N4.46

Effects of concentrate level and starch degradability on expression of mammary lipogenic genes in goats receiving a diet supplemented with sunflower oil.

L. Bernard, C. Leroux, Y. Faulconnier, D. Durand, Y. Chilliard*

INRA, Herbivore Research Unit, Theix, France. * email : chilliar@clermont.inra.fr

Nutritional factors are efficient means to modify milk fatty acid (FA) composition in lactating ruminants including goats (Chilliard *et al*., 2003) that could be used to improve the nutritional quality of milk fat. Milk FA have 2 main origins: they are either synthesized *de novo* in the mammary gland or extracted from the arterial blood. These pathways involve numerous mammary enzymes. The aim of this experiment was to relate, in lactating goats receiving a lipid supplement rich in C18:2 n-6 , the effect of different forage:concentrate ratio and different degradable starch in concentrate on milk FA to mammary metabolism assessed by gene expression and enzyme activities of few "candidate" genes representing the main pathways involved in lipid synthesis.

Animals, diets and mammary tissue

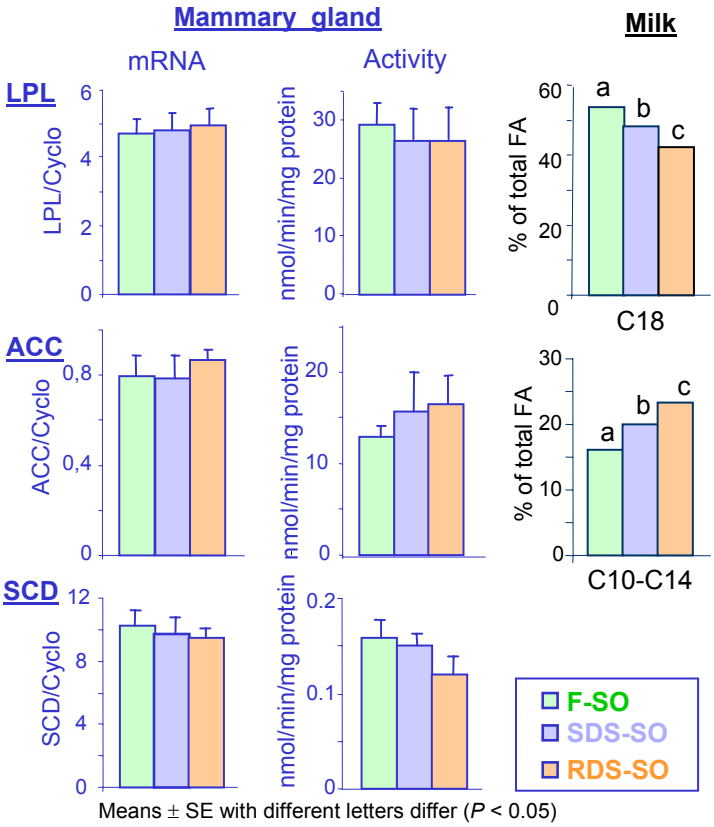
Fourteen mid-lactating goats fed, in a 3 X 3 Latin Square design, received 3 diets supplemented with 130 g/d of sunflower oil (SO; i.e. 5.8% of diet DM) differing in concentrate level: 0.8 kg/d (**F-SO**) vs 1.4 kg/d and, for the latter, ruminal degradability of starch (DS), either corn grain (**S**low**DS-SO**) or flattened wheat (**R**apid**DS-SO**) at 1 kg/d. Mammary tissues were taken by biopsy (end of 3-week periods, n=3X14 per dietary treatment) using a Bard Monopty instrument (Bard, Inc. Covington, Georgia) and at slaughter (end of experiment; n = 5 for **F-SO** and **RDS-SO**, n = 4 for **SDS-SO**) for mRNA and enzyme activities measurements, respectively.

Assays

- Milk FA composition, by GLC (Trace GC 2000 Series, ThermoFinnigan, France) after preparation of methyl esters, and separation on a 100 m x 0.25 mm i.d. fused silica capillary column (CP Sil 88) (Loor *et al*., 2005),
- Activities and mRNA level by real-time RT-PCR (Bernard *et al*., 2005) of enzymes involved in FA uptake of circulating TG (lipoprotein lipase LPL), *de novo* lipogenesis (acetyl-CoA carboxylase ACC, fatty acid synthase FAS), and delta-9 desaturation (stearoyl-CoA desaturase, SCD), as well as mRNA level of an housekeeping gene (Cyclophilin, Cyclo).

Results

Dietary treatments (level and nature of concentrate) had no significant effect ($P > 0.05$) on mRNA abundance and enzyme activities of LPL, ACC, FAS and SCD. However, even if not significant mainly due to individual variability, ACC activity increased by 21% and 27%, and milk secretion of C8-C16 FA by 15 and 30%, respectively for **SDS-SO** and **RDS-SO** compared to **F-SO**. Similar trends were observed for ACC (by 9%) and FAS (by 10%) mRNA abundances with the high concentrate diet when the starch was rapidly degradable in the rumen (**RDS-SO**). In contrast, SCD activity tended to decrease (-22%; $P > 0.2$) for **RDS-SO** compared to other diets, although there was no effect on the desaturation ratios for 14:0, 16:0 and 18:0 that could be related to SCD activity (results not shown). LPL activity was not modified by the dietary treatment even though there was a decrease ($P < 0.05$) in the secretion of C18 FA by 10 and 21 % respectively for **SDS-SO** and **RDS-SO** diets, as compared to **F-SO**. Whatever the nature of starch, increasing the level of concentrate increased milk *trans*-10 18:1 (see Poster N4-45).



Means ± SE with different letters differ ($P < 0.05$)

We report that gene expression responses to dietary treatments is only partly related to the corresponding milk FA responses, due to individual variability and/or other factors (*i.e.* substrate and cofactors availability). SCD mRNA did not vary and its activity tended to decrease with RDS-SO compared to other diets. Moreover, increasing *trans*10-18:1 secretion with high starchy concentrate level in the diet was not related to activities changes of enzymes involved in mammary FA uptake (LPL) and *de novo* lipid synthesis (ACC, FAS). *This work was funded by EU BIOCLA Project QLK1-2002-02362.*

References

Bernard L *et al.* 2005. J. Dairy Sci. 88, 1478-1489.
Chilliard Y *et al.* 2003. J. Dairy Sci. 86, 1751-1770.
Loor J *et al.* 2005. J. Dairy Sci. 88, 726-740.