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To cite this version :

Zened, Asma and Combes, Sylvie and Cauquil, Laurent and Mariette, J and Rousseau, C and Klopp, C and Troegeler, Annabelle and Enjalbert, Francis *The ruminal level of trans-10 fatty acids of dairy cows is linked to the composition of bacterial community*. (2011) In: 4th Congress of European Microbiologists, 26-30 June 2011, Geneva, Switzerland.

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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

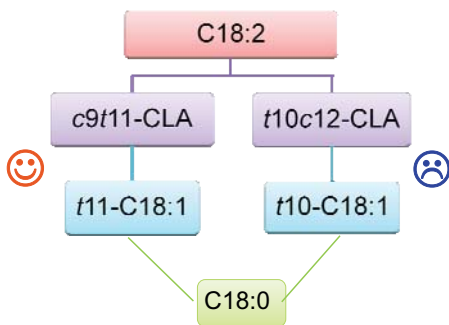


Fig.1 Biohydrogenation of linoleic acid (C18:2)

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.

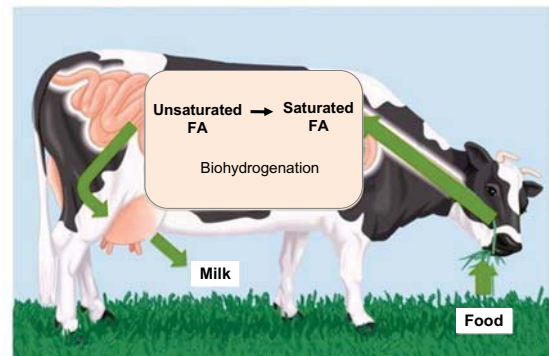
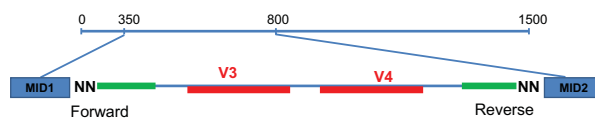


Fig. 2

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



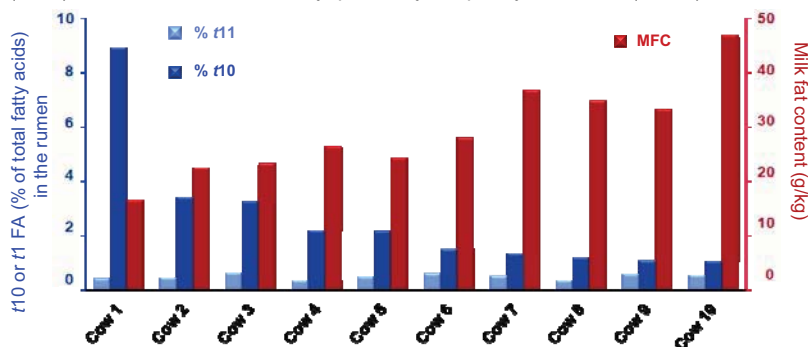
Barcoded reads of the V3-V4 regions of the 16S rRNA genes, were obtained from a 454 GS-FLX sequencer

Taxonomic assignments were performed using the open-source software Mothur V. 1.12.3 (www.mothur.org)



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(≥ 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