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Genetic correlations of mid-infrared-predicted milk fatty acid groups with milk production traits

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ABSTRACT

The objective of this research was to estimate the genetic correlations between milk mid-infrared-predicted fatty acid groups and production traits in first-parity Canadian Holsteins. Contents of short-chain, medium-chain, long-chain, saturated, and unsaturated fatty acid groupings in milk samples can be predicted using mid-infrared spectral data for cows enrolled in milk recording programs. Predicted fatty acid group contents were obtained for 49,127 test-day milk samples from 10,029 first-parity Holstein cows in 810 herds. Milk yield, fat and protein yield, fat and protein percentage, fat-to-protein ratio, and somatic cell score were also available for these test days. Genetic parameters were estimated for the fatty acid groups and production traits using multiple-trait random regression test day models by Bayesian methods via Gibbs sampling. Three separate 8- or 9-trait analyses were performed, including the 5 fatty acid groups with different combinations of the production traits. Posterior standard deviations ranged from <0.001 to 0.01. Average daily genetic correlations were negative and similar to each other for the fatty acid groups with milk yield (−0.62 to −0.59) and with protein yield (−0.32 to −0.25). Weak and positive average daily genetic correlations were found between somatic cell score and the fatty acid groups (from 0.25 to 0.36). Stronger genetic correlations with fat yield, fat and protein percentage, and fat-to-protein ratio were found with medium-chain and saturated fatty acid groups compared with those with long-chain and unsaturated fatty acid groups. Genetic correlations were very strong between the fatty acid groups and fat percentage, ranging between 0.88 for unsaturated and

0.99 for saturated fatty acids. Daily genetic correlations from 5 to 305 d in milk with milk, protein yield and percentage, and somatic cell score traits showed similar patterns for all fatty acid groups. The daily genetic correlations with fat yield at the beginning of lactation were decreasing for long-chain and unsaturated fatty acid groups and increasing for short-chain fatty acids. Genetic correlations between fat percentage and fatty acids were increasing at the beginning of lactation for short- and medium-chain and saturated fatty acids, but slightly decreasing for long-chain and unsaturated fatty acid groups. These results can be used in defining fatty acid traits and breeding objectives.

Key words: fatty acid, production trait, genetic correlation, Gibbs sampling

INTRODUCTION

Interest is growing in broadening selection objectives in dairy cattle breeding to include novel traits to improve milk quality, cow health, and fertility so as to complement selection for production traits. The composition of milk fat is meaningful for human health and nutrition (Parodi, 2004), but also as a potential indicator for the metabolic and health status of the cow and novel traits such as energy balance and methane emissions (Jorjong et al., 2015; van Gastelen and Dijkstra, 2016). Emerging consumer concern over the health effects of the products they consume has elicited research into the possibility of altering the fatty acid content of milk. Bovine milk fat is a source of many fatty acids with potential health benefits (Parodi, 2004), and increased proportions of those fatty acids promoting good health may be a worthy breeding goal.

The fatty acid profile of milk can be altered through the feeding of specialized diets to lactating dairy cows (Palmquist et al., 1993; Chilliard et al., 2000; Kliem and Shingfield, 2016); however, these changes are only temporary and depend on feed availability and prices.

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Likewise, limitations exist to the amount of fat that can be fed to dairy cows and the availability of these dietary lipids to the mammary gland to be used for milk production (Kliem and Shingfield, 2016). The fatty acid composition of milk is also influenced by the genetics of the cow (Soyeurt et al., 2007; Stoop et al., 2008; Bastin et al., 2011; Pegolo et al., 2016), thus providing the possibility for genetic selection to permanently enhance the milk fatty acid profile for the entire cow population.

The implementation of a new trait into a selection program requires an affordable means of phenotyping the trait routinely on a large scale. Mid-infrared (MIR) spectroscopy is already used to record fat and protein percentage, MUN, and BHB contents in milk during routine milk recording. More recently, studies have shown that milk fatty acid contents can also be predicted from the MIR spectra of a milk sample (Soyeurt et al., 2006; Rutten et al., 2009; De Marchi et al., 2011; Fleming et al., 2017). The prediction of milk fatty acid contents using MIR technology facilitates the collection of large numbers of these phenotypes for all milk-recorded cows. Genetic evaluation and selection for these traits is thus achievable for the dairy industry. To avoid unwanted correlated responses with other important traits, knowledge of these genetic correlations is important before implementation of fatty acid composition traits into breeding goals. To our knowledge, no studies have investigated genetic correlations across the lactation between fatty acid groups and milk production traits in dairy cattle, with the exception of Bastin et al. (2011, 2013), who used daily EBV correlations to approximate genetic correlations between fatty acids and select milk traits. The objective of our study was to estimate the genetic correlations of milk fatty acid group contents with milk production traits in the Canadian Holstein population using multiple-trait animal models.

MATERIALS AND METHODS

Data

Milk MIR spectra obtained during routine milk recording from 1 of 2 MilkoScan FT6000 spectrometers

(Foss, Hillerød, Denmark) at CanWest DHI (Guelph, ON, Canada) or Valacta (Sainte-Anne-de-Bellevue, QC, Canada) milk laboratories were stored in a database. Spectra were collected between January 2013 and July 2015 and standardization of spectra between the 2 machines was performed per Bonfatti et al. (2017). The database contained a total of 2,053,396 spectra of individual milk samples from Holstein cows.

Prediction equations developed by Fleming et al. (2017) for 5 groups of fatty acids, expressed as grams per deciliter of milk, were applied to the historical spectra. Fatty acid groups were defined by saturation (SFA and UFA) and by chain length [short-chain (SCFA; 4 to 10 carbons), medium-chain (MCFA; 11 to 16 carbons), and long-chain (LCFA; 17 to 22 carbons)]. The individual fatty acids used to devise the groups are given in Table 1. Fatty acid contents were examined on a per-milk basis instead of on a per-fat basis because of the greater prediction accuracies achieved. The coefficients of determination of cross-validation for the prediction equations were 0.94, 0.84, 0.72, 0.90, and 0.83 for the SFA, UFA, SCFA, MCFA, and LCFA groups, respectively. Fatty acid predictions were deleted for samples with MIR spectral data considered as outliers and dissimilar to those used to develop the calibrations. Spectral outliers were determined using the root mean square error for standardized predictors, calculated when the prediction equations by Fleming et al. (2017) were applied. Sample spectra with a mean square error greater than 3 standard deviations above the mean value were considered outliers and removed. All 5 groups of fatty acids were predicted for 1,957,353 Holstein milk samples with spectra saved in the database. Test day production records included milk, fat, and protein yields, SCC, and fat to protein ratio (**F:P**) and were obtained from the Canadian Dairy Network (Guelph, ON, Canada) for the test-day records with fatty acid contents predicted. The SCC was log-transformed to SCS according to the formula proposed by Ali and Shook (1980). The total number of milk samples with predicted fatty acid contents, along with complete test-day production records and lactation information for the corresponding test-day, was 1,780,089 from 514,795 Holstein cows in 6,768 herds.

Table 1. Individual fatty acids included in the defined short-chain (SCFA), medium-chain (MCFA), long-chain (LCFA), SFA, and UFA groups of fatty acid traits

Trait	Fatty acids included
SCFA	C4:0, C6:0, C8:0, C10:0
MCFA	C11:0, C12:0, C13:0, C14:0, C14:1, C15:0, C16:0, C16:1
LCFA	C17:0, C17:1, C18:0, C18:1n-9 <i>trans</i> , C18:1n-9 <i>cis</i> , C18:2n-6 <i>trans</i> , C18:2n-6 <i>cis</i> , C18:3n-3, C18:2n <i>cis</i> -9, <i>cis</i> -12, C22:6n-3
SFA	C4:0, C6:0, C8:0, C10:0, C11:0, C12:0, C13:0, C14:0, C15:0, C16:0, C17:0, C18:0
UFA	C14:1, C16:1, C17:1, C18:1n-9 <i>trans</i> , C18:1n-9 <i>cis</i> , C18:2n-6 <i>trans</i> , C18:2n-6 <i>cis</i> , C18:3n-3, C18:2n <i>cis</i> -9, <i>cis</i> -12, C22:6n-3

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