

Effects of Different Combinations of Alfalfa & Oat Hay on Production Performance, Digestion Metabolism & Ruminal Microflora of Dairy Cows

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The objective of this study was to explore the effects of different combinations of alfalfa and oat hay on the production performance, digestion metabolism and ruminal microflora of dairy cows. Sixty Holstein cows in mid lactation were selected (body weight 595.9 ± 22.5 kg, milk yield 26.34 ± 0.86 kg/d) and randomly allocated to 3 groups with 4 replicates in each group and 5 cows in each replicate. The dairy cows were fed with basic diet in AA group, and oat hay was used to replace 1/4 and 1/2 alfalfa hay in QO and HO groups, respectively. The pre-test period lasted for 14 days, and the trial period lasted for 56 days. Then three Holstein cows with permanent rumen fistulae were randomly selected and fed the same diet as group AA, QO and HO, respectively. The pre-test period lasted for 20 days, and the trial period lasted for 3 days. The results showed that: 1) Compared with AA group, the dry matter intake (DMI) and milk yield in QO group were significantly increased ($P < 0.05$), while those in HO group were significantly decreased ($P < 0.05$). 2) The milk fat rate of QO group was higher than that of AA and HO groups ($P < 0.05$), and the milk protein content was higher than that of HO group ($P < 0.05$). 3) The apparent digestibility of dry matter (DM), crude protein (CP) and neutral detergent fiber (NDF) in QO group was significantly higher than that in AA group ($P < 0.05$), and the rumen disappearance rate of DM, NDF and acid detergent fiber (ADF) were the highest in this group at most time points. 4) At the phylum level, the relative abundance of *Bacteroidetes* in AA, HO and QO groups were 54.07%, 44.72% and 38.31%, respectively, and AA group was significantly higher than QO group ($P < 0.05$). The relative abundance of *Proteobacteria* in AA, HO and QO groups were 4.08%, 23.33% and 26.64%, respectively, among which HO and QO groups were significantly higher than AA group ($P < 0.01$). 5) At the genus level, compared with AA group, *Succinivibrionaceae_UCG-001* in HO and QO groups were significantly increased ($P < 0.01$), and *norank_f_Lachnospiraceae* was significantly decreased ($P < 0.01$). *Prevotella_1* in QO group and *Rikenellaceae_RC9_gut_group* in HO group were also significantly lower than those in AA group ($P < 0.05$). At the same time, *norank_f_Bacteroidales_BS11_gut_group* and *Butyrivibrio_2* enriched in AA group ($P < 0.05$), and *Roseburia* enriched in HO group ($P < 0.01$). 6) The apparent digestibility of NDF had positive correlations with *Succinivibrionaceae_UCG-001* ($R = 0.7167$, $P = 0.0298$), and had negative correlations with *norank_f_Lachnospiraceae* ($R = -0.7167$, $P = 0.0298$). While the milk protein had positive correlations with *Rikenellaceae_RC9_gut_group* ($R = 0.7000$, $P = 0.0358$) and *norank_f_Lachnospiraceae* ($R = 0.7500$, $P = 0.0199$). In conclusion, when alfalfa and oats are combined in a ratio of 3:1, it can promote the degradation of feed fiber and protein by changing the rumen microbial composition, and then to improve the production performance, milk quality, degradation rate and apparent digestibility of nutrients in the rumen of dairy cows.

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