platform, with a throughput of 8,000,000 paired-end reads per sample. Reads were trimmed and low-quality sequences were removed. Host reads were mapped to the *Bos taurus* genome (ARS-UCD1.2) with STAR software. Differential expression (DE) analyses were performed using DESeq2 software and analyzed to predict potential regulatory target genes with Targetscan and DIANA miRPath v3.021 softwares. Functional enrichment of target genes was performed with WEB-based Gene seT AnaLysis Toolkit. In total, 163 expressed miRNAs were identified, being seven miRNAs more expressed in the efficient group; bta-miR-126 ($p$adj =0.0019), bta-miR-30a ($p$adj =0.0042), bta-miR-196a ($p$adj =0.0164), bta-miR-205 ($p$adj =0.0401), bta-miR-27b ($p$adj =0.0517), bta-miR-143 ($p$adj =0.0965), and bta-miR-155 ($p$adj =0.0942). Target genes from bta-miR-143 were enriched for PI3K-Akt signaling pathway and target genes from bta-mir-27b were enriched for Type II diabetes mellitus, Insulin resistance, TNF, and Insulin signaling pathway. Previous studies also identified these pathways related to RFI in a Nelore population. Altogether, these results point to miRNAs identified from the stool as potential regulators of feed efficiency, which may provide the knowledge to develop future strategies to manipulate the microbiome.

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Microbial diversity in the stool of Bos indicus divergent for feed efficiency

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Microbiome research is gaining attention in livestock species, as it assists in understanding host biological processes under the prism of symbiotic microorganisms. Feed efficiency is a livestock production trait with economic and environmental impacts, and there is increasing evidence that the gut microbiota plays a vital role in its regulation, suggesting that the modulation of an animal's microbiota composition can promote more sustainable and efficient livestock production. 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 feed efficiency. For this study, stool samples were collected from the rectal ampulla of 16 Nelore bulls divergent for Residual Feed Intake (RFI) value. DNA extraction was performed using the Quick-DNA™ Fecal/Soil Microbe Miniprep Kit (ZYMO Research Corp), using 150 mg of stool. PCR target amplification for bacterial 16S rRNA was performed using designed primers and amplicons were sequenced in an Illumina Hiseq platform (2×250 bp) using the Illumina V3 sequencing kit. After sequencing, raw reads were filtered for quality (>Q25) and trimmed at positions 220 (F) and 175 (R) using QIIME 2 version 2018.8. The filtered data was submitted to the DADA2 package to generate amplicon sequence variants (ASVs) and bacterial sequences were annotated using the SILVA database version 132. The resulting ASV table was used to determine alpha diversity (number of ASVs and the Shannon–Wiener index) with QIIME2. We identified a total of 5006 bacterial ASVs in the Nelore bulls' microbiomes. The most prominent bacterial phyla identified in the both groups were Firmicutes and Proteobacteria. Comparison of samples from different groups using alpha diversity metrics (Chao I index and Shannon index) revealed no significant difference ($p > 0.10$) in the richness of bacteria populations between efficient and inefficient groups. Nonetheless, Pearson correlation analysis between the Shannon index and RFI showed significant association ($p < 0.10$), indicating a relationship between feed efficiency and microbial diversity.

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RNA-seq profiling of milk somatic cells in four cattle breeds reared in different management systems

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The lactation cycle is a continuous process where several developmental and physiological changes occur in the mammary gland in particular changes in its functionality, milk yield and milk composition, and mammary epithelial cells (MECs). MECs are involved in the synthesis and secretion of milk, and in the immune response. The principal aim of the present study was to profile the transcriptome of bovine milk somatic cells (BMSCs) in four cattle breeds, some of which not previously investigated: Holstein (HO), Simmental (SM), and Simmental × Holstein (SM × HO) reared in Monterotondo (Italy) in an intensive production system, under the same management and feeding

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