Metagenomic analysis of sheep rumen microbiome for carbohydrate-active genes discovery

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The breakdown of plant biomass into simple sugars for bioethanol production is still inefficient and costly due to the recalcitrant nature of plant fiber. The search for new lignocelulolytic genes in microbial communities naturally evolved in a biomass-degrading ecosystem is a promising strategy for identification of new genes. In this context, this study aimed to explore the sheep rumen microbiome using metagenomics for genes discovery. Six male sheep (Ovis aries) were used in the experiment where three animals were fed with a basal diet and three were fed with a diet including sugarcane bagasse for 60 days. To characterize carbohydrate-active enzymes (CAE), total DNA was isolated from the solid contents of rumen followed by shotgun sequencing generating 4.68 GB of metagenomic data. The assembled contigs allowed identification of 27 different CAE (NCBI-nr), including 11 lignocellulases, 13 amylases and 3 other putative CAE from animals under the control treatment and 106 putative partial CAE representing a total of 52 lignocellulases, 46 amylases and 8 other putative CAE from animals fed with diet amended with sugarcane bagasse. Fifty-four complete CAE genes, including, 6 Beta-glucosidase, 1 Glucan endo-1,3-beta-D-glucosidase, 1 Xylan 1,4-beta-xylosidase, 6 Beta-mannosidase, 4 Chitinase, 8 Beta-N-acetylhexosaminidase, 8 Beta-galactosidase, 9 Cellulase, 4 Alpha-galactosidase, 6 Alpha-amylase and 1 Endo-1,4-beta-xylanase, were identified. The preliminary data analysis showed that addition of sugarcane bagasse in the sheep diet affects the diversity of CAE and their relative abundance.

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