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Differences in milk fat composition predicted by mid-infrared spectrometry among dairy cattle breeds in the Netherlands

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ABSTRACT

The aim of this study was to estimate breed differences in milk fatty acid (FA) profile among 5 dairy cattle breeds present in the Netherlands: Holstein-Friesian (HF), Meuse-Rhine-Yssel (MRY), Dutch Friesian (DF), Groningen White Headed (GWH), and Jersey (JER). For this purpose, total fat percentage and detailed FA contents in milk (14 individual FA and 14 groups of FA) predicted from mid-infrared spectra were used. Mid-infrared spectrometry profiles were collected during regular milk recording from a range of herds with different combinations of breeds, including both purebred and crossbred cows. The data set used for the analyses contained 41,404 records from a total of 24,445 cows. In total 7,626 cows were crossbreds belonging to the breeds HF, MRY, DF, GWH, and JER; 1,769 purebreds (≥87.5%) belonging to the breeds MRY, DF, GWH, and JER; and the other 15,050 cows were HF. Breed effects were estimated using a single-trait animal model. The content in milk of short-chain FA C4:0, C6:0, C8:0, C10:0, C12:0, C14:0, and C16:0 was higher for JER and the content in milk of C16:0 was lower for GWH compared with the other breeds; when adjusting for breed differences in fat percentage, however, not all breed differences were significant. Breed differences were also found for *cis*-9 C14:1, *cis*-9 C16:1, C18:0, and a number of C18 unsaturated FA. In general, differences in fat composition in milk between HF, MRY, and DF were not significant. Jerseys tended to produce more saturated FA, whereas GWH tended to produce relatively less saturated FA. After adjusting for differences in fat percentage, breed differences in detailed fat composition disappeared or became smaller for several short- and medium-chain FA, whereas for several long-chain unsaturated FA, more significant breed differences were found. This indicates that short- and medium-chain FA are for all breeds more related to total fat percentage than long-chain FA. In conclusion, between breed differences were found in detailed FA composition and content of individual FA. Especially, for FA produced through de novo synthesis (short-chain FA, C12:0, C14:0, and partly C16:0) differences were found for JER and GWH, compared with the breeds HF, MRY, and DF.

Key words: milk, fatty acid, mid-infrared spectrometry, cattle breed

INTRODUCTION

Bovine milk fat is composed of a wide range of FA, which can be distinguished based on their number of carbons, the saturation of their carbon chain, and the conformation of double bonds. These different FA can roughly be divided into SFA with no double bounds, which make up around 70% of the total milk fat, and unsaturated FA (**UFA**) with 1 (25% MUFA) or multiple double bounds (5% PUFA). The detailed FA composition in milk is variable and can differ between cows and herds (e.g., Stoop et al., 2008). Extending the knowledge on variation in detailed FA composition is of major interest for the dairy industry because of the expected effects of dairy fat intake on human health (Mensink et al., 2003; Palmquist et al., 2006) and associations between FA composition with milk processability (e.g., Smet et al., 2009) and individual methane emission (Dijkstra et al., 2011). The variation in FA composition in milk can be partly explained by differences in the diet of the cows (e.g., Baumgard et al., 2001; Sterk et al., 2011). Besides diet, a considerable part of the variation also has a genetic origin. For instance, Mele et al. (2009) reported heritabilities for individual FA in milk of Italian Holstein-Friesians (**HF**) ranging from 0.03 to 0.17 and Stoop et al. (2008) reported heritabilities for individual FA in milk of Dutch HF ranging from 0.22 to 0.71. This indicates that a considerable part of the variation in FA composition is due to genetics. Breeding, therefore, can be a tool to change the FA composition in bovine milk. In addition to genetic variation within

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breeds, difference between dairy breeds in FA composition might be relevant. Furthermore, identification of specific breed characteristics could provide arguments for breed conservation. Differences in FA composition between herds with different dairy breeds in the Netherlands were reported by Maurice-Van Eijndhoven et al. (2011). Breed differences in FA composition were also found by DePeters et al. (1995) in which differences were reported between HF, Jersey (**JER**), and Brown Swiss Beaulieu and Palmquist (1995), in which differences were reported between HF and JER, and Lawless et al. (1999) found differences for several individual FA between Irish HF, Dutch HF, Montbéliardes, and Normandes in Ireland. In the first study (Maurice-Van Eijndhoven et al., 2011), however, the structure of the data did not allow separation of breed and herd effects.

To accurately disentangle breed and herd effects, data across a range of herds with multiple combinations of breeds are needed. The latter is a major challenge if the majority of herds only have purebred cows from 1 breed. To be able to identify breed differences, a large number of records including detailed milk FA profiles are needed. Unfortunately, the most commonly used method to determine FA composition in milk is gas chromatography (**GC**). Gas chromatography is relatively expensive and time consuming and, therefore, less suitable to assess the detailed milk fat composition for large numbers of milk samples. An alternative method to predict FA composition is mid-infrared spectrometry (**MIRS**) as described by Soyeurt et al. (2007b), Rutten et al. (2009), and De Marchi et al. (2011). Mid-infrared spectrometry is less expensive and time consuming and commonly used by milk laboratories to analyze the major milk components such as fat and protein content, which makes MIRS attractive for routine prediction of FA and for large-scale experiments. For example, Soyeurt et al. (2007a) reported heritabilities calculated using individual FA predicted using MIRS profiles in milk of dairy cattle in the Walloon region of Belgium, ranging from 0.05 to 0.38. In another study of Soyeurt et al. (2006b), using predicted FA databased on MIRS, some breed differences in FA composition were reported among the dairy breeds dual-purpose Belgian Blue, HF, JER, Montbéliarde, and Meuse-Rhine-Yssel (**MRY**) participating in the Walloon milk recording in Belgium.

The aim of this paper is to identify breed differences in FA composition among the dairy cattle breeds HF, MRY, Dutch Friesian (**DF**), Groningen White Headed (**GWH**), and JER. This was achieved by comparing the predicted FA composition for those different cattle breeds in the Netherlands using a data set with MIRS profiles from regular milk recording, including a range of herds with different combinations of breeds, considering both purebred and crossbred animals.

MATERIALS AND METHODS

Data Collection and Data Editing

Mid-infrared spectrometry profiles of milk samples were collected via the Dutch milk recording system of CRV BV (Arnhem, the Netherlands) between October and December 2006. Samples were treated immediately with 0.03% (wt/wt) sodium azide to avoid microbiological growth. The MIRS profiles were obtained using 3 Fourier-transformed interferogram machines (MilkoScan FT 6000; Foss Electric A/S, Hillerød, Denmark) at the laboratory of Qlip N.V. (Leusden, the Netherlands). The sampled herds were a random representation of all herds participating in the milk recording system of CRV BV.

The initial data set contained 372,429 test-day records of 230,995 cows. Data-editing steps included the deletion of records and cows for the following reasons: less than 75% of the breed composition known, unknown sire, incomplete milk recording data (e.g., unknown birthdate or DIM), 2 records from the same cow on the same sample date, cows with records in more than 1 herd, cows reported sick at sampling date, cows in parity 11 or higher, cows before 5 or after 365 d in lactation, and cows in herds with less than 5 purebred cows of the same breed (HF, MRY, DF, or GWH) per herd. To detect records with possible errors, due to, for example, swapped samples, fat content recorded via the regular milk control (predicted by QLIP N.V.) was compared with the values obtained using the RobustMilk prediction equations (Soyeurt et al., 2011). The correlation coefficient between fat content predicted by QLIP N.V. and fat content predicted using the RobustMilk prediction equations was 0.996. When the absolute difference in both predictions for fat percentage was more than 0.35 the record was removed. Finally, complete records with extreme outliers in at least 1 of all predicted traits ($\pm$5 SD of the mean) were deleted. After these editing steps, the data set contained 307,656 records.

A large number of these records were from HF animals from herds without crossbreds or animals from breeds other than HF. Because these records do not contribute to the breed estimates and makes the data set heavily unbalanced, only animals from herds with at least 3 animals with >25% genes from MRY, DF, GWH, or JER were kept in the data set. The final data set used for the analyses contained 41,404 records of 24,445 cows from 445 farms. A total of 7,626 cows were crossbreds belonging to the breeds HF, MRY, DF, GWH, and JER; 1,769 purebreds ($\geq$87.5%) belonging