Effect of dietary linseed oil and propionate precursors on ruminal bacterial community, composition and diversity in Yanbian Yellow steers

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■ Abstract

The rumen microbial ecosystem is a complex system and rumen fermentation processes include interactions among microorganisms. There are important relationships between dietary variety and ruminal bacterial composition. We investigated ruminal fermentation characteristics and compared the ruminal bacterial communities using tag amplicon pyrosequencing analysis in Yanbian Yellow steers fed linseed oil and propionate precursors (malate, fumarate). Supplementation of linseed oil and propionate precursors in the diet increased ruminal pH, total VFA concentrations and the molar proportion of propionate in our study. The most abundant bacterial operational taxonomic units in the rumen content are those related to feed differences. Surveys on the rumen microbiota, indicates a core microbiota composed of Firmicutes and Bacteroidetes phyla. Further analysis indicated that Bacteroidetes was the most abundant member of the ruminal bacterial communities and genus Prevotella was highly represented in our shared microbial community when steers fed linseed oil and propionate precursors. However, for control and linseed oil diets, Firmicutes was the most abundant phylum and the genus Ruminococcaceae was absolutely predominant. Overall, feeding a diet supplemented with a moderate level of linseed oil and propionate precursors may alter the ruminal fermentation pattern, and this alteration was accompanied with changes in overall bacteria communities and similarities in rumen ecosystem in Yanbian Yellow steers.

Key words: linseed oil, propionate precursors, bacterial community, diversity

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