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Genetic analysis of predicted fatty acid profiles of milk from Danish Holstein and Danish Jersey cattle populations

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ABSTRACT

The objective of this paper was to assess the genetic variability of the detailed fatty acid (FA) profiles of Danish Holstein (DH) and Danish Jersey (DJ) cattle populations. We estimated genetic parameters for 11 FA or groups of FA in milk samples from the Danish milk control system between May 2015 and October 2016. Concentrations of different FA and FA groups in milk samples were measured by mid-infrared spectroscopy. Data used for parameter estimation were from 132,732 first-parity DH cows and 21,966 first-parity DJ cows. We found the highest heritabilities for test day measurements in both populations for short-chain FA (DH = 0.16; DJ = 0.16) and C16:0 (DH = 0.14; DJ = 0.16). In DH, the highest heritabilities were also found for saturated FA and monounsaturated FA (both populations: 0.15). Genetic correlations between the fatty acid traits showed large differences between DH and DJ for especially short-chain FA with the other FA traits measured. Furthermore, genetic correlations of total fat with monounsaturated FA, polyunsaturated FA, short-chain FA, and C16:0 differed markedly between DH and DJ populations. In conclusion, we found genetic variation in the mid-infrared spectroscopy-predicted FA and FA groups of the DH and DJ cattle populations. This finding opens the possibility of using genetic selection to change the FA profiles of dairy cattle.
Key words: fatty acid profile, genetic parameter, dairy cow, population

INTRODUCTION

Milk contains important nutrients for young animals and humans. A major component in milk, fat consists almost entirely (~98%) of triglycerides, which are composed of a glycerol backbone and 3 fatty acids (**FA**). More than 400 individual FA have been discovered in milk (Jensen et al., 1991), which are typically divided into SFA (65–70% of total fat), MUFA (27–33%), and PUFA (3–5%). From a human nutritional standpoint, it would be beneficial to increase the unsaturated fat content of milk. Ingestion of unsaturated fats has a generally positive effect on serum cholesterol levels; however, a direct negative effect of SFA is debatable (Lawrence, 2013; Bier, 2016; Parodi, 2016). Furthermore, C16:0 has been associated with negative effects on cardiovascular disease in humans (Mensink et al., 2003; Givens, 2010).

In Denmark, interest has increased regarding the development of new dairy products with fat as an important component. The formation of FA in milk is influenced by many factors, including lactation stage (Craninx et al., 2008; Stoop et al., 2008), season (Heck et al., 2009), management or feeding regimen (Moate et al., 2007; Coppa et al., 2013), and genetics (Soyeurt et al., 2006b; Stoop et al., 2008; Krag et al., 2013). For changing the FA profile in milk by genetic selection, it is important to clarify the genetics underlying milk FA in different dairy cattle breeds. This clarification requires large amounts of phenotypic data (i.e., FA measurements). However, measuring the FA concentration in milk has been a challenge, because the gold standard for measuring FA is GC. Owing to its time-consuming and costly nature, GC is not well suited for large-scale screening. Alternatively, mid-infrared spectrometry (**MIRS**) can be used for the high-throughput analysis of milk samples (Soyeurt et al., 2006a; De Marchi et al., 2014).

In the current study, we investigated the possibility of differentiating the milk FA profile by genetics. For that purpose, the Danish dairy cattle population was routinely screened for different FA groups by using MIRS. We present the results of the genetic and phenotypic analyses of FA data from the Danish Holstein (**DH**) and Danish Jersey (**DJ**) cattle populations.

MATERIALS AND METHODS

Data and Animals

Milk samples were collected during regular herd testing from May 2015 to October 2016 from primiparous

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Table 1. Total number of fatty acid observations (8–305 DIM) and number of cows per breed and production system after editing, based on data from May 2015 to October 2016

	Production system					
	Conventional		Organic		Total	
Breed	Cows	Observations	Cows	Observations	Cows	Observations
Danish Holstein	121,337	558,198	11,394	54,123	132,731	612,321
Danish Jersey	20,155	88,023	1,812	7,897	21,967	95,920
Total	141,492	646,221	13,206	62,020	154,698	708,241

DH and DJ cows participating in the Danish herd testing scheme. Samples were analyzed at a certified laboratory (Eurofins, Vejen, Denmark) with a MilkoScan FT+/FT6000 (Foss, Hillerød, Denmark) equipped with special software (Foss Application Note 64, Foss) for predicting 7 FA fractions, namely SFA, MUFA, PUFA, short-chain FA (**SCFA**), medium-chain FA (**MCFA**), long-chain FA (**LCFA**), and *trans* FA (**TFA**), as well as 4 individual FA, namely C14:0, C16:0, C18:0, and C18:1. Raw FA measurements, provided as grams of FA per 100 g of milk, were stored in the Danish Cattle Database (SEGES, Skejby, Denmark). In addition to FA measurements, information about milk yield, total fat content, calving date, parity, breed, and production system was extracted from the Danish Cattle Database (SEGES).

We applied numerous consecutive editing procedures to ensure that we obtained high-quality FA observations. Observations were checked for the following conditions and removed if any condition was met. (1) One or more of the 11 FA fractions was missing from an observation. (2) The PUFA concentration was greater than or equal to the MUFA concentration. (3) The ratio of the sum of the SFA, MUFA, and PUFA contents to the total fat content was less than 0.825 or greater than 1.075 (values chosen such that 5% of remaining observations were removed). (4) The ratio of the sum of the SCFA, MCFA, and LCFA contents to the sum of the SFA, MUFA, and PUFA contents was less than 0.84 or greater than 1.04 (values chosen such that 1% of remaining observations were removed). Finally, (5) each FA fraction was checked for outliers. The size of extreme values was chosen such that 1% of remaining observations were removed. If more than 1 observation per cow per herd test day was observed, then the mean value of the observations was used. Moreover, an observation was removed if the daily milk yield was less than 2 kg or the total fat percentage was greater than 8 or 12% for DH and DJ, respectively, as these conditions could indicate the presence of a metabolic disease (e.g., ketosis). The lactation period was defined as 8 to 305 DIM. This interval was chosen to avoid any interference caused by colostrum production in the beginning of lactation, and because 305 DIM defines the endpoint of lactation when performing genetic evaluation of dairy cattle in Nordic countries.

Three additional editing steps were performed. (1) Daughters of a sire with fewer than 10 daughters were removed from the data set. (2) Cows that changed herd during the sampling period were removed from the data set. (3) The last step was reduction of the number of animals to enable both phenotypic and genetic analyses of especially the large DH data. This was done by randomly removing all records from every second cow from the data set. Means and variances of the FA variables were checked to ensure that data were unbiased after reduction. The sizes of the final data sets are shown in Table 1.

Definition of Traits

For each FA fraction, 2 trait groups were defined: (1) total test day FA production in grams and (2) percentage of test-day FA, defined as the ratio of the content of the FA fraction to the sum of the SFA, PUFA, and MUFA contents. Total fat in grams was determined across the lactation (8–305 DIM). Genetic parameters were estimated based on test day measurements across the lactation period. The average number of observations per cow across the lactation period was 4.6 (SD = 2.7) for DH and 4.4 (SD = 2.5) for DJ. Minimum number of observations per cow was 1 for both breeds.

Data Analysis

Descriptive statistical analysis was performed by using the HPMIXED procedure in SAS (version 9.3, SAS Institute Inc., Cary, NC) to study the effects of breed (2 levels; DH and DJ), production system (2 levels; organic and conventional), month × year (18 levels), 30-d lactation interval (10 levels), and production system × (month × year). The following linear mixed model was used:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Qh} + \mathbf{Za} + \mathbf{e}, \quad [1]$$