Title: PROSPECTING OF GENE 16S rRNA IN NELORE CATTLE USING THE ILLUMINA PLATFORM

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Abstract:

The rumen is an open ecosystem in which food consumed by ruminants is fermented to release short chain fatty acids and microbial protein, which serve as sources of energy and protein for the animal, respectively. Species of microorganisms in the rumen have developed a series of complex interactions that represent one of the best examples of symbiosis between microorganisms in nature. Conventional taxonomic methods based on culture techniques are being replaced by molecular techniques that are faster and more accurate. The molecular techniques are based on the 16S rRNA sequence, which provides the phylogenetic classifications used to identify and quantify the bacterial community. To evaluate rumen bacterial diversity in this study, three rumen-cannulated Nellore cattle were used. The liquid and solid fractions of the rumen contents were processed to extract metagenomic DNA, and then the amount and integrity of the samples were tested. Next, PCR was performed based on the V1 and V2 hypervariable regions of the 16S rRNA. Following the PCR, a sequence library was constructed, and sequencing was performed using the Illumina platform. Data were analyzed using the software programs MG-RAST and MOTHUR for bacterial relationships. Using this next-generation sequencing technology, it was possible to identify 27 phyla, 5 of which represented 70% of the reads. Approximately 11,407,000 reads of adequate quality were generated, and 812 operational taxonomic units (OTUs) were found at the species level. The combination of whole genome association (WGA) and the Illumina platform allowed for the evaluation of a wide range of organisms in the rumen microbiome and highlighted the possibility of future bioprospecting for genes that can be applied in animal nutrition.

Keywords: bacteria, Firmicutes, Illumina, rumen, 16S rRNA