Feeding different lipid supplements during lactation cycle in dairy goats: 2 effect on mammary gene expression

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To sustain the development and production of goat milk products, the guarantee of milk technological (high dry matter content, rennet coagulation) and sensorial (flavour) qualities is central. To achieve these goals along a lactation period, it is necessary to supply the goat with sufficient energy, which could be a challenge, especially for high yielding goats in early lactation. Dietary fat supplements are used as a mean to increase the total energy concentration of the diet. The aim of the present study was to examine the effect of different lipid supplements on mammary gene expression and milk production and composition in dairy goats over a lactation period.

Thirty Norwegian dairy goats with kidding in February 2011 were fed a control diet with a concentrate mixture (0.9 kg/d) consisting of barley, rape seed meal (expro 00SF), soy bean meal, beet pulp, molasses and mineral/vitamin premix until 60 days in milk (DIM). After 60 DIM and until the end of the experiment, the goats were assigned to three experimental groups (balanced for their parity, genotype at the αS1 casein locus) each of 10 goats that received 3 dietary treatments: 'Control', 'Saturated' and 'Unsaturated' that differ in the composition of the concentrate mixtures. The two lipid supplemented treatments consisted of the same concentrate mixture as the 'Control', with addition of 8% of a source of 'Saturated' (Akofeed Gigant 60; rich in C16:0) and 'Unsaturated' (rapeseed oil, rich in cis-9-18:1 and cis-9, cis-12-18:2) fat. The experiment consisted of three different periods: 1) Spring indoor feeding period from 1 to 120 DIM; 2) Summer mountain grazing period from 120 to 200 DIM; 3) Autumn indoor feeding period from 200 to 230 DIM. In the indoor feeding periods during spring and autumn, the goats received silage according to appetite, and the silage intake was registered three subsequent days every week. Milk yield was measured three subsequent days every second week. The experiment included seven sampling points from 10 to 230 DIM including various milk analyses and body conditions measures as well as arterio-venous differences of metabolites across the mammary gland. Mammary biopsies were performed at 30, 60, 120, 200 and 230 DIM for analysis the mRNA abundance of 18 candidate genes by RT qPCR. These genes were involved in different pathways (lipid metabolism, lactose synthesis, apoptosis, glucose metabolism) or specifying the major milk proteins and proteins of the milk fat globule membrane. Data were expressed as mRNA copy number relative to the geometric mean of 3 reference genes.

Dietary treatments (addition of saturated or unsaturated fat to concentrate) had no effect on the mRNA abundance of the candidate genes in the mammary gland, that were not related to the observed increase in milk fat content in 'Saturated' compared to 'Control' and 'unsaturated' groups. Conversely, the lactation stage affected the mRNA abundances of most of the genes studied, in particular those involved in lipid metabolism that generally increased and then decreased over the lactation period, and their relationship with the milk components secretion need to be further explored.