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Genetic relationships of clinical mastitis, cystic ovaries, and lameness with milk yield and somatic cell score in first-lactation Canadian Holsteins

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ABSTRACT

The objective of this study was to investigate the genetic relationships of the 3 most frequently reported dairy cattle diseases (clinical mastitis, cystic ovaries, and lameness) with test-day milk yield and somatic cell score (SCS) in first-lactation Canadian Holstein cows using random regression models. Health data recorded by producers were available from the National Dairy Cattle Health System in Canada. Disease traits were defined as binary traits (0 = healthy, 1 = affected) based on whether or not the cow had at least one disease case recorded within 305 d after calving. Mean frequencies of clinical mastitis, cystic ovaries, and lameness were 12.7, 8.2, and 9.1%, respectively. For genetic analyses, a Bayesian approach using Gibbs sampling was applied. Bivariate linear sire random regression model analyses were carried out between each of the 3 disease traits and test-day milk yield or SCS. Random regressions on second-degree Legendre polynomials were used to model the daily sire additive genetic and cow effects on test-day milk yield and SCS, whereas only the intercept term was fitted for disease traits. Estimated heritabilities were 0.03, 0.03, and 0.02 for clinical mastitis, cystic ovaries, and lameness, respectively. Average heritabilities for milk yield were between 0.41 and 0.49. Average heritabilities for SCS ranged from 0.10 to 0.12. The average genetic correlations between daily milk yield and clinical mastitis, cystic ovaries, and lameness were 0.40, 0.26, and 0.23, respectively; however, the last estimate was not statistically different from zero. Cows with a high genetic merit for milk yield during the lactation were more susceptible to clinical mastitis and cystic ovaries. Estimates of genetic correlations between daily milk yield and clinical mastitis were moderate throughout the lactation. The genetic correlations between daily milk yield and cystic ovaries were near zero at the beginning of lactation and were highest at mid and end lactation. The average genetic correlation between daily SCS and clinical mastitis was 0.59 and was consistent throughout the lactation. The average genetic correlation between daily SCS and cystic ovaries was near zero (−0.01), whereas a moderate, but nonsignificant, correlation of 0.27 was observed between SCS and lameness. Unfavorable genetic associations between milk yield and diseases imply that production and health traits should be considered simultaneously in genetic selection.

Key words: disease, milk yield, somatic cell score, genetic correlation

INTRODUCTION

Breeding for disease resistance is becoming increasingly important for economic reasons, as well as animal welfare concerns and consumer demands for healthy and naturally produced products. In Canada, a national dairy cattle health and disease data recording system was started in 2007. Eight diseases that are known to affect herd profitability are recorded by producers on a voluntary basis: clinical mastitis, displaced abomasum, ketosis, milk fever, retained placenta, metritis, cystic ovaries, and lameness. The feasibility of using producer-recorded health data from Canada for genetic evaluations has been shown previously by Neuenschwander (2010) and Koeck et al. (2012b).

Milk yield, one of the main selection criteria for dairy cattle during the last few decades, is genetically unfavorably correlated with disease resistance (e.g., Hooijer et al., 2001; Carlén et al., 2004; König et al., 2008). Due to lack of disease recording systems, selection for disease resistance in many countries is based on genetically correlated traits, such as SCS, which is used as a mastitis indicator. Most literature estimates of genetic correlations between disease traits and milk yield or SCS are from lactation-average models. Recently, Negussie et al. (2008a, 2010) and Mrode et al. (2012) applied random regression models to investigate genetic relationships between mastitis and milk yield or SCS throughout lactation. The advantage of such an

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Table 1. Summary statistics of analyzed data

Item	Clinical mastitis	Cystic ovaries	Lameness
Cows (no.)	61,086	45,641	36,001
Test-day records (no.)	453,829	346,579	266,082
Sires (no.)	3,080	2,530	2,431
Pedigree (no.)	4,106	3,518	3,376
Disease frequency (%)	12.7	8.2	9.1
Mean test-day milk yield (kg)	29.5	29.4	29.6
Mean test-day SCS ($\log_2$)	2.2	2.1	2.1

analysis is that all information in the data are utilized, as SCS and milk production traits vary with stage of lactation.

In previous studies of Canadian Holsteins, the genetic correlation between clinical mastitis and lactation average SCS was estimated to be in the range of 0.63 to 0.69 (Koeck et al., 2012a,c). Genetic associations between diseases and milk yield throughout the lactation have never been studied in this population. Therefore, the objective of this study was to investigate the genetic relationships of the 3 most frequently reported dairy cattle diseases (clinical mastitis, cystic ovaries, and lameness) with test-day milk yield and SCS in first-lactation Canadian Holstein cows using random regression models.

MATERIALS AND METHODS

Data

Data for clinical mastitis, cystic ovaries, and lameness recorded by dairy producers from April 1, 2007, to April 20, 2011, as well as monthly test-day records of milk yield and SCC, were obtained from the Canadian Dairy Network (Guelph, ON, Canada). To ensure that all cows were from herds with reliable disease recording, several editing criteria were applied separately for each disease. Only herds having at least 2 records of the disease being analyzed were considered. The first and last record in a herd had to be at least 180 d distant. This criterion would remove herds that had recorded for only a short time. In addition, minimum disease frequencies were applied to ensure continuous data recording within individual herds. Minimum frequencies (reported cases per herd and year) were 5% for clinical mastitis and 1% for cystic ovaries and lameness.

Because not all herds record all diseases (Koeck et al., 2012b), 3 data sets, one for each disease, were created by matching test-day data to health records. In all data sets, only records from first-lactation Holstein cows with an age at calving between 19 and 43 mo and at least 1 test-day observation were considered. For each of the 3 data sets, a sire pedigree file was generated by tracing the pedigrees of sires and maternal grandsires back as far as possible. Summary statistics for the analyzed data sets are given in Table 1.

Trait Definitions

In Canada, cases of clinical mastitis, cystic ovaries, and lameness are recorded by producers according to the disease definitions described by Kelton et al. (1998). Clinical mastitis, cystic ovaries, and lameness were defined as binary traits (0 = healthy, 1 = affected) based on whether or not the cow had at least one disease case recorded within 305 d after calving. Test-day records between 5 and 305 DIM were considered for milk yield and SCC. Test-day SCC was transformed to SCS, to achieve an approximately normal distribution, as follows: $\text{SCS} = \log_2 (\text{SCC}/100{,}000) + 3$.

Models

For genetic analyses, a Bayesian approach using Gibbs sampling was applied. Bivariate linear sire random regression model analyses were carried out between the 3 diseases (clinical mastitis, cystic ovaries, and lameness) and test-day milk yield or SCS. Legendre polynomials of the second degree were used to describe regression curves for milk yield and SCS, whereas only the intercept term was fitted for disease traits. As disease frequencies were low, the disease traits were defined on a lactation basis. An alternative approach would be to define disease traits as longitudinal traits. However, as shown by Carlén et al. (2009), the application of random regression models was unstable and sensitive for estimation of genetic parameters for clinical mastitis.

Linear models were applied for disease traits, even though these traits are binary. Although threshold models are, at least in theory, more appropriate to analyze binary traits, the literature indicates they have little effect on the ranking of animals (e.g., Ramirez-Valverde et al., 2001). Moreover, Negussie et al. (2008b) analyzed clinical mastitis in bivariate analyses with production traits (SCS, milk, protein, and fat yields) by using both a threshold-linear and linear-linear model and found