Ruminal bacterial community change in response to diet-induced variation of ruminal trans-10 fatty acids

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Background and Objective

Trans fatty acids (FA) are produced during the biohydrogenation of linoleic acid in the rumen. Because of their health-promoting properties, trans-11 isomers, which are usually the most abundant biohydrogenation intermediates, are most desirable (1). However, in high yielding dairy cows, when high concentrate diets containing fat are fed to cows, a shift from trans-11 to trans-10 FA can occur, therefore, trans-10 isomers can become the predominant biohydrogenation intermediates, inducing milk fat depression in dairy cows (2) and having possible detrimental effects on human health (3).

The aim of this work was to study the bacterial community dynamics in response to diet-induced trans-10 FA shift.

Methods

Four cannulated dairy cows were used in a 4x4 arrangement. Each period comprised 15 days with a control diet (C diet, 20% of starch) followed by 14 days with either C diet, a 40% starch diet (S diet), a 5% sunflower oil diet (O diet) or a 40% starch plus 5% oil diet (SO diet).

During each period, rumen fluids were taken on days 15, 25, 27 and 29.

The bacterial communities were assessed using PCR-CE-SSCP of the V3 region of the 16S rRNA genes.

The CE-SSCP data processing was computed with StatFingerprints package used in R software (4).

The bacterial communities were compared using the pairwise Euclidean distances of the CE-SSCP profiles. To explore this distance matrix, nonmetric multidimensional scaling (nMDS) was carried out. Pairwise analyses of similarities (R-ANOSIM) were performed on the distance matrix to test the effect of the diet (R > 0.75: well separated groups; 0.50 < R < 0.75: separated but overlapping groups; 0.25 < R < 0.50: separated but strongly overlapping groups).

Results & Conclusions

On day 15, trans-10 FA proportion and Simpson index values were similar among the 16 cow x period combinations (0.9 % of total FA and 7.7 on average, respectively).

No differences in the structure of the bacterial community was noticed on day 15 (□).

On days 25-29 (full symbols), the structure of ruminal bacterial community of cows receiving SO diet differed from those receiving C and O diets, and S diet resulted in an intermediate structure.

The increase in trans-10 FA proportion was noticed in the rumen only with the starch + oil diet. Starch + oil addition to the diet of cows modified the structure of the microbiome and both starch alone and starch + oil addition reduced its diversity. Oil addition in a low starch diet did not affect bacterial community.

References