--ANALYSIS OF FECAL MICROBIOME DIVERSITY IN NELORE CATTLE UNDER DIFFERENT ENVIRONMENTAL CONDITIONS

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Abstract:

The microbiome is composed of a complex community of microorganisms, which interact in an intricate way, playing a crucial role in the health, performance and adaptation of cattle to different environments. Understanding how the microbiota can vary under different environmental conditions can provide important insights into such interactions between the intestinal microbial community of these ruminants and the environment they are exposed to. To this end, this work aimed to analyze the diversity of fecal microbiota in Nelore cattle during different periods: grazing during the dry season, grazing during the rainy season and feedlot. Samples from 85 Nelore cattle derived from the " Meat Quality" trial (June 2020 to July 2021) were collected directly from the animals' rectal ampulla, submerged in nitrogen and stored at -80°C. Fecal samples were extracted using Quick-DNA™ Fecal/Soil Microbe Miniprep Kit and subsequently sequenced using next-generation sequencing on Illumina PE250 platform with specific primer-set-pairs for amplification of ribosomal 16S gene of bacteria and Archaea. The QIIME 2 software was used for data processing and analysis. The quality (>Q25) of the sequences were evaluated and trimmed at positions 250 forward and reverse. The DADA2 plugin was used to cluster the raw sequences into Amplicon Sequence Variants (ASVs), which were annotated and compared to the SILVA database version 138.1 for taxonomic assignment. Alpha and Beta diversities were calculated to provide an overview of the abundance, distribution, difference or similarity of this biological community in the different samples using the phyloseq package in RStudio v. +386 software. Based on the Shannon index, we observed that there is a greater bacterial diversity during the grazing period in the dry season compared with the rainy season and feedlot period (p-value $\leq$ 0.05, Wilcoxon test). Additionally, the Shannon index also revealed that the diversity of Archaea was higher during the dry and rainy seasons than the feedlot period (p-value $\leq$ 0.05, Wilcoxon test). Considering the bacterial samples, beta diversity using Non-Metric Multidimensional Scaling (NMDS) and Bray-Curtis distance showed a segregation of each period, with the rainy season period being more closely related to feedlot. Regarding Archaea, Beta diversity exhibited greater clustering and closer proximity of samples among the three periods. This analysis of fecal microbiome diversity in Nelore cattle under different environmental conditions may contribute to new approaches and strategies for management and nutrition, potentially enhancing the efficiency and sustainability of animal production and expanding knowledge about microbial ecology and its impacts on cattle. It could also contribute to reducing the noise in genetic evaluations.

Palavras-chave: Microbiome; Nelore cattle; Fecal microbiota diversity; Environmental conditions; Metabarcoding

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