Liver DNA methylation profile in Nelore cattle extremes for feed efficiency

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The production cost of cattle is high, especially the fraction related to animal nutrition. The increase in feed efficiency may provide increased efficiency in beef production, minimizing feed expenditures, methane gas emission and nitrogen excretion. Residual feed intake (RFI) is one of the most adopted measurements of feed efficiency, which is a complex trait controlled by different metabolic processes and environmental factors. For this reason, understanding gene expression profile and its regulation may help to understand the outcomes in phenotypic variation. Therefore, using the reduced representation bisulfite sequencing (RRBS) methodology, this study aimed to determine the DNA methylation profile in hepatic tissue of Nelore cattle exhibiting extreme RFI phenotypes. Differentially methylated cytosines (DMCs) and regions (DMRs) were determined using the new version of the bovine reference genome (ARS-UCD1.2). We detected 1,493 DMCs and 279 DMRs between high residual feed intake (or less efficient) and low residual feed intake (or more efficient) animal groups. DMCs and DMRs were analyzed according to their distribution on the bovine chromosomes, annotation and proximity to the closest gene. It was found one DMC in the *IDH2* gene and one DMR in the *KCNQ3* gene, and both genes were previously identified as associated with feed efficiency by gene expression studies in cattle. Other DMCs and DMRs are being compared with results from previous gene expression analyzes to understand their role on the regulation of the closest gene. These results will add new layers of information to molecular regulatory mechanisms related to feed efficiency in cattle.

Keywords: feed efficiency, gene expression regulation, RRBS, differential methylation.

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