The desperate need for alternative sources of fuel has been abundantly clear in the past few years. Biofuel production through utilizing and characterising putative enzymes that are responsible for efficient lignocellulosic biomass degradation with the purpose of sugar/saccharide extraction is the future for employing such biomass. This untapped fuel source is degraded naturally in the microbiome within the rumen of the Moose (Alces alces alces). Therefore, in this study we analyzed the microbiomes of six moose rumen samples; three from each of the two regions of Öland & Växjo/Småland in Sweden. Taxonomic analysis through Sortmerna (16S & 18S rDNA) and RDP classifier demonstrated the dominance of phylums Bacteroidetes and Firmicutes, both of which are known to possess cellulolytic activity. Upon the assembly of the six samples for an input of 75 GB (following quality trimming & normalization), producing around 166,000 contigs, the entire assembly was then annotated through the Community Cyber infrastructure for Advanced Microbial Ecology Research and Analysis (CAMERA for short). A total of 682328 genes were predicted, of which around 17,663 were predicted to encode carbohydrate-active enzymes. Delving more into the unique carbohydrate-active enzymes and their acting substrates will substantially improve upon the possible utility of such enzymes in the industrial path of the lignocellulosic biomass degradation through enzyme cocktails.

Keyword: Metagenomics, Microbiome, Next generation sequencing, CAZy