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

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ABSTRACT

Direct comparison of cow and goat performance and milk fatty acid responses to diets known to induce milk fat depression (MFD) in the bovine reveals relevant species-by-diet interactions in ruminal lipid metabolism. Thus, this study was conducted to infer potential mechanisms responsible for differences in the rumen microbial biohydrogenation (BH) 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 × 3 Latin square design with 25-d experimental periods. On the last day of each period, fatty acid composition (by gas chromatography) and bacterial community (by terminal-RFLP), as well as fermentation characteristics, were measured in rumen fluid samples. Results showed significant differences in the response of cows and goats to dietary treatments, although variations in some fermentation parameters (e.g., decreases in the acetate-to-propionate ratio due to FO or SOS) were similar in both species. Main alterations in ruminal BH pathways potentially responsible for MFD on the SOS diet (i.e., the shift from *trans*-11 to *trans*-10 18:1 and related increases in *trans*-10,*cis*-12 18:2) tended to be more pronounced in cows, which is consistent with an associated MFD only in this species. However, changes linked to FO-induced MFD (e.g., decreases in 18:0 and increases in total *trans*-18:1) were stronger in caprine rumen fluid, which may explain their unexpected susceptibility (although less marked than in bovine) to the negative effect of FO on milk fat content. Altogether, these results suggest that distinct ruminal mechanisms lead to each type of diet-induced MFD and confirm a pronounced interaction with species. With regard to microbiota, differences between cows and goats in the composition of the rumen bacterial community might be behind the disparity in the microorganisms affected by the experimental diets (e.g., *Ruminococcaceae*, *Lachnospiraceae*, and *Succinivibrionaceae* in the bovine, and *Pseudobutryrivibrio*, *Clostridium* cluster IV, *Prevotella*, and *Veillonellaceae* in the caprine), which hindered the assignation of bacterial populations to particular BH steps or pathways. Furthermore, most relevant variations in microbial groups corresponded to as yet uncultured bacteria and suggest that these microorganisms may play a predominant role in the ruminal lipid metabolism in both cows and goats.

Key words: biohydrogenation, fatty acid, rumen bacteria, milk fat depression

INTRODUCTION

Milk fat depression (**MFD**) represents a situation where milk fat concentration and yield can decrease up to 50%, often as a result of changes in diet composition (Bauman and Griinari, 2001; Shingfield et al., 2010a). Inducing MFD might have applications as a management tool in dairy cow farming (Bauman et al., 2011), but has a potential negative effect on the subsequent manufacture of cheese. Although goats were thought, for many years, to be less sensitive to diet-induced MFD (Shingfield et al., 2010a; Toral et al., 2014), more recent studies have demonstrated their susceptibility when fed marine lipids at a high dose (2.2% DM; Toral et al., 2015).

The effect of nutrition on milk fatty acid (**FA**) composition is largely determined by rumen lipid metabolism, particularly by the biohydrogenation (**BH**) process (AbuGhazaleh et al., 2002; Loor et al., 2005; Toral et al., 2012). Alterations in rumen BH pathways may explain the basis for diet-induced MFD (Bauman and Griinari, 2001), but the underlying mechanisms remain uncertain and might differ depending on factors such as diet or host animal species.

Starting with the diet, despite differences in MFD induced by feeding either marine lipids or high-starch

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rations and plant oils (Chilliard et al., 2007; Shingfield and Griinari, 2007), no direct comparative study exists testing the hypothesis that distinct ruminal mechanisms lead to each type of diet-induced MFD.

Regarding the host animal, interspecies variations in rumen digestion and microbiota (Moon et al., 2010; Lee et al., 2012) are well known in ruminant nutrition. Conversely, knowledge of putative species-specific differences in BH pathways only arises from indirect comparisons (Loor et al., 2004; Boeckaert et al., 2008; Toral et al., 2012), often by extrapolating data from milk FA, due to the scarcity of available studies on this issue, particularly in the caprine (Chilliard et al., 2014; Li et al., 2014).

Accordingly, a first direct comparison study was performed in cows and goats, both receiving diets known to induce MFD in bovine, to describe milk fat yield and FA composition (Toral et al., 2015). In that study, milk FA profiles showed a significant species by diet interaction in ruminal responses (Toral et al., 2015). Furthermore, the lack of MFD in goats fed a starch-rich diet supplemented with sunflower oil was attributed to a putatively greater stability in BH pathways compared with cows, whereas the decrease in milk fat content in both species when fed fish oil at 2.2% DM (–30 and –21% in cows and goats, respectively) was associated with a strong inhibition of ruminal 18:1 saturation (i.e., the same mechanism in cows and goats). Nevertheless, even though the reasons for this interaction are expected to be linked to species differences in the structure and composition of the rumen bacterial community (Moon et al., 2010; Lee et al., 2012), knowledge is still limited on the microbial ecology of FA metabolism, especially in goats (Huws et al., 2011; Toral et al., 2012; Zhu et al., 2012). Additionally, application of culture-independent molecular techniques, including next-generation sequencing methodologies, has revealed that the effect of lipids on bacterial populations remains largely unknown (Castro-Carrera et al., 2014; Huws et al., 2015).

On this basis, a comparative study with lactating cows and goats was undertaken to test the following hypotheses: (1) ruminal mechanisms underlying MFD induced by marine lipid supplements or by diets containing high amounts of starch and plant oils are different, and (2) rumen microbial BH 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 (**SOS**). Then, changes in rumen FA composition, bacterial community, and fermentation characteristics were measured and used to infer potential mechanisms responsible for differences in the regulation of ruminal lipid metabolism 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 the European Union Directive 2010/63/EU. 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. Unfortunately, 1 goat had to be withdrawn from the experiment because it suffered diarrhea. All animals were offered grass hay ad libitum supplemented with concentrates containing no additional lipid (control), FO, or SOS. 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 fish oil (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 feeding out. The fish oil represented 2.2% and the sunflower oil 5.3% of total DMI. The remaining alfalfa pellets and part of the corn grain were replaced by flattened wheat grain (37.4% DM) in SOS concentrate. Hay refusals were weighed daily and used to adjust the amounts of concentrate offered the following day to maintain the targeted dietary forage to concentrate ratio (40:60 on a DM basis). Diets were offered as 2 equal meals at 0830 and 1600 h. Formulation, chemical composition, and FA profile of the concentrates and hay have been reported previously (Toral et al., 2015). Experimental diets were formulated to be isoproteic (139 g of CP/kg of DM), and the mean starch concentrations (values for the control, FO, and SOS diets, respectively) were 232, 239, and 325 g/kg of DM and those of NDF were 365, 349, and 296 g/kg of DM. Fish oil and sunflower oil supplied 400 and 953 g of FA/d in cows and 48 and 114 g of FA/d in goats, respectively. Animals had access to a constant supply of fresh water and were milked at 0800 and 1530 h.

Rumen Sample Collection

On d 25 of each experimental period, rumen fluid was collected by stomach tube from each animal after an overnight period without concentrate distribution (but with ad libitum access to hay) and before morning feeding. This technique has been validated as a