Effect of cow diet on the ruminal microflora and its *in vitro* fatty acid production

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The objective of this study was to investigate the effects of donor's cow diet (hay or maize silage plus concentrates) on ruminal bacteria count, flora diversity and fatty acids profile (FA) of ruminal inoculum for *in vitro* cultures, and on *in vitro* biohydrogenation (BH) of C18:2.

Material et methods :
Two dry cows fitted with a ruminal canula were used in a 2×2 design. Each period included three weeks of diet adaptation and two weeks of sampling. The cows were fed twice daily either a diet (H) composed of grass (38%) and alfalfa hay (62%) or an acidogenic diet (A) composed of maize silage (38%), wheat (57%) and soybean meal (5%). Ruminal fluid was sampled and centrifugated (150g, 5min., 39°C) in order to remove large food particles. 80 mL of the ruminal inoculum obtained were mixed with 80mL of buffer, a fermentative substrate and grape seed oil as source of C18:2 before being incubated during 6 hours at 39°C in anaerobic and dark conditions.
Biodiversity was estimated by the Simpson index modified by Haegeman et al.[1] after SSCP analysis, and FA were analysed by GLC. Bacteria counting was realised according to Oblinger and Koburger[2] (1975).

Results :
Total and cellulolytic bacteria contents were higher in inoculum A than in inoculum H ($9.3.10^9$ vs. $2.4.10^8$/mL for total bacteria and $2.4.10^8$ vs. $1.6.10^7$/mL for cellulolytic bacteria). No difference in the biodiversity of the inoculums was noticed according to the cow or the diet, but diversity during period 1 tended to differ (P=0.09) from period 2, suggesting a time variation of flora biodiversity.
Before incubation, the ruminal inoculum from the cow receiving diet A contained significantly (P<0.01) more C18:2, trans-10 and trans-11 isomers, and odd-chain FA than inoculum from the cow receiving diet H.
After incubation, inoculum A resulted in significantly (P<0.01) greater BH of C18:2 than inoculum H (Figure 1), and produced (P<0.01) more trans-10 isomers, trans-11 isomers and odd-chain FA (Figure 2).

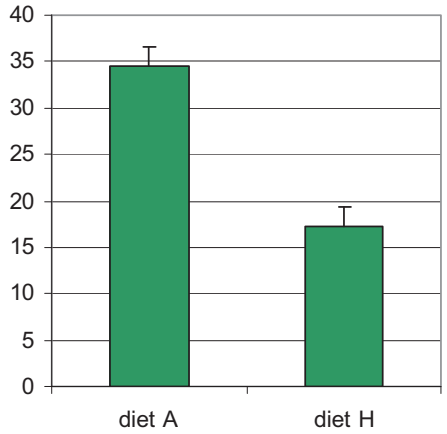

Figure 1 : Percent of C18:2 disappeared during the 6h incubation with ruminal inoculum from cow fed diet A or diet B.

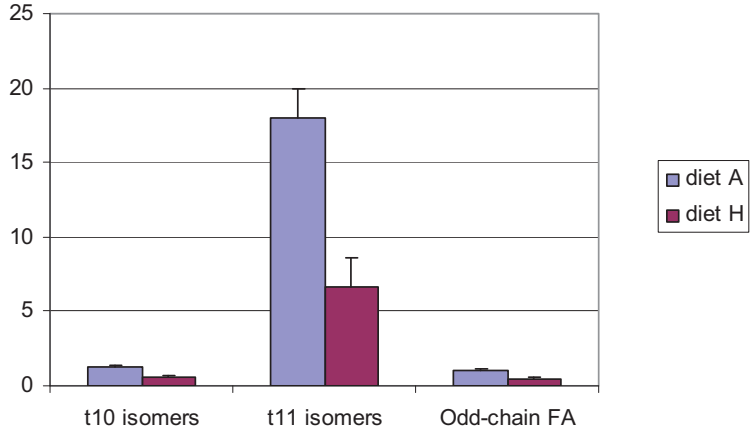

Figure 2 : Production (mg) of FA in the in vitro media with ruminal inoculum from cow fed diet A or diet H.

Discussion :
Trans-10 and odd-chain FA are known to be increased by a high concentrate diet, which explains that inoculum A was richer in these FA than inoculum H. The ruminal flora selected *in vivo* by diet A continued the production of these FA *in vitro* production. The greater content of trans-11 isomers and of C18:2 in the inoculum A could be explained by the greater C18:2 content of the diet A. During incubation with added C18:2, inoculum A continued to produce more trans-11 along with a higher C18:2 BH than inoculum H, which could be due to the higher concentration of cellulolytic bacteria in the inoculum A. The lack of cellulolytic bacteria in the inoculum H could be due to the hay diet leading to a sample poor in bacteria, the centrifugation eliminating many bacteria with large food particles which were quantitatively more in the sample from cow fed diet H, or both.

Conclusion : A centrifugated ruminal inoculum from a cow fed a diet only composed of hay was not able to hydrogenate in a large extent C18:2, possibly because of a lack of total and cellulolytic bacteria.

1. Haegeman, B., J.-J. Godon, B. Sen, & J. Hamelin (2007) personal communication.
2. Oblinger JL & Koburger JA (1975) *J. milk food technol.* 38, 540-545.