in the Ion PGM Platform and monitored nutritional aspects for each animal for six months. We performed data filtering and analysis in the R environment following the Brazilian Microbiome Project recommendations. Our data suggested microbial community structure of saliva, ruminal fluid, and feces present significant differences ($p = 0.001$). Rumen showed a lower richness of microorganisms compared to the other sources ($p < 0.05$). Those findings contradict the idea of estimating the ruminal microbiota from saliva samples. Animals with higher abundances of potentially pathogenic genera such as *Moraxella*, *Porphyromonas*, and *Alysiella* in saliva presented lower ADG. *RF16* group and genera from the family *Prevotellaceae*, both correlated to improvements on processement of complex carbohydrates such as starch and lignin, were the taxa most related to higher ADG in the rumen. The higher ADG group also presented in feces the genus *Prevotellaceae* UCG-004 as increased, a group previously linked to improving the growth of young ruminants. Our data highlighted the differences in microbes from different sources in cattle and provided insights about which ones of these microorganisms may improve cattle nutrition and gain of weight. Our findings may be useful in further works focused on biomarkers of cattle performance and nutrition supplementation targeting higher ADGs in bovines.

Keywords: cattle breeding, compositional data, microbiome, rumen microbiota.

Development Agency: Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES).