

CARBOHYDRATE ACTIVE ENZYMES IN METAGENOME-ASSEMBLED GENOMES FROM RUMINAL AND STOOL MICROBIOMES OF NELORE CATTLE**Liliane Costa Conteville¹; Bruno Gabriel Andrade²; Adhemar Zerlotini³; Gerson Mourão⁴; Luiz Lehmann Coutinho⁴; Luciana de Almeida Regitano¹**

¹. São Carlos, SP, Brazil. Embrapa Pecuária Sudeste; ². Cork, Ireland. Computer Science Department, Munster technological University; ³. Campinas, SP, Brazil. Embrapa Informática Agropecuária; ⁴. Piracicaba, SP, Brazil. Center for Functional Genomics, Department of Animal Science, University of São Paulo

Abstract:

The cattle rumen is specialized in the breakdown of dietary matter into energy and nutrients, which is mainly performed by enzymes encoded by the microbiome. Among these enzymes, the carbohydrate-active enzymes (CAZymes) play a crucial role in the processing of complex dietary carbohydrates into components that can be absorbed by the host. Considering that the rumen and stool microbiome composition and genetic content are largely determined by the host's diet, here, we recovered draft genomes from 52 Brazilian Nelore bulls' microbiomes to explore the effects of different diets on the set of CAZymes. These animals belong to two feed intervention treatment groups, of which 26 received a conventional diet and 26 received a by-product-based diet. Total DNA extracted from the rumen and stool samples were used to construct metagenomic libraries, which were sequenced on an Illumina NextSeq equipment. Raw paired reads were trimmed and quality filtered. Reads that mapped the host genome were removed. A total of 2.6 billion read pairs remained after these steps. For genome recovery, the metagenomes were co-assembled and single-assembled using MEGAHIT. Binning and de-replication were performed using MetaBat2 and dRep, respectively. High-quality bins were taxonomically assigned with GTDB-Tk. Predicted proteins from the MAGs were searched against the CAZy database using dbCAN2. With this, we recovered 447 ruminal and 469 stool metagenome-assembled genomes (MAGs). Most ruminal and stool MAGs were classified as belonging to the Clostridia class, mainly represented by the orders Oscillospirales and Lachnospirales, and to the Bacteroidia class, represented by the Bacteroidales order. Among the putative CAZymes genes identified in the MAGs, the majority encode glycoside hydrolases (GHs) and glycosyltransferases (GTs). The most abundant GHs in both ruminal and fecal MAGs are members of the GH13, GH3, GH2, GH5, GH43 and GH77 families. These families comprise oligosaccharide degrading enzymes, but also cellulose, hemicellulose and starch degradation enzymes. The diversity in the functions and pathways to which the CAZymes are associated may be a reflection of the different diets that were administered to the animals. This study has the potential to unravel the repertoire of enzymes involved in feed degradation and their potential impact on cattle phenotypes such as feed efficiency and methane emission.

Palavras-chave: Metagenome-Assembled Genomes; Rumen Microbiome; Fecal Microbiome; Nelore; CAZymes

Support / Acknowledgment

Funded by National Council for Scientific and Technological Development, CNPq (grant number: 456191/2014-3) and The São Paulo Research Foundation - FAPESP (grant number: 2019/04089-2). L.C.Conteville is funded with a fellowship from FAPESP (process number 2020/15565-7)