MICROBIOTA DIVERSITY AND COMPOSITION OF YOUNG NELORE BULLS

Liz Jiannine Fuentes Rojas [1,2]; Gabriel Alexander Colmenarez [3]; Wanderson Anjos da Silva [1,2]; Bárbara Cunha Padilha Antonio [1,2]; Liliane Costa Conteville [2]; Tainã Figueiredo Cardoso [4]; Priscila Silva Neubern de Oliveira [1,2]; Gerson Barreto Mourão [5]; Cintia Righetti Marcondes [2]; Luciana Correia de Almeida Regitano [2]

[1]. São Carlos, SP, Brazil. Department of Genetics and Evolution, Federal University of São Carlos; [2]. São Carlos, SP, Brazil. Embrapa Southeast Livestock; [3]. Foz do Iguaçu, PR, Brazil. Federal University of Latin American Integration; [4]. 08193 Bellaterra, Spain. Centre for Research in Agricultural Genomics (CRAG), CSIC-IRTA-UAB-UB, Universitat Autònoma de Barcelona; [5]. Piracicaba, SP, Brazil. Center for Functional Genomics, Department of Animal Science, University of São Paulo (ESALQ - USP)

Abstract:
Ruminants depend on a complex and diverse microbial community that is responsible for the development, health and productivity of the host, establishing important levels of association. The study of microbial populations within the gastrointestinal tract represents a potential avenue for understanding host biological processes from the perspective of symbiotic microorganisms. Next generation sequencing studies have used 16S rRNA sequencing to describe the microbiota composition, stating that metabarcoding can offer new opportunities to use microbial composition to assess animal performance phenotypes, such as feed efficiency. The present study aimed to explore the abundance and taxonomic diversity of the fecal microbiota of 487 Nelore bulls at ages between 18 and 30 months, participating in the 2019 to 2022 editions of the National Young Bull Evaluation Program (PNAT). Fecal samples were collected from the rectal ampulla of Nelore bulls and DNA extraction was performed from 150 mg of stool using the Quick-DNA ™ Fecal/Soil Microbe Miniprep Kit (ZYMO Research Corp). PCR target amplification for 16S rRNA was performed using designed primers and amplicons were sequenced in an Illumina NovaSeq platform (2 × 250 bp). After sequencing, raw reads were filtered for quality (>Q25) and trimmed at positions 250 (F) and 250 (R) using QIIME 2 v.2022.8. The filtered data was submitted to the DADA2 package to generate amplicon sequence variants (ASVs) and sequences were annotated using the SILVA database v.138.1 . The resulting ASV table was used to determine alpha diversity (number of ASVs and the Shannon-Wiener index) and beta diversity (NMDS, Bray Curtis Method) with RStudio version 4.2.2. We identified a total of 132.208 bacterial ASVs and 2.018 archaeal ASVs in the young Nelore bulls' microbiomes. Based on the alpha diversity, we could observe a large intra-year diversity considering both bacteria and archaeal populations. When comparing the Shannon index between each pair of years, we observed that all four groups were significantly different ($p <= 0.05$, Wilcoxon test) from each other regarding bacterial diversity, but that there were no significant differences ($p > 0.05$, Wilcoxon test) regarding archaeal diversity. Regarding Beta diversity, we observed a marked clustering of bacteria population among samples of each year. In all four years, the most abundant genus identified in archaea was Methanobrevibacter, of the family Methanobacteriaceae and the phylum Euryarchaeota. The most abundant genus identified in bacteria was Rikenellaceae RC9 gut group, the family Lachnospiraceae and the phylum was Firmicutes. Further analysis will be performed to associate these Alfa and Beta diversities and microbial abundances with the cattle's performance traits and other phenotypes of economic importance, such as feed efficiency.
Palavras-chave: Metabarcoding; Microbiota; Taxonomic diversity; Microbial abundances; Nelore bulls

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