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**AREA: Microbiologia Ambiental - Divisão B**

**SUB-AREA: Ecologia Microbiana Molecular**

**Deep into to the bacterial communities living in sheep rumen**

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**Resumo:**

The rumen microbiome is specialized in degrading plant biomass by using a variety of enzymes to break down the cell wall, allowing the adaptation of ruminants to different nutritional regimes. Many studies have been conducted toward a full understanding of the host-microorganism relationships focusing on the discovery of new enzymes for biofuel production. In the present study, we aimed to evaluate the bacterial taxonomic composition of the sheep rumen microbiome by high-throughput Ion Torrent PGM sequencing of the 16S rRNA gene (V6 region). Sheep of Santa Inês breed were submitted to two different diet regimes during 60 days, where three animals were fed with a base diet and the other three animals were fed with a sugarcane bagasse based diet. Ruminal fiber samples were collected at 0, 15, 30, 45, and 60 days after the establishment of the experiment, and the total DNA was extracted for sequencing. PCoA analysis indicated two distinct sample clusters, one composed by samples collected at 0, 15 and 30 days; and other by samples collected at 45 and 60 days. We found that ruminal bacterial community richness was similar in both treatments, while the relative abundances of specific groups were different between the two treatments. Overall, the Bacteroidetes (24%) was the dominant phylum in the sheep rumen microbiome, followed by the Firmicutes (23.7%), Proteobacteria (4.2%) and Actinobacteria (4%). It is interesting to note that Fibrobacteres was more abundant in the animals fed with sugarcane bagasse when compared with sheep fed with base diet, indicating the importance of this phylum during the biomass degradation process. Fibrobacteres is an important taxonomic group playing a role during the biomass degradation; consequently it is a potential candidate to be used for the discovery of new enzymes to be applied in biofuel production from sugarcane bagasse.

**Palavras-chaves:** Fiber, DNA, gene, bagasse, sugarcane

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