PS.25.005 MOLECULAR DIVERSITY OF BACTERIA AND ARCHAEA IN THE RUMEN OF GOATS FROM THE SEMI-ARID REGION OF BRAZIL

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The rumen is a complex ecosystem harboring a rich microbial community. Ruminants have a powerful system for fiber fermentation, mainly due to the presence of anaerobic organisms. The aim of this study was to assess the diversity of the microbial ecosystem associated with the rumen of goats from the semi arid region of Brazil using a molecular approach. Total DNA was extracted from the solid and liquid fractions of the rumen; PCR was used to amplify 16S rDNA using primers for the domains Bacteria and Archaea. Approximately 200 non-chimeric sequences with lengths greater than 400 bp were obtained for each Bacteria library and 80 sequences for each library of Archaea. The rarefaction curves revealed that at the distance level of 3%, the sampling effort was sufficient to cover the diversity existing in all libraries. Analysis of 16S rDNA sequences from the Bacteria domain showed the presence of 5 phyla: *Bacteroidetes, Firmicutes,* TM7, *Verrucomicrobia, Actinobacteria* as well as unclassified bacteria representing 27.5% in the solid fraction and 15% in the liquid fraction. The dominant classes: *Clostridia* and *Bacteroidetes*, with 34% and 23% in the solid fraction and 52% and 30% respectively in the liquid fraction, are known to play an important role in the degradation of fibers in other ruminants. Within the domain Archaea, only the phylum *Euryarcheota* was obtained, especially sequences belonging to the methanogenic archaea *Methanobrevibacter* and *Methanosphaera*. In our study we have identified a group of Archaea sequences not previously reported to be associated with the rumen of animals. Despite the fact that the rumen has been studied for years with traditional techniques, the relatively high number of sequences belonging to Bacteria not yet classified and a new group of Archaea found in this study demonstrate that
the microbiota of the rumen of goats is not well known.

Abstract Category
25 The Gut Microbiome