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J. Dairy Sci. 100:1–14 https://doi.org/10.3168/jds.2017-12789 © American Dairy Science Association[®]. 2017.

Comparison of mammary lipid metabolism in dairy cows and goats fed diets supplemented with starch, plant oil, or fish oil

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ABSTRACT

A direct comparison of cow and goat performance and milk fatty acid (FA) responses to diets known to induce milk fat depression in the bovine has suggested interspecies differences in rumen and mammary lipid metabolism. Thus, this study was conducted to infer some potential mechanisms responsible for the differences in mammary lipogenesis due to diet and ruminant species. To meet this objective, 12 cows and 15 goats were fed a basal diet (control), a similar diet supplemented with 2.2% fish oil (FO), or a diet containing 5.3% sunflower oil and additional starch (+38%; SOS) according to a 3 \times 3 Latin square design with 26-d experimental periods. Milk yield, milk composition, FA profile, and FA secretion were measured. On the last day of each period, the mRNA abundance of 19 key genes in mammary metabolism or the enzyme activity or both were measured in mammary tissue sampled by biopsy or at slaughter or both. The results show significant differences in the response of cows and goats to the dietary treatments. In cows, milk fat content and yield were lowered by FO and SOS (-31%), whereas only FO decreased milk fat content in goats (-21%) compared with the control. In cows and to a lesser extent in goats, FO and SOS decreased the secretion of <C16 and C16 FA, and FO lowered >C16 FA output (mmol/kg of BW). However, SOS increased the secretion of >C16 FA in goats. These changes in milk fat content and FA secretion were not associated with modifications in mammary expression or the activity of 19 proteins involved in the major lipogenic pathways. This absence of variation may be attributable to posttranscriptional regulation for these genes or related to the time of sampling of the mammary tissue relative to the previous meal and milking. Otherwise, the abundances of 15 mRNA among the 19 encoding for genes involved in lipid metabolism in the mammary gland were different among species, with 9

more abundant in cows (FASN, FADS1, SCD1, GPD1, LALBA, SREBF1, LXRA, PPARA, and PPARG1) and 6 more abundant in goats (G6PD, GPAM, SCD5, XDH, CSN2, and SP1). Similarly, a significant effect of the species was observed in the 4 enzyme activities measured; glycerol-3-phosphate dehydrogenase and malic enzyme were higher in cows, and FA synthase and glucose-6-phosphate dehydrogenase activities were higher in goats. In conclusion, the differences between cow and goat performance and milk FA responses to the FO and SOS treatments were not related to changes in the measured mammary lipogenic gene expression. Furthermore, the data provide evidence that the major mammary lipogenic pathways differ between the caprine and the bovine, whose biological significance remains to be unraveled.

Key words: cow, goat, lipogenic gene expression, milk fatty acid, milk fat depression

INTRODUCTION

In milk, fat is the major energy constituent and represents a significant proportion of the total energy requirements for lactation in ruminants. Moreover, fat is an important component contributing to the technological, organoleptic, and nutritional properties of milk (Palmquist et al., 1993; Chilliard and Ferlay, 2004). Nutrition is the major environmental factor that regulates milk fat secretion and composition and constitutes a rapid, reversible, and efficient means to modulate milk fat synthesis and composition (Chilliard et al., 2007). Thus, a better understanding of milk fat synthesis regulation within the mammary gland is central to the development of nutritional strategies to limit milk energy secretion, improve the energy balance of lactating ruminants, and enhance the nutritional value of milk for human consumers. Under certain dietary conditions, such as starch-rich diets or the addition of plant oil or marine oils, dairy ruminants may experience milk fat depression (MFD), and milk fat concentration and yield may decrease dramatically (up to 50%; Bauman and Griinari, 2003). Several theories have been

Received February 23, 2017.

Accepted July 24, 2017.

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proposed to explain the causes of MFD (Bauman and Griinari, 2003; Shingfield and Griinari, 2007), with the biohydrogenation (**BH**) theory being the most universal. This theory attributes diet-induced MFD to an inhibition of mammary lipogenesis by specific fatty acid (FA) intermediates that form in the rumen on certain diets due to alterations in ruminal BH pathways (Bauman and Griinari, 2003; Shingfield et al., 2010). The BH theory provides a basis for explaining most cases of MFD on starch-rich diets or with plant oil in cows via a direct inhibition of mammary lipogenesis by BH intermediates with confirmed or putative antilipogenic effects [trans-10, cis-12 CLA (Baumgard et al., 2000), cis-10, trans-12 CLA (Sæbø et al., 2005), and trans-9, cis-11 CLA (Perfield et al., 2007). However, these intermediates do not, in isolation, explain MFD in cows or sheep fed diets containing marine oils (Loor et al., 2005; Gama et al., 2008; Toral et al., 2010). Thus, for dietary conditions with marine oil, Shingfield and Griinari (2007) proposed also including the role of changes in the availability of preformed long-chain FA to the mammary gland in the explanation of MFD. This would involve both a shortage of 18:0 for endogenous cis-9 18:1 synthesis in the mammary gland and an increase in the supply of *trans* FA formed in the rumen, which would increase the milk fat melting point and thereby lower the rate of fat removal in mammary epithelial cells (Loor et al., 2005; Gama et al., 2008).

An indirect comparison of cow and goat performance and milk FA responses to diets known to induce MFD in the bovine reveals relevant species-by-diet interactions, with goats being less sensitive to diet-induced MFD (Shingfield et al., 2010; Toral et al., 2014) even though recent studies have demonstrated their susceptibility when fed marine lipids at a relatively high dose (2.2%)DM; Toral et al., 2015). The reasons for the differential lipogenic responses between these ruminant species are not well understood, but based on indirect comparisons of milk FA composition, differences in ruminal BH and mammary lipid metabolism (Chilliard et al., 2007, 2014; Shingfield et al., 2010) could be implicated. Faced with the absence of direct interspecies comparisons of diet-induced MFD among these species, a comparative study with lactating cows and goats was undertaken to determine the mechanisms underlying the differences of mammary lipogenic responses between these ruminant species. From this study, animal performance responses including milk fat yield, FA composition (Toral et al., 2015), and rumen metabolism (Toral et al., 2016) were reported and revealed relevant interspecies differences and species-by-diet interactions. The present study aimed to provide further insight into the mechanisms regulating mammary lipogenesis in ruminants. In the mammary gland, milk fat is controlled via the expression of a network of lipogenic genes (Bionaz and Loor, 2008), and alterations in mammary lipogenic gene expression may partly explain the basis for diet-induced MFD. However, the underlying mechanisms might differ depending on factors such as dietary conditions or animal species.

On this basis, a direct comparative study with lactating cows and goats was undertaken to test the hypotheses that (1) the mammary mechanisms underlying MFD induced by marine lipid supplements or by diets containing high amounts of starch and plant oils are different and (2) mammary lipid metabolism responses vary between animal species. To meet this objective, cows and goats were fed a basal diet (control), a similar diet supplemented with fish oil (FO), or a diet containing sunflower oil and additional starch from wheat (SOS). Then, changes in animal performance and milk FA, the mammary expression of several genes involved in the major lipogenic pathways, and the activity of a few enzymes related to corresponding proteins were measured and used to infer the potential mechanisms responsible for differences in the regulation of mammary lipogenesis due to diet and ruminant species.

MATERIALS AND METHODS

Animals, Experimental Design, Diets, and Management

All procedures involving animals were approved by the Animal Care Committee of INRA in accordance with the guidelines established by European Union Directive 2010/63/EU. The details of the experimental design have been described in Toral et al. (2015). Briefly, 12 multiparous nonpregnant Holstein cows and 15 multiparous nonpregnant Alpine goats were allocated to 1 of 3 groups (4 cows and 5 goats each) and used in a replicated 3×3 Latin square to test the effects of 3 treatments during three 25-d experimental periods. One goat had to be withdrawn from the experiment because it suffered from diarrhea. All animals were offered grass hay ad libitum supplemented with concentrates (control, FO, or SOS). Formulation of experimental concentrates and chemical composition of concentrates and grassland hay were described in Toral et al. (2015). Briefly, the control concentrate was based on (% DM) cracked corn grain (54.9), pelleted dehydrated alfalfa (29.4), soybean meal (14.3) and a mineral-vitamin premix (1.4). In the FO and SOS concentrates, both FO (3.6% DM) and sunflower oil (9.0% DM) replaced alfalfa pellets on a proportionate basis and were mixed manually with other ingredients immediately before being fed out. The FO represented 2.2% of total DMI, and the sunflower oil represented 5.3% of total DMI. Download English Version:

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