

Dynamics of the sheep rumen microbiome and its relationship with the degradation of biomass

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Considering diet as a modulator of the ruminal microbiome, this work aimed to investigate the impact of sugarcane bagasse on the composition and function of microbial species inhabiting the sheep (*Ovis aires*) rumen. Six cannulated male animals were used in the experiment, where three individuals were fed on a diet consisting of 70% forage and 30% concentrate (control treatment), and three were fed on a similar diet, but with sugarcane bagasse replacing 14% of the forage portion (bagasse treatment). The ruminal contents, i.e., liquid and fiber, were sampled every two weeks during 60 days. We assessed the structure of microbial communities by sequencing regions of bacterial 16S rRNA genes and the fungal intergenic region (ITS2). The 16S rRNA amplicon sequencing analyses revealed a microbial community dominated mainly by Firmicutes and Bacteroidetes throughout the experimental period. The genera *Prevotella* and *Ruminococcus* accounted for 20% and 4% of the bacterial community of rumen, respectively. In the fungal community, the phylum Neocallimastigomycota accounted for 91% of sequences and the main genera adhered on the ruminal fiber were *Piromyces*, *Neocallimastix*, *Orpinomyces*, *Anaeromyces*, *Caecomyces*, and *Cyllamyces*. Furthermore, metagenomic data analysis showed a significant increase in the frequency of enzymes, such as α -1,4-glucanase, α -galactosidase, endo-1,4- β -xylanase, β -xylosidase, xylose isomerase, cellobiose phosphorylase and α -N-arabinofuranosidase in the bagasse treatment. The results of this study demonstrate the potential to increase the discovery and/or recovery of biomass degrading enzymes from ruminants, as well as the possibility to enrich specific microbial groups or functions in the sheep rumen by changing diet.