Development of Genetic Evaluations for Metabolic Disease Traits for Canadian Dairy Cattle

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Abstract

The overall goal of this study was to develop genetic evaluations for metabolic disease traits in Canadian dairy cattle. The specific objective was to estimate genetic parameters for metabolic diseases and their main predictors in Canadian Holsteins. Health data recorded by producers were available from the National Dairy Cattle Health System. Records from first to fifth lactation were considered for ketosis (KET), displaced abomasum (DA), milk fever (MF), fat to protein ratio (F:P) and milk ß-hydroxybutyrate (BHBA), whereas for body condition score (BCS) only records from first lactation cows were available. Binary disease traits (0 = no case, 1 = at least one case), F:P and milk BHBA were treated as different traits in first and later lactations. Records for MF in first lactation were not considered in the present study as the frequency of this disease was near zero and a preliminary analysis revealed a heritability of zero. Bivariate and multivariate linear sire models were fitted using AI-REML. Heritability for metabolic disease traits ranged from 0.011 to 0.047. Higher heritabilities were found for BCS, F:P and milk BHBA, with estimates ranging from 0.10 to 0.22. First lactation KET was strongly correlated with DA (0.76) and milk BHBA (0.75), whereas lower genetic correlations were found with BCS and F:P (-0.54 and 0.37, respectively). Displaced abomasum in first lactation was moderately correlated with BCS (-0.40) and F:P (0.19). Similar genetic correlations were estimated in later lactation cows. Milk fever, which was only evaluated in second and later lactation cows, was moderately correlated with KET (0.39) and milk BHBA (0.33). Genetic correlations of disease traits between first and later lactations were relatively high (0.79 for KET and 0.86 for DA).

Key words: metabolic disease, milk ß-hydroxybutyrate, fat to protein ratio, body condition score, genetic parameters

Introduction

This study is part of a larger project whose overall objective is to develop routine genetic evaluations for disease resistance traits in Canadian dairy cattle. The aim of this study was to estimate genetic parameters for metabolic diseases [clinical ketosis (**KET**), displaced abomasum (**DA**), milk fever (**MF**)] and its predictors. Based on the results of previous studies (Loker *et al.*, 2012; Koeck *et al.*, 2013; Koeck *et al*., 2014) the following indicator traits were selected: body condition score (**BCS**), fat to protein ratio at the first test-day (5-40 DIM; **F:P**) and milk ß-hydroxybutyrate at the first test-day (5-40 DIM; **BHBA**).

Materials and Methods

Health data recorded by dairy producers and veterinarians from April 2007 to December 2014, as well as records for BCS and F:P were obtained from the Canadian Dairy Network (Guelph, Ontario). A minimum disease frequency (reported cases per herd and year) of 1% was applied for KET, DA and MF to ensure continuous data recording within individual herds. Data editing was applied separately for each disease, because not all herds record all disease. Diseases were defined as binary traits (0 = no case, 1 = at least one case) based on whether or not the cow had at least one disease case recorded within 100 d after calving for KET, within 100 d after

calving for DA and within 30 d after calving for MF. Body condition score was routinely recorded by professional type classifiers on a scale from 1 (very thin) to 5 (very fat) in increments of 0.25. Only first classifications within 305 DIM were used, reclassification records were not considered. Test-day records for milk BHBA recorded between 5 and 100 DIM from October 2011 to December 2014 was obtained from Valacta (Sainte-Anne-de-Bellevue, QC, Canada). Test-day milk samples were analyzed by a MIR spectrometer (MilkoScan FT+, Foss, Hillerød, Denmark) with previously developed calibration equations for milk BHBA from Foss (Hillerød, Denmark). Milk BHBA test-day records with missing milk test-day measurement were excluded from further analyses. For genetic analyses, the milk BHBA concentrations were $\log_e$ transformed to normalize their distribution. To allow a log transformation of the data, a constant of 1.00 was added to milk BHBA concentrations to prevent negative and zero values, for which $\log_e$ is not defined. Data on Holstein cows from lactation 1 to 5 were considered. Sequential edit of cow lactation records was applied for each disease trait separately, which means that cows with a given lactation record have a record in all previous lactations. Disease data was then merged with data on BCS, F:P and milk BHBA. A summary statistics of the analyzed data set is given in Table 1. The sire pedigree file was generated by tracing back the pedigrees of sires and maternal grandsires as far as possible.

Table 1. Summary statistics - number of records and mean and SD in parentheses for each trait.

Trait	Records	Lactation	
		1	2-5
KET, %	120,497	4.1	6.9
DA, %	296,539	3.0	3.7
MF, %	207,903	0.1	2.9
BCS, score	230,222	2.82 (0.35)	-
F:P, ratio	410,253	1.33 (0.27)	1.32 (0.27)
BHBA, mmol/L	55,623	0.101 (0.078)	0.109 (0.083)

Statistical Analysis

Univariate and multivariate linear sire models were fitted using the AI-REML procedure in the DMU package (Madsen and Jensen, 2008). Disease traits (KET, DA and MF), F:P and milk BHBA were treated as different traits in first and later lactations. Records for MF in first lactation were not considered in the present study as the disease frequency was near zero and a preliminary analysis revealed a heritability of zero.

The bivariate models were applied to:

- KET_1 and KET_{2-5}
- DA_1 and DA_{2-5}

The multivariate models were applied to:

- KET_1, DA_1, BCS, $F{:}P_1$ and $BHBA_1$
- KET_{2-5}, DA_{2-5}, MF_{2-5}, $F{:}P_{2-5}$ and $BHBA_{2-5}$

The model for disease traits in first lactations included fixed effects of age at calving, year-season of calving and herd-year of calving, random additive genetic sire effect and random residual effect. The model for BCS included fixed effects of age at calving-stage of lactation, herd-round-classifier of calving, random additive genetic sire effect, and random residual effect. The model for F:P and milk BHBA in first lactations included fixed effects of age at calving, year-season of calving, herd-year of calving and days in milk, random additive genetic sire effect and random residual effect.

Models for disease, F:P and milk BHBA traits in later lactations are the same as for the first lactation data; only a fixed effect of lactation (2, 3, 4, 5) was fitted instead of an age at calving effect. The permanent environmental effect was included for later lactation traits to account for repeated observations on a cow. However, it was not considered for DA as a preliminary analysis revealed a permanent environmental variance close to zero for this trait.

Results and Discussion

Genetic correlations of disease traits between first and later lactations were relatively high, 0.79 (0.11) for KET and 0.86 (0.05) for DA.
Genetic parameters for KET, DA and MF and their predictors are shown in Tables 2 and 3. Heritability for metabolic disease traits ranged from 0.011 to 0.047. Higher heritabilities were found for BCS, F:P and milk BHBA, with estimates ranging from 0.10 to 0.22. First lactation KET was strongly correlated with DA (0.76) and milk BHBA (0.75), whereas moderate genetic correlations were found with BCS and F:P (-0.54 and 0.37, respectively). Displaced abomasum in first lactation was moderately correlated with BCS (-0.40) and F:P (0.19). Similar genetic correlation estimates were estimated in later lactation cows. Milk fever, which was only evaluated in later lactation cows, was moderately correlated with KET (0.39) and milk BHBA (0.33).

Table 2. Heritabilities (in bold on the diagonal, SE in parentheses) and genetic correlations (above the diagonal, SE in parentheses) in first lactation cows.

Trait	KET_1	DA_1	BCS	$F:P_1$	$BHBA_1$
KET_1	**0.018 (0.003)**	0.76 (0.06)	-0.54 (0.08)	0.37 (0.08)	0.75 (0.08)
DA_1		**0.047 (0.005)**	-0.40 (0.05)	0.19 (0.06)	0.15 (0.09)
BCS			**0.220 (0.011)**	-0.30 (0.04)	-0.43 (0.08)
$F:P_1$				**0.158 (0.009)**	0.32 (0.08)
$BHBA_1$					**0.097 (0.015)**

Table 3. Heritabilities (in bold on the diagonal, SE in parentheses) and genetic correlations (above the diagonal, SE in parentheses) in later lactation cows.

Trait	KET_{2-5}	DA_{2-5}	MF_{2-5}	$F:P_{2-5}$	$BHBA_{2-5}$
KET_{2-5}	**0.028 (0.006)**	0.54 (0.10)	0.39 (0.16)	0.57 (0.08)	0.75 (0.09)
DA_{2-5}		**0.022 (0.004)**	0.15 (0.15)	0.24 (0.09)	-0.03 (0.12)
MF_{2-5}			**0.011 (0.003)**	-0.02 (0.13)	0.33 (0.15)
$F:P_{2-5}$				**0.119 (0.009)**	0.25 (0.08)
$BHBA_{2-5}$					**0.105 (0.016)**

The use of a multivariate model significantly increased the reliability of sire EBV for KET, whereas for DA and MF only a slight increase was observed (Figures 1 and 2).

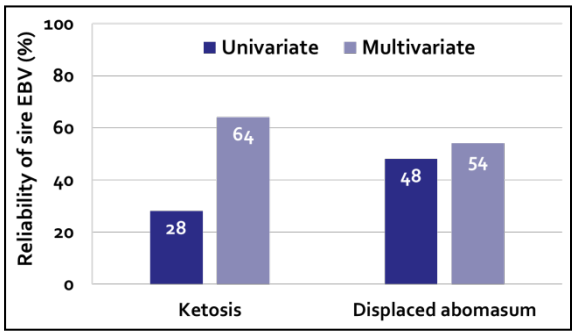

Figure 1. Reliability of sire EBV (sires with 51 to 100 daughters in first lactation).

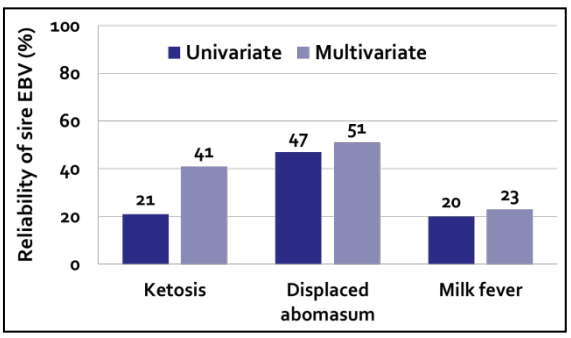

Figure 2. Reliability of sire EBV (sires with 51 to 100 daughters in later lactations).

Conclusions

- Ketosis is strongly correlated with milk BHBA, therefore, more milk BHBA records will be accumulated.
- Milk fever will not be included in routine genetic evaluation, because of a) very low frequency in first parity cows; b) lack of good predictors; and c) low reliability of sire EBV.

Acknowledgements

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