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

A. ZENED1, S. COMBES1, L. CAUQUIL1, J. MARIETTE2, C. ROUSSEAU3, C. KLOPP2, A. TROEGELER-MEYNADIER1, F. ENJALBERT1

1UMR 1289 Tandem, INRA / INPT-ENSAT / ENVT, Castanet-Tolosan, France, France
2Plateforme bio-informatique Genotoul, Biométrie et Intelligence Artificielle, INRA, Castanet-Tolosan, France
3INPT-ENSAT, Castanet-Tolosan, France

a.zened@envt.fr

Objective and Methods

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.

Results and conclusions

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

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.

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