

Effects of Glucogenic and Lipogenic Diets on Ruminal Microbiota and Metabolites in Vitro

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Abstract : To improve the energy status of dairy cows in the early lactation, lots of jobs have been done on adjusting the starch to fiber ratio in the diet. As a complex ecosystem, the rumen contains a large population of microorganisms which plays a crucial role in feed degradation. Further study on the microbiota alterations and metabolic changes under different dietary energy sources is essential and valuable to better understand the function of the ruminal microorganisms and thereby to optimize the rumen function and enlarge feed efficiency. The present study will focus on the effects of two glucogenic diets (G: ground corn and corn silage; S: steam-flaked corn and corn silage) and a lipogenic diet (L: sugar beet pulp and alfalfa silage) on rumen fermentation, gas production, the ruminal microbiota and metabolome, and also their correlations in vitro. The gas production was recorded consistently, and the gas volume and producing rate at times 6, 12, 24, 48 h were calculated separately. The fermentation end-products were measured after fermenting for 48 h. The ruminal bacteria and archaea communities were determined by 16S RNA sequencing technique, the metabolome profile was tested through LC-MS methods. Compared to the diet G and S, the L diet had a lower dry matter digestibility, propionate production, and ammonia-nitrogen concentration. The two glucogenic diets performed worse in controlling methane and lactic acid production compared to the L diet. The S diet produced the greatest cumulative gas volume at any time points during incubation compared to the G and L diet. The metabolic analysis revealed that the lipid digestion was up-regulated by the diet L than other diets. On the subclass level, most metabolites belonging to the fatty acids and conjugates were higher, but most metabolites belonging to the amino acid, peptides, and analogs were lower in diet L than others. Differences in rumen fermentation characteristics were associated with (or resulting from) changes in the relative abundance of bacterial and archaeal genera. Most highly abundant bacteria were stable or slightly influenced by diets, while several amylolytic and cellulolytic bacteria were sensitive to the dietary changes. The L diet had a significantly higher number of cellulolytic bacteria, including the genera of Ruminococcus, Butyrivibrio, Eubacterium, Lachnospira, unclassified Lachnospiraceae, and unclassified Ruminococcaceae. The relative abundances of amylolytic bacteria genera including Selenomonas_1, Ruminobacter, and Succinivibrionaceae_UCG-002 were higher in diet G and S. These affected bacteria was also proved to have high associations with certain metabolites. The Selenomonas_1 and Succinivibrionaceae_UCG-002 may contribute to the higher propionate production in the diet G and S through enhancing the succinate pathway. The results indicated that the two glucogenic diets had a greater extent of gas production, a higher dry matter digestibility, and produced more propionate than diet L. The steam-flaked corn did not show a better performance on fermentation end-products than ground corn. This study has offered a deeper understanding of ruminal microbial functions which could assist the improvement in rumen functions and thereby in the ruminant production.

Keywords : gas production, metabolome, microbiota, rumen fermentation

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