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Transcriptional regulation of lipid metabolism and inflammation in transition dairy goats by fish oil and stearate.

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Abstract

To better understand the interaction between saturated or unsaturated fatty acids and its effect on expression of genes involved in subcutaneous adipose tissue metabolism, 23 second parity alpine dairy goats were enrolled in the experiment and fed either a non fat-supplemented basal diet (C; n=8), the basal diet supplemented with stearic acid (ST; n=7) or the basal diet supplemented with fish oil (FO; n=8). 30g/head/d supplemental fatty acids during the dry period and 50g/head/d during lactation were delivered starting one week before parturition up to 21 days in milk. Subcutaneous adipose tissue samples were harvested at day -7, 7 and 21 relative to kidding and mRNA levels of genes involved in inflammation were measured via qPCR. Data were analyzed using the MIXED procedure of SAS. No significant effects for treatment were observed, however eight genes were significant for time. *HP* and *SAA3* expression peaked at day 7 postpartum, to then return at prepartum level around 21 d relative to kidding, while *IL8*, *IL10*, and *IL18* expression constantly increased along the transition period. Vice versa, expression of *IL1 β* , *IL6R*, and *RXRA* decreased in response to kidding, with a subsequent increase at day 21. The obtained results led us to hypothesize that goats face a postponed lipomobilization after kidding, probably related to their reduced production. The next step will involve the analysis of miRNA related to immune cell infiltration, adipocyte inflammation and lipolysis and positive regulation of adipogenesis to better understand the complex network of lipid metabolism in periparturient goats.

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