Prokaryotic Diversity Present in the Semi-Arid Goat Rumen and Its Biotechnological Potential.

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The degradation of fibers and fermentation of sugars occur in the rumen mainly due to the presence of anaerobic microorganisms. Metagenomic studies address the genetic structure of a microbial community without the need for cultivation of microorganisms. The aim of this study was to use a metagenomic approach to characterize the bacterial community present in the rumen of goats adapted to semi-arid conditions and to determine its biotechnological potential for the identification of new enzymes. 16S rDNA gene libraries were constructed from the solid and liquid fractions of the rumen. Approximately 200 non-chimeric sequences with greater 400 bp were obtained for each library. The sequences identified were divided into 5 phyla: Bacteroidetes, Firmicutes, TM7, Verrucomicrobia, Actinobacteria, as well as unclassified bacteria (27.5% of the sequences present in the solid fraction and 15% in the liquid fraction). The high number of sequences belonging to unclassified Bacteria shows that the microbiota of the goat rumen is not is not well known and therefore this microbial community represents a wealth of metabolic pathways. A metagenomic expression library was constructed and clones with activities such as amylase, lipase, β-glicosidase and celobiohydrolase were identified.

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