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# The effect of different forage on rumen microbiota and milk composition of Holstein late lactation milking cows (1)

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## Abstract

The objective of this was to compare the milking cow's microbiota profiles and milk composition by feeding different forage total mix rations. A total of 10 late lactation milking cows with similar milk production and lactation days were selected, and five lactating cows were in each Pangola hay (P) or Bermuda hay (B) group. In the experimental period, cows were pre-fed for 18 days. Milk samples were collected in the last three days, and rumen fluid samples were only collected at the end of the experimental period. The results showed 2,071 and 1,974 DNA barcoding of unique microbial species in the rumen of dairy cows in groups P and B, respectively, and between different treatment groups. At the phylum level, the rumen microorganisms of the P and B groups were dominated by four dominant bacteria, including *Bacteroidetes, Firmicutes, Proteobacteria, and Tenericutes*. Nevertheless, the relative abundance of the dominant phylum in the samples of the two treatment groups was different. The relative abundance of Bacteroides as the first dominant phylum in the samples of group P was 69.81%, which was higher than that of 67.22% in group B. The genus with the highest relative abundance in group P and B cattle samples was Prevotella, accounting for 49.45% and 50.38%, respectively. PCA analysis indicated that *Prevotella* was the major bacteria with higher contributions to variability, *Pseudobutyrivibrio, Kineothrix, Butyrivibrio, and Alistipes* were major contributors to PC2 variability. No significant differences existed between groups P and B of milk yield, fat, protein, lactose, solids not-fat, urea nitrogen, and citric acid content. However, the content of *de novo* fatty acids (0.98 vs. 0.75 g/100 g of milk) in the milk of group P was significantly higher than that of group B ($p < 0.05$). To summarize the results, the composition of rumen microbiota in milking cows fed with different ration compositions was similar, but the proportions differed. Understanding the changes in rumen core microbial composition and milk composition of milking cows with different forage complete mixed diets will help to develop the most suitable ratio of domestic forage that is stable in the rumen and capable of utilizing production capacity.

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