In vitro fermentation of key dietary compounds with rumen fluid: A genome-centric perspective

The anaerobic decomposition of organic substrates leads to the generation of gases, such as methane, which can either be a valuable energy carrier in industrial applications or can be considered as a main greenhouse gas when it is naturally emitted. In this study we investigated in vitro the effect of dietary compounds, such as starch and proteins, on the microbial community present in the rumen fluid. High throughput shotgun sequencing, followed by metagenomic assembly and binning allowed the extraction of 18 genome bins. A composite bioinformatic analysis led to the prediction of metabolic pathways involved in the degradation of dietary compounds and in the biosynthesis of crucial products like propionate, methane and ammonia. The identification of genomes belonging to poorly characterized phyla such as Thermoplasmata and Elusimicrobia shed light on their putative role. The high abundance of methylotrophic archaea in the inoculum suggests a relevant role in methane production.

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