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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**.

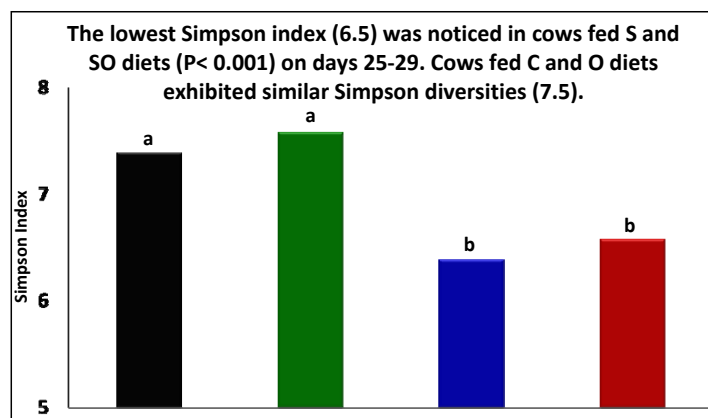
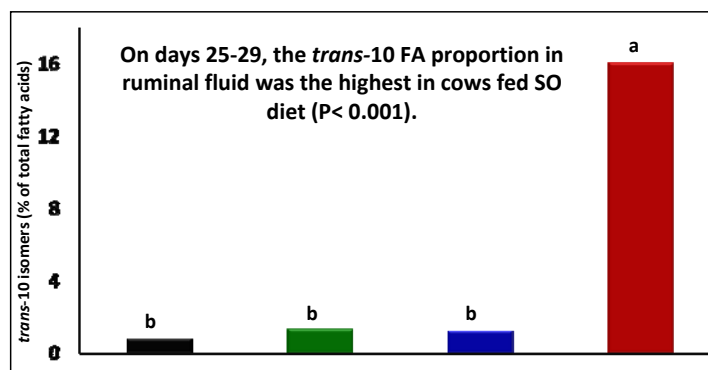
The bacterial communities were assessed using **PCR-CE-SSCP** of the V3 region of the 16S rRNA genes.



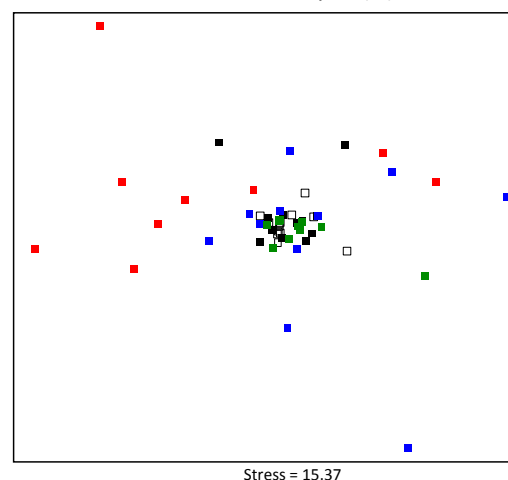
The CE-SSCP data processing was computed with StatFingerprints package used in R software⁽⁴⁾. The bacterial communities were compared using the pairwise Euclidean distances of the CE-SSCP profiles. To explore this distance matrix, nonmetric multidimensional scaling (**nMDS**) was carried out. Pairwise 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.

R-Anosim (d25-29)	C diet	O diet	S diet	SO diet
C diet		0.01	0.14	0.44
O diet			0.25	0.51
S diet				0.18

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 microbiote and both starch alone and starch + oil addition reduced its diversity. Oil addition in a low starch diet did not affect bacterial community.

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