MICROBIAL ABUNDANCE AND EXPRESSION IN THE RUMEN MICROBIOME OF NELORE CATTLE

Juliana Virginio da Silva[1,2]; Liliane Costa Conteville[2]; Bruno Gabriel Andrade[3]; Adhemar Zerlotini Neto[4]; Gerson Barreto Mourão[5]; Luiz Lehmann Coutinho[5]; Luciana Correia de Almeida Regitano[2]

[1]. São Carlos, São Paulo, Brasil. Universidade Federal de São Carlos; [2]. São Carlos, São Paulo, Brasil. Embrapa Pecuária Sudeste; [3]. Cork, Ireland. Munster technological University; [4]. Campinas, São Paulo, Brasil. Embrapa Informática Agropecuária; [5]. Piracicaba, São Paulo, Brasil. Universidade de São Paulo

Abstract:

The study of the microbiome related to fermentation in ruminants can help to optimize the conversion of animal protein. However, most species present in the rumen are unculturable , which makes the study of such microorganisms challenging. Advances in scientific knowledge, especially in the areas of molecular biology, biotechnology and bioinformatics, have paved the way to provide deeper genetic information on the rumen microbiome. Within this scenario, metagenomics and metatranscriptomics have been filling some gaps and deepening our knowledge about the microbiome. By integrating both approaches, we can elucidate not only the taxonomy of the microorganisms present in the rumen but also study the gene expression within this community. Therefore, in the present work we analyzed the gene expression of the most abundant genera identified in the rumen metagenomes of 50 Nelore cattle. For this, the total DNA and the total RNA of the rumen contents were extracted and sequenced on an Illumina NextSeq equipment. The raw DNA and RNA paired-end reads were trimmed and quality filtered. The rRNA reads were then separated from the non-rRNA reads using SortMeRNA software. The host's genetic material was filtered using the BBmap software. The filtered sequences of both DNA and RNA were submitted to the Kraken pipeline. The 20 most abundant genera identified on the metagenomes and metatranscriptomes were selected. Pearson's correlations between the 20 most abundant genera in the metagenome and their respective degrees of expression in the metatranscriptome were obtained. The results indicate that out of 20 most abundant genera in the metagenomes, 10 also stood out in the metatranscriptomes, being the most active. They were: *Prevotella, Bacteroides, Clostridium, Methanobrevibacter, Blautia, Fibrobacter, Ruminococcus, Alistipes and Butyrivibrio*. These genera play important roles in starch degradation and utilization, polysaccharide degradation, cellulose degradation, proteolytic activity, lipolytic activity, and fermentation of soluble carbohydrates. Pearson's correlation analysis indicates that there is a positive correlation ($p = 0.91$) between the mean abundance obtained in the metagenome and the mean expression level of the metatranscriptome. The results found throughout this work indicate that there is a relationship between the abundance of microorganisms present in the rumen content and their respective degrees of expression. Therefore, this study provides a preliminary comparison between high-throughput sequencing metagenome and metatranscriptome data generated from Nelore rumen contents and may serve as a basis for future studies.

Palavras-chave: Metatranscriptome; Metagenome; Rumen Microbiome; ;

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