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Genetic parameter estimation for major milk fatty acids in Alpine and Saanen primiparous goats

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ABSTRACT

Genetic parameters for 18 fatty acids or groups of fatty acids (FA), milk production traits, and somatic cell score (SCS) were estimated by restricted maximum likelihood with a repeatability animal model, using 45,259 test-day records from the first lactations of 13,677 Alpine and Saanen goats. Fatty acid data were collected as part of an extensive recording scheme (PhénoFinLait), and sample testing was based on mid-infrared spectra estimates. The total predicted FA content in milk was approximately 3.5% in Alpine and Saanen goats. Goat milk fat showed similar saturated FA to cattle and sheep, but higher contents of capric (C10:0) FA (~9.7 g/100 g of milk fat). Heritability estimates ranged from 0.18 to 0.49 for FA and estimates were generally higher when FA were expressed in g/100 g of milk fat compared with g/100 g of milk. In general, the 3 specific short- and medium-chain goat FA, caproic acid (C6:0), caprylic acid (C8:0), and especially capric (C10:0) acid, had among the highest heritability estimates (from 0.21 to 0.37; average of 0.30). Heritability estimates for milk yield, fat and protein contents, and SCS were 0.22, 0.23, 0.39, 0.09, and 0.24, 0.20, 0.40, and 0.15, in Alpine and Saanen goats, respectively. When FA were expressed in g/100 g of milk, genetic correlations between fat content and all FA were high and positive. Genetic correlations between the fat content and FA groups expressed in g/100 g of fat led to further investigation of the association between fat content and FA profile within milk fat. Accordingly, in both Saanen and Alpine breeds, no significant genetic correlations were found between fat content and C16:0, whereas the correlations between fat content and specific goat FA (C6:0 to C10:0) were positive (0.17 to 0.59). In addition, the genetic correlation between fat content and C14:0 was negative (−0.17 to −0.35). The values of the genetic correlations between protein content and individual FA were similar, although genetic correlations between protein content and FA groups were close to zero. Genetic correlations of milk yield or SCS with the FA profile were weak. Results for genetic parameters for FA, however, should be further validated, because the low predicting ability of certain FA using mid-infrared spectra and the limited calibration data set might have resulted in low accuracy. In conclusion, our results indicated substantial genetic variation in goat milk FA that supported their amenability for genetic selection. In addition, selection on protein and fat contents is not expected to have an undesirable effect on the FA profile in regard to specificity of goat products and human health.

Key words: fatty acid, dairy goat, milk composition, genetic parameters

INTRODUCTION

Total worldwide goat milk production was 51,235 million tonnes in 2008. About 5% of this production was from European countries and France is the leading goat milk producer in Europe, with production of 584,000 t of milk in 2009 (Institut de l'Élevage, 2010). In France, goat milk is mainly used for commercial and farmhouse cheeses, with a production of about 109,900 t and an average consumption of about 2 kg per person and year in 2009 (Institut de l'Élevage, 2010).

Goat milk fat represents approximately 4% of the total milk constituents. Goat and cow milks have similar FA composition, although some specific short- and medium-chain FA—caproic acid (C6:0), caprylic acid (C8:0), and capric acid (C10:0)—are more abundant in goats; they form 15 to 18% (compared with up to 10% in cow milk) of the total FA (Chilliard et al., 2006; Raynal-Ljutovac et al., 2008).

Fatty acids are well known for their importance in human nutrition. Numerous studies, reviewed in Arnould and Soyeurt (2009), have reported that SFA, and especially lauric (C12:0), myristic (C14:0), and

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palmitic acids (C16:0), have an unfavorable relation with some heart diseases, diabetes, and obesity (Mensink et al., 2003; Haug et al., 2007). In contrast, unsaturated fatty acids (**UFA**), usually called "healthy" fatty acids, are reported to have a favorable effect on health, especially on cholesterol levels. However, some short- and medium-chain SFA, such as C6:0 to C10:0, which are well known for their role in the specific goat flavor (C8:0), seem to be of medical interest in humans (malabsorption syndromes, infant malnutrition, cardiovascular diseases, nonallergenic properties; Haenlein, 2004). Moreover, FA are reported to play an important role in the techno-functional properties of cheese making, including organoleptic properties and cheese yield (Martin, 2008).

Therefore, interest in FA composition has been increasing over the last 10 yr. Many studies have investigated the short-term improvement of FA composition based on a feeding approach (Chilliard et al., 2001, 2002, 2003, 2008; Chilliard and Ferlay, 2004; Ollier et al., 2009). Another permanent and cumulative approach is to focus on genetic selection. To study the feasibility of a genetic change of milk FA composition, genetic parameters for FA have to be estimated. A few studies on the estimation of the genetic parameters in cattle were published several years ago (Renner and Kosmack, 1974; Karijord et al., 1982) and more recently (Soyeurt et al., 2007; Bobe et al., 2008; Soyeurt and Gengler, 2008; Stoop et al., 2008; Gion et al., 2011). To our knowledge, no equivalent study on FA composition in goats has been published to date. One genetic study on Norwegian goats (Skjevdal, 1979) reported a heritability of goat flavor of approximately 0.25, providing an indirect and rough estimation of C8:0 heritability.

In France, since 2008, an important research and development project has been performed to establish detailed phenotypes for milk composition (FA and proteins) and genotypes in cattle, sheep, and goats. The "PhénoFinLait" project is supported by a consortium of scientific and economic stakeholders from the milk industry (Brochard et al., 2009). The project involved a large-scale, on-farm phenotyping scheme for milk components based on the use of mid-infrared (**MIR**) spectra. Estimation equations were developed by Ferrand et al. (2011) to estimate FA composition in a manner similar to previous work carried out on bovine species (Soyeurt et al., 2006a, 2011; Rutten et al., 2010). This method of estimation, already used by milk recording organizations for the estimation of fat or protein content, is faster and cheaper and allows the testing of many more samples and animals than the reference estimation method by GC; MIR spectra estimates, however, are less reliable than GC.

The aim of the present study was to estimate genetic parameters for caprine milk FA using the MIR spectra collected during the PhénoFinLait project and genetic correlations of FA with milk production-related traits in primiparous goats.

MATERIALS AND METHODS

Animals and Milk Sampling

From December 2009 to December 2010, 269,296 milk samples were collected from 71,384 goats from the 2 main French dairy breeds (Alpine and Saanen) in 210 herds, as part of the PhénoFinLait project. Samples were analyzed by using 6 MIR spectrometers (MilkoScan FT6000 and MilkoScan FT+; Foss Electric, Hillerød, Denmark) in 3 laboratories. Herds were selected using several criteria: they had to be part of French milk recording, located in areas with a high concentration of goat herds, and close to a laboratory producing MIR spectra. Moreover, they had to be representative of the most common goat husbandry systems in France; that is, a feeding regimen using forages, concentrates, or both, with a kidding period in autumn or spring. Additionally, herds were chosen according to their high AI rate, to further conduct QTL detection in a daughter design. For each herd involved in the program, the database contained 2 to 6 test dates (**TD**) with individual MIR spectral information of goats. Additional information on SCC, milk yield, and fat and protein contents, collected monthly by the milk recording organization, were extracted from the national goat database (CTIG, Centre de Traitement de l'Information Génétique, INRA, Jouy-en-Josas, France).

Only data from the first lactation were considered for estimation of genetic parameters. Preliminary studies showed that fat content showed a considerable residual standard error during the earlier stages of lactation (between 5 and 20 DIM). Therefore, records with DIM of <20 or >364 were discarded. Additional edits were applied according to the following inclusion criteria: (1) herds with at least 5 FA profile records by herd within test-day (**HTD**) classes; (2) animals from Alpine and Saanen purebred, with known sires and at least 2 TD during the lactation; and (3) sires with at least 5 daughters.

Moreover, selection was applied based on the milk recording method. Only methods A and AT were considered: in the A milk recording method, 2 samples of milk (one from the evening and one from the morning) were collected but only one sample (a mix of both collected samples) was analyzed; in the AT milk recording method, alternative samples from evenings or mornings were collected and analyzed.