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# The ruminal level of *trans*-10 fatty acids of dairy cows is linked to the composition of bacterial community

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## Objective and Methods

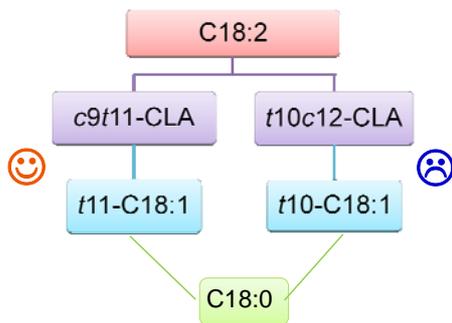


Fig.1 Biohydrogenation of linoleic acid (C18:2)

In dairy cows, *trans*-10 fatty acids (*t10*-FA) are produced by ruminal bacteria during lipid digestion, in particular during C18:2 biohydrogenation (Fig. 1), thereafter absorbed and secreted into milk (Fig. 2).

High *t10* FA production causes milk fat depression and is detrimental for human consumer health.

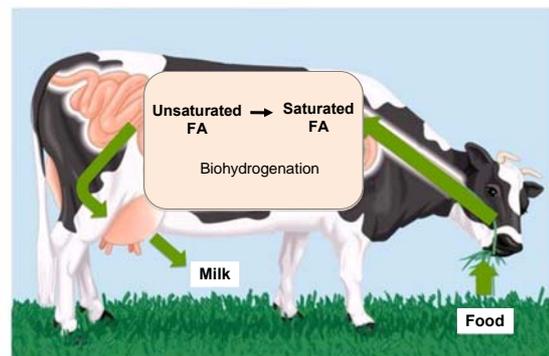
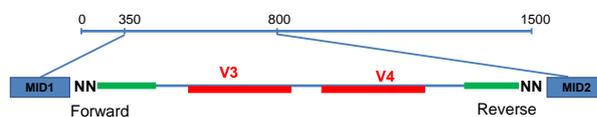


Fig. 2

**This study investigated the relationship between the ruminal proportion of *t10* FA and the composition of rumen bacterial community in a dairy cow herd.**

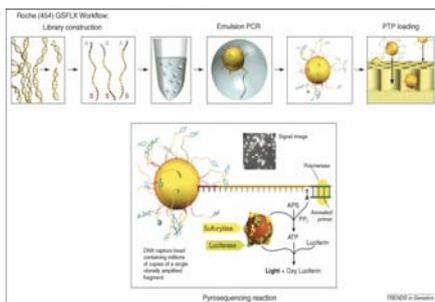
Ruminal fluids of 10 cows receiving the same diet and exhibiting a high heterogeneity of *t10*-FA ruminal proportions

DNA extraction



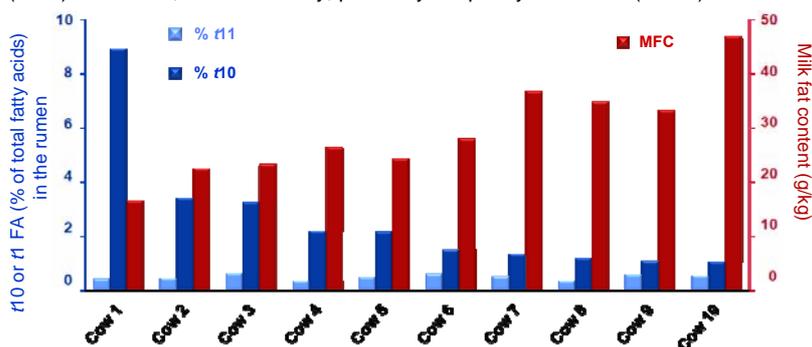
Barcoded reads of the V3-V4 regions of the 16S rRNA genes, were obtained from a 454 GS-FLX sequencer

Taxonomic assignments were performed using the open-source software Mothur V.1.12.3 ([www.mothur.org](http://www.mothur.org))



## Results and conclusions

A negative correlation ( $R=-0.7$ ) was noticed between *t10* FA and milk fat content (MFC) which was, on the contrary, positively but poorly correlated ( $R=0.2$ ) to *t11* FA.



**Variation in ruminal percentage of *t10* FA was associated with changes in the ruminal bacterial community**

A relationship between lactic acid production and high levels of *t10* FA has already been observed. In this study, an increase in Veillonellaceae family and *Lactobacillus* genus, which are consumers and producers of lactic acid respectively, is noticed in ruminal fluids exhibiting high *t10* FA percentage.

The abundance of other bacteria were also linked to *t10* FA production but their functions are not yet well-established.

Phylum	Order	Family	Genus	R( $\geq 0.7$ )	P-value	Abundance (%)
Firmicutes	Clostridiales	Lachnospiraceae		0.8	***	18.05
Firmicutes	Clostridiales	Lachnospiraceae	<i>Syntrophococcus</i>	0.9	***	0.87
Firmicutes	Clostridiales	Lachnospiraceae	<i>Butyrivibrio-Pseudobutyrvibrio</i>	-0.8	**	0.18
Firmicutes	Clostridiales	Veillonellaceae	<i>Dialister</i>	0.7	**	0.97
Firmicutes	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>	0.8	***	0.14
Bacteroidetes	Bacteroidales	Prevotellaceae	uncultured	-0.7	*	1.91
Bacteroidetes	Bacteroidales	RF16		-0.7	**	0.70
Actinobacteria	Coriobacteriales	Coriobacteriaceae		0.9	***	0.80

\* <0.05  
 \*\* <0.01  
 \*\*\*<0.001