

Metagenomics of sheep rumen microbiome under two diet. LD Lopes^a, LRF Silva^b, EM Romagnoli^a, C Ferreira^a, RG Taketani^a, H Louvandini^b, AL Abdalla^b, R Mendes^a. ^aEmbrapa Environment, Laboratory of Environmental Microbiology, Rod. SP340 km 127.5, Jaguariuna SP, 13820-000, Brazil. ^bCentre for Nuclear Energy in Agriculture, University of Sao Paulo, Av. Centenario 303, Piracicaba SP, 13400-970, Brazil.

The rumen microbiome is a dynamic system in which the microbial diversity and community structure are shaped when exposed to different diet compositions. The relative abundance of microbial groups in the rumen microbiome shifts when a given substrate is able to enrich specific groups in detriment of less favoured ones. In this study, we generated more than 3.5 million of 16S rRNA sequences from the microbiome of sheep rumen to identify the bacterial community structure associated to animals under two diet conditions. Fistulated Santa Inês sheep were fed for four weeks with (1) the control diet (corn plus soybean meal 60% and Tifton-85 grass *Cynodon spp.* 40%) or with (2) the diet in which the soybean was fully replaced by *P. platycephala*, a Fabaceae family plant. Twenty-five mL of the ruminal fluids were sampled from four animals for each treatment. Thereafter, samples were anaerobically incubated *in vitro* at 39°C with 0.5 g of the same proportion diet composition used during animal feeding and 50 mL of buffer solution for 24 hours. After the incubation period, total DNA was isolated and 16S rRNA gene was amplified for subsequent metagenomic sequencing by using the PGM Ion Torrent sequencer. Overall, the sheep microbiome was dominated by Firmicutes (17%), Bacteroidetes (8%) and Proteobacteria (7%) phyla. Although the total abundance of dominant bacterial phyla did not show significant shifts when the animals were submitted to different diets, the initial clustering analysis suggests a distinct bacterial community structure associated to each treatment. A significant fraction of the metagenome dataset was comprised by unclassified bacterial sequences (66%), revealing the potential of the sheep rumen to be used as a source for genome discovery and biotechnological applications.