

## **FECAL BACTERIAL MICROBIOME OF CLOSE TO WEANING NELORE ASSOCIATED WITH FEED EFFICIENCY**

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### **Abstract:**

An integrative perspective on microbial ecology based on microbial modules can aid in comprehending the microbial interactions associated with animal phenotypes. The present study aimed to analyze fecal bacterial profiles obtained close to the weaning period associated with the residual feed intake (RFI) phenotype measured during feedlot Nelore cattle. Stool samples were collected from the animals' rectal ampulla. DNA extraction was performed using the Quick-DNA™ Fecal/Soil Microbe Miniprep Kit. Target PCR amplification for bacterial 16S rRNA was performed using specific primers and the amplicons were sequenced on an Illumina platform. After sequencing, the raw reads were filtered and clipped using QIIME 2 v.2022.8. The filtered data was submitted to the DADA2 package to generate amplicon sequence variants (ASVs) and the sequences were annotated using the SILVA database v.138.1. Extreme animals for RFI trait were selected: eight efficient and eight inefficient. Weighted correlation network analysis was performed to construct a microbiome network and to identify microbial modules using the CEMiTool R package. A total of 11 ASVs modules were identified. Among these modules, 10 showed significant correlation with RFI trait, with modules M1 and M2 being the most prominent. M1 exhibited a negative normalized enrichment score (NES) of -5.23 regarding the efficient group, and a NES = 5.14 regarding the inefficient group, indicating that an increase of these bacteria tends to increase RFI values, thus reducing feed efficiency. On the other hand, M2 exhibited a positive NES of 4.72 compared to the efficient group (and a NES = -4.73 for the inefficient group), so the increase of these bacteria grouped in this module tends to decrease RFI values, improving the feed efficiency. In M1, top hub ASVs stood out to the families *Muribaculaceae*, *Anaerovoracaceae*, and *Oscillospiraceae*. On the other hand, in M2 we highlight the hub ASVs corresponding to the *Monoglobaceae* and *Lachnospiraceae* families. Interestingly, ASVs belonging to the *Ruminococcaceae* family were associated with both low RFI (more efficient) and high RFI (less efficient) steers, implying that distinct genera within this family may perform diverse functions that result in contrasting impacts on the feed efficiency phenotype. In previous works, our group have already highlighted the presence of these bacteria associated with RFI. In conclusion, our results indicate that the microbiome communities can be classified by network analysis, pointing to weaning as a promising period to provide early indicators of performance biomarkers.

**Palavras-chave:** Biological networks; Fecal microbiota; Livestock microbiome; Nelore; RFI

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