

TITLE: SUPPLEMENTED GRASSLANDS ALTERS THE GUT MICROBIAL COMMUNITIES BUT NOT RUMINAL COMMUNITIES IN HEIFERS

AUTHORS: TAKAGAKI, B.M.^{1,2}; FREITAS, A.S.²; DAVID, D.B.³; TÓTOLA, M.R.¹; ROESCH, L.F.W.²

INSTITUTIONS: 1. UNIVERSIDADE FEDERAL DE VIÇOSA, VIÇOSA, MG (AV. P.H. ROLFS, S/N - CAMPUS UNIVERSITÁRIO, CEP 36570-900, VIÇOSA – MG, BRAZIL).

2. UNIVERSIDADE FEDERAL DO PAMPA, SÃO GABRIEL, RS (AVENIDA ANTÔNIO TRILHA, 1847, CEP 97300-000, SÃO GABRIEL – RS, BRAZIL).

3. DEPARTAMENTO DE DIAGNÓSTICO E PESQUISA AGROPECUÁRIA, SECRETARIA DE AGRICULTURA, PECUÁRIA E IRRIGAÇÃO, SÃO GABRIEL – RS, BRAZIL.

ABSTRACT:

Ruminants' gastrointestinal tract harbors a large amount of microorganisms specialized in fermentation of compounds, most of them composed of lignocellulose. In addition, many studies indicate that changes in feeding, such as inclusion of a higher concentration of proteins by ingestion of grains results in changes in ruminal microbiota. In this context, the aim of this work was to evaluate the changes in the microbial community from gut and from rumen of heifers from two different grasslands in the municipality of São Gabriel-RS. Fecal and ruminal fluid samples were collected as representative samples from gut and rumen environment, respectively, after the morning grazing cycle of 20 Brafford heifers. Animals were divided in two groups: one treated on natural grassland and other on a grassland supplemented with fertilizers, leguminous and ryegrass. Samples were stored in sterile conical tubes until extraction of the microbial DNA. Microbial DNA was extracted using PowerSoil DNA Isolation kit (MO BIO, Carlsbad, CA). The amplification of the V4 region of the 16S rRNA gene was done and the amplicons were sequenced using the Ion Torrent PGM platform. Sequences were processed using the pipeline proposed by the Brazilian Microbiome Project and were grouped into Operational Taxonomic Units (OTUs) at 97% similarity. Group comparisons, diversity analysis and differential abundance test were performed in the R environment. One outlier sample was excluded from analysis to avoid possible bias. Sequencing provided a total of 442,458 sequences grouped into 3396 OTUs. Alpha and beta diversity analyzes showed significant differences ($p=0.01$) between the treatments in the fecal samples, but not in ruminal fluid ($p>0.05$). OTU belonging to the family *Paraprevotellaceae* was differentially abundant in fecal samples, being increased in the treatment with supplemented grasslands. This family support the degradation of proteins and carbohydrates, being that the genus CF231 has already been described as increased in certain dosages of nitrates when administered as a supplement to ruminant feed. The greater selectivity of the ruminal environment (mainly pH) may result in lower influences of the grassland on those samples. In short, we showed the gut microbial communities of heifers were affected by different treatments of the grasslands, while the rumen samples kept more stable.

Keywords: Feces, Natural grassland, Rumen, 16S rRNA.

Development Agency: Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq).