TLP-396. Metagenomic analysis of microbiome structure and functions in sheep rumen

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Introduction. Plant biomass is a resource available at large scale with important application for second-generation biofuel production. The enzymes costs associated with their low efficiency represent a big barrier for biofuel production economically viable from biomass. However, biomass degrading enzyme recovery from naturally enriched environments, such as the rumen, offers a promising strategy for identification of new enzymes with higher lignocellulosic activity. Search for biomass degrading enzymes in the rumen of sheep fed with a diet amended with sugarcane bagasse in comparison with control treatment.

Materials and methods. Sheep were fed for 60 days with a diet including sugarcane bagasse or without bagasse (control) under experimental conditions considering three replicates. Metagenomic DNA was extracted from the solid contents of rumen followed by sequencing using miseq illumina plataform. The illumina sequence data was quality filtered and assembled according to the mg-rast pipeline. The scaffolds were subject gene prediction using mg-rast and comparative analysis were performed using stamp.

Results. The bacteria domain represented CA. 97% of reads considering the total community. Bacteroidetes phylum was the most abundant (~48%), followed by firmicutes (~33%) and proteobacteria (6%). Pcoa analyses showed no significant difference between microbiome structures across treatments, nevertheless, samples from different treatments clustered when the functional profile was considered. Targeting specific hydrolase enzymes in the metagenomes revealed that beta-xylosidase, family gh43 ($p=0.023$) and diadenosine tetraphosphate (ap4a) hydrolase ($p=0.047$) are significantly more abundant in the animals fed with a diet amended with sugarcane bagasse.

Conclusions. Considering the sheep rumen as an untapped source of potential biomass degrading enzymes using a diet amended with sugarcane bagasse is possible to increase the abundance of hydrolases genes.