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Beef meat is one of the products with the highest intensity of greenhouse gas emissions in livestock production chains. Emissions are mainly in the form of methane (CH₂) produced by enteric fermentation. This process is carried out by the symbiotic ruminal microbiota and causes a loss of energy for the host which may decrease the feed efficiency (FE). There are numerous related studies that investigate the relationships between the rumen microbiome and diverse expressed phenotypes of ruminants. Ross et al. (2013) support that a metagenomic approach could be a powerful tool that may surpass prediction accuracies based only on host genome, and there are confirmed by Roehe et al. (2016); Wallace et al. (2017), Delgado et al. (2019), and so on. Metagenomic studies allow profiling the microbial community of a sample and infer gene functions of those species found to determine associations to studied traits. The current research defines a guideline to perform untargeted metagenomics sequencing studies with the objective of determine genetic markers associated with CH₄ emissions and FE. In order to accomplish this, we sampled ruminal contents of two groups of Hereford steers (n = 36) selected based on their high and low efficiency. Samples were frozen at -80 °C, freeze dried and stored until the time of DNA isolation and complete sequencing. At this moment, metadata information of each sample was recorded in a database and once multiple nucleotide sequences are obtained, we will perform the bioinformatic processing and statistical analysis following the present guideline. This work will be significant in animal genetic improvement programs for future selection of superior cattle using genomic information to predict phenotypes that are complex and expensive to measure, as well as contribute to mitigation of CH_4 emissions while improve FE.

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