J. Dairy Sci. 101:1–12
https://doi.org/10.3168/jds.2017-13479
© 2018, THE AUTHORS. Published by FASS Inc. and Elsevier Inc. on behalf of the American Dairy Science Association®.
This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/3.0/).

Somatic cell count–based selection reduces susceptibility to energy shortage during early lactation in a sheep model

J. Bouvier-Muller,*† C. Allain,* F. Enjalbert,* Y. Farizon,* D. Portes,‡ G. Foucras,† and R. Rupp*[1]
*GenPhySE, Université de Toulouse, INRA, INPT, ENVT, Castanet Tolosan, F-31326, France
†Interactions Hôtes—Agents Pathogènes (IHAP), Université de Toulouse, ENVT, Toulouse, F-131076, France
‡Domaine de La Fage, INRA, Roquefort sur Soulzon, F-12250, France

ABSTRACT

During the transition from late gestation to early lactation ruminants experience a negative energy balance (NEB), which is considered to increase susceptibility to mammary infections. Our previous study in 2 divergent lines of sheep selected for high and low somatic cell score (SCS) suggested an association between the response to NEB and genetic susceptibility to mastitis. Forty-eight early-lactation primiparous dairy ewes from the 2 SCS genetic lines were allocated to 2 homogeneous subgroups—an NEB group, which was energy restricted and received 60% of the energy requirements for 15 d, and a control-fed group—to obtain 4 balanced groups of 12 ewes: high-SCS positive energy balance, low-SCS positive energy balance, high-SCS NEB, and low-SCS NEB. High-SCS ewes showed greater weight loss and increased plasmatic concentrations of β-hydroxybutyrate and nonesterified fatty acids than low-SCS ewes when confronted with an induced NEB. The aim of this study was to further characterize this interaction by combining transcriptomic and phenotypic data with a generalized partial least squares discriminant analysis using mixOmics package framework. A preliminary analysis using 3 blocks of phenotypes (fatty acids, weight and production, blood metabolites) revealed a high correlation between fat-to-protein ratio, β-hydroxybutyrate, and nonesterified fatty acids concentrations with milk long-chain fatty acid yields. These phenotypes allowed good discrimination of the energy-restricted high-SCS ewes and confirmed a high level of adipose tissue mobilization in this group. A second analysis, which included RNA-seq data, revealed high correlations between the long-chain fatty acid yields in milk and *PDK4*, *CPT1A*, *SLC25A20*, *KLF10*, and *KLF11* expression, highlighting the relationship between mobilization of body reserves and enhanced fatty acids utilization for energy production in blood cells. Finally, analysis of milk composition measured in 1,025 ewes from the 2 genetic lines over 10 yr confirmed significant higher fat-to-protein ratio in high-SCS ewes in early lactation. Altogether, our results strongly confirmed a genetic link between susceptibility to mastitis and metabolic adaptation to energy shortage. Improving genetic resistance to mastitis using SCS should be accompanied by a favorable effect on the response to metabolic stress, especially in highly stressful early lactation. Moreover, this study suggests that the fat-to-protein ratio could be used as a low-cost tool for monitoring energy balance and ketosis during this critical phase of lactation.

Key words: mastitis resistance, negative energy balance, dairy ruminant, data integration

INTRODUCTION

Mastitis, an inflammation of the mammary gland, is caused mainly by bacteria that proliferate in the gland lumen following colonization of the teat canal. This disorder is the most costly and frequent infectious disease of dairy cattle (Wells et al., 1998; Barkema et al., 2009) and sheep (Bergonier et al., 2003). Although much work has been carried out in dairy ruminants to understand the complex physiological and cellular events that occur in the mammary gland in response to pathogens (Kehrli and Shuster, 1994; Sordillo, 2005), the protective mechanisms are still obscure. Data in the literature, however, corroborate the importance of a rapid influx of neutrophils and macrophages into the mammary gland to allow effective and early clearance of the pathogen and to control the inflammatory process (Paape et al., 2002; Wellnitz and Bruckmaier, 2012). This massive cell recruitment in the udder leads to a dramatic increase in the milk SCC. Accordingly, SCC has been widely advocated as an easy-to-measure tool for predicting mastitis and discriminating between chronically infected and noninfected animals (Kehrli and Shuster, 1994; Bergonier and Berthelot, 2003).

The existence of a genetic basis for mastitis susceptibility has been well documented in dairy ruminants

---

Received July 11, 2017.
Accepted November 20, 2017.
[1] Corresponding author: rachel.rupp@toulouse.inra.fr

(Mrode and Swanson, 1996; Heringstad et al., 2000; Rupp and Boichard, 2003). The estimated heritability of SCC, one of the most widely studied predictors, ranges from 10 to 20% (Rupp and Foucras, 2010) and is genetically strongly positively correlated with resistance to mastitis. In this context, a divergent selection of Lacaune dairy sheep was developed based on extreme breeding values of the SCS (Rupp et al., 2009). In particular, milk bacteriology showed that the high-SCS line has a higher rate of mammary infections in natural conditions, which is associated with a lower capacity for bacterial clearance during experimental challenges compared with the low-SCS line (Bonnefont et al., 2011).

The risk of dairy ruminants developing mastitis is increased during the periparturient period, when most animals experience some degree of negative energy balance (**NEB**). This is due to a low feed intake relative to high energy demands for growth of the fetus and uterus and milk synthesis, especially in high-yielding animals (Drackley, 1999). The severity and duration of NEB leads to extensive mobilization of fatty acids (**FA**) from the adipose tissue and results in higher blood nonesterified FA (**NEFA**) or BHB concentrations (Dann et al., 2006). There is growing evidence of a relationship between severe NEB, impairment of the immune response, and an increased risk of mastitis in early lactation, in particular in dairy cows (Suriyasathaporn et al., 2000; Jánosi et al., 2003; Nyman et al., 2008).

A genetic association between mastitis susceptibility and energy metabolism was also suggested in a previous study in dairy ewes (Bouvier-Muller et al., 2016). This report described the consequences of experimentally induced NEB during early lactation on production traits and metabolic response in high-SCS and low-SCS ewes. A noteworthy interaction between genetic background and energy balance on metabolic parameters and BW was demonstrated. High-SCS ewes showed a greater decrease in BW and higher NEFA and BHB concentrations than low-SCS ewes when subjected to NEB. However, the mechanisms underlying the relationship between energy balance and mastitis susceptibility remained unclear.

In the present study, additional phenotypes such as milk FA composition and blood RNA-seq transcriptomic profiling were scrutinized to provide additional insight into these mechanisms. A sparse partial least squares–discriminant analysis (**sPLS-DA**) model, based on the integration of multiple phenotypes and transcriptomic data sets, was used to describe the interaction between genetic background for mastitis susceptibility and energy balance. Field data on the genetic lines were also analyzed to confirm our hypothesis of a genetic dependence of ketosis frequency in relation to susceptibility to mammary infection.

MATERIALS AND METHODS

All procedures involving animals received approval from the Ethics Committee on Animal Experimentation of Toulouse (France), agreement no. 01557/01.

Experimental Design

A detailed description of the experimental design can be found in Bouvier-Muller et al. (2016). Briefly, 48 primiparous Lacaune ewes from each of 2 genetic lines (high SCS and low SCS; Rupp et al., 2009) were allocated to 2 groups per line 2 wk after lambing according to milk yield, milk composition, BW, and litter size. One group received a control (positive energy balance; **PEB**) diet that met energy requirements, and the other group (NEB) received a low-energy diet that met only 60% of their energy requirements. This resulted in 4 balanced groups of 12 ewes: high-SCS PEB, low-SCS PEB, high-SCS NEB, and low-SCS NEB. Both diets met the protein requirements. After 10 d on either the NEB or PEB diet, the healthiest half-udder in all ewes was injected with a sterile solution of Pam3CSK4 (10 μg/mL; InVivogen, Toulouse, France) and muramyl dipeptide (10 μg/mL; InVivogen) to induce local inflammation. As shown in Figure 1, the first day of restriction was referred to as d 0 in the experiment timeline.

Phenotypes and Sample Collection for Blood Metabolites Analyses

A detailed description of the phenotypes collection can be found in Bouvier-Muller et al. (2016). Milk yield, fat, and protein contents and SCC were measured on d −2, 8, and 14. The SCC were measured with a Fossomatic cell counter (Foss, Hillerød, Denmark). Daily values of SCC, fat, and protein contents were calculated as the average of the morning and evening milking values weighted by milk yield. The daily fat-to-protein ratio was calculated from the daily averages for fat and protein contents. Daily SCC data were normalized as follows to give a daily SCS: SCS = 3 + log2(SCC/100,000).

The NEB was characterized by weighing the ewes on d −1, 8, and 14. During the restriction period, BW was corrected in NEB ewes by adding their average decrease in BW between d −1 and d 1 (3.3 kg) to compensate for the decrease in digestive tract contents due to the lower DMI. Body condition score was assessed on d −10, 6, and 14 using the 5-point scale proposed by Rus-

Download English Version:

https://daneshyari.com/en/article/8501397

Download Persian Version:

https://daneshyari.com/article/8501397

Daneshyari.com