Index for Mastitis Resistance and Use of BHBA for Evaluation of Health Traits in Canadian Holsteins

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Abstract

A routine genetic evaluation for mastitis resistance will be officially implemented in Canada in August 2014 for Holstein, Ayrshire and Jersey breeds. The model is a multiple-trait linear animal model including mastitis, average SCS in early lactation, standard deviation of SCS, excessive test-day SCC, fore udder attachment, udder depth and body condition score. Genetic evaluations for clinical mastitis in first lactation as well as in second and later lactations are calculated and expressed as relative breeding values with a mean of 100 and a standard deviation of 5, where higher values are desirable. An index for Mastitis Resistance was developed that includes both the two clinical mastitis traits and the official SCS evaluation, with equal weights.

Hyperketonemia or ketosis is one of the most frequent diseases in dairy cattle and the level of milk ß-hydroxybutyrate (BHBA) is an indicator of subclinical ketosis. Heritability estimates for milk BHBA in Canadian Holstein cows were between 0.13 and 0.29. Higher milk BHBA in early lactation was genetically associated with a higher frequency of clinical ketosis and displaced abomasum. Milk BHBA can be routinely analyzed in milk samples at test-days, and, therefore, provides a potential alternative for breeding cows with a lower susceptibility to hyperketonemia.

Key words: mastitis resistance, genetic evaluation, ß-hydroxybutyrate, metabolic disease

Genetic Evaluation for Mastitis Resistance

Introduction

In August 2014, Canadian Dairy Network (CDN) will release the first official run of genetic evaluations for mastitis resistance (Jamrozik *et al*., 2013) for Holstein, Ayrshire and Jersey breeds. The model is a multiple-trait linear animal model including clinical mastitis, mean somatic cell score (SCS) in early lactation (5-150 days in milk), standard deviation of SCS, excessive test-day SCC, fore udder attachment, udder depth and body condition score. Traits for mastitis and SCS are for first parity cows and for second and later parity cows. Genetic evaluations for clinical mastitis in first lactation as well as for clinical mastitis in second and later lactations are calculated and expressed as relative breeding values (**RBV**) with a mean of 100 and a standard deviation of 5, where higher values are desirable. Those are the only estimated breeding values that will be published from this evaluation system. The other traits are included in the evaluation system as they are well correlated with mastitis and most of them have much higher heritabilities. Therefore, their inclusion provides a significant increase in reliability for the genetic evaluations for clinical mastitis, which are the traits of interest. The objective of this part of the study was to develop a Mastitis Resistance index for official publication that includes the RBV for the two measures of clinical mastitis as well as officially published genetic evaluations for SCS that originate from the Canadian Test Day Model.

Index for Mastitis Resistance

Boettcher *et al*. (1998) developed an udder health index for use in sire selection for an aggregate genotype that included subclinical mastitis (measured by SCS) in lactations 1 and ≥2, clinical mastitis in lactations 1 and ≥2, and

milking time. Estimated economic weights were -$12, -$31, -$15, -$59 and -$11, respectively, per genetic standard deviation. At that time clinical mastitis was not recorded, thus traits in the selection index were milking speed, udder conformation and SCS in first and later lactations. In August 2014, CDN will release the first official run of genetic and genomic evaluations for Clinical Mastitis in First lactation (**CM-F**) and Clinical Mastitis in Later lactations (**CM-L**) using a multiple trait evaluation model (Jamrozik *et al*., 2013). Based on the work by Boettcher *et al*. (1998), an index for Mastitis Resistance was developed that included both the clinical mastitis traits (CM-F and CM-L) and the official SCS evaluation, which has equal weights on SCS in first, second and third lactation. All traits were standardized before applying the relative weights and the overall Mastitis Resistance index was then standardized as an RBV with an average of 100 and standard deviation of 5.

Selection Response

The response to selection per year (Table 1) for different index weights was calculated and it was based on the following assumptions:

1) Heritability for CM-F, CM-L and SCS = 0.03, 0.05, 0.20, respectively
2) Genetic correlations among the three traits: CM-F with CM-L = 0.60 and 0.55 for the other 2 combinations
3) Reliability of RBV for MR traits = 0.30, and for SCS = 0.50 (conservative estimates)
4) Selection only on Mastitis Resistance (with various combinations/emphasis of traits)

An index for Mastitis Resistance with equal weights (of 1/3) on CM-F, CM-L and SCS provided a reasonable genetic progress for both CM traits and SCS and it will be officially published in Canada. It also allows newly proven bulls for production to have an official index, as the emphasis on CM-F is large enough to reach the publishable reliability threshold.

Correlations among sire evaluations for each of clinical mastitis evaluation (CM-F and CM-L), SCS and the Mastitis Resistance index are shown in Table 2 based on sires with at least 45% reliability for either CM-F or CM-L. The Mastitis Resistance index was highly correlated with the evaluations for each of the individual traits.

Genetic Trends

As shown previously by Miglior *et al*. (2012), genetic trends for SCS improved markedly since 2004, becoming favorable instead of unfavorable (Figure 1). Also, the genetic trend for CM-F and CM-L (Figure 1) was favorable over the last years due to indirect selection for lower SCS.

Implementation

Official Mastitis Resistance evaluations for the Holstein, Ayrshire and Jersey breeds will be officially published in August 2014. For now, official genomic evaluations will be only computed for the Holstein breed, as there are not enough reference bulls for Ayrshire and Jersey. The minimum criteria for receiving an official proof for Mastitis Resistance are applied to the evaluation for Clinical Mastitis in first lactation: at least 20 daughters in 10 herds and reliability ≥ 45 (Holstein) and ≥ 35 (Ayrshire and Jersey).

Use of BHBA for Evaluation of Health Traits

Introduction

Hyperketonemia or ketosis is one of the most frequent diseases in dairy cattle and the level of milk ß-hydroxybutyrate (**BHBA**) is an indicator of subclinical ketosis. Since October 2011 screening for hyperketonemia based on BHBA analysis by mid infrared spectrometry of test-day milk samples is offered in Canada by Valacta (Sainte-Anne-de-Bellevue, QC, Canada), the Canadian DHI organization responsible for Québec and Atlantic provinces. The objectives of this study were to estimate genetic parameters for milk BHBA and to determine their relationship with clinical ketosis and displaced abomasum.

Materials and Methods

Data set 1. A total of 466,330 test-day records for milk BHBA recorded between 5 and 100 DIM from October 2011 to November 2012 was obtained from Valacta. 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). Only first lactation Holstein cows with an age between 19 and 43 months were considered. A summary of statistics of the analyzed data set is given in Table 3. An animal pedigree file was generated by tracing the pedigrees of cows with records 7 generations back and contained 300,812 animals.

Data set 2. For the subsequent analysis, health data were obtained from the Canadian Dairy Network (Guelph, Ontario). Clinical ketosis and displaced abomasum were recorded by producers on a voluntary basis. A minimum disease frequency (reported cases per herd and year) of 1% was applied for both diseases to ensure continuous data recording within individual herds. Both diseases were defined as binary traits (0 = healthy, 1 = sick) based on whether or not the cow had at least 1 case of the respective disease recorded within the first 100 d after calving. Milk BHBA data from data set 1 were merged with health data. Table 4 gives an overview of analyzed traits in data set 2.

Models. Data were analyzed with linear animal models using the AI-REML procedure in DMU (Madsen and Jensen, 2008).

Genetic Parameters for Milk BHBA. Univariate and bivariate linear animal models were applied to milk BHBA at 5-20 DIM, 21-40 DIM, 41-60 DIM, 61-80 DIM and 81-100 DIM using data set 1. In matrix notation, the model was as follows:

$$\mathbf{y} = \mathbf{X\beta} + \mathbf{Z_h h} + \mathbf{Z_a a} + \mathbf{e}, \qquad [1]$$

where **y** is a vector of observations; **β** is a vector of systematic effects, including fixed effects of age at calving, season of calving and DIM; **h** is a vector of random herd of calving effects; **a** is a vector of random animal additive genetic effects; **e** is a vector of random residuals; and **X**, $\mathbf{Z_h}$, and $\mathbf{Z_a}$ are the corresponding incidence matrices. Age at first calving had 16 classes, in which <22 and >35 months were the first and last classes, respectively, and other classes were single months. Seasons were formed by combining three consecutive months (January-March, April-June, July-September and October-December). DIM was defined in classes, with each day representing a single class.

Associations Between Milk BHBA and Metabolic Diseases. A 3-variate linear animal model was fitted for milk BHBA at the first test-day (5-40 DIM), clinical ketosis and displaced abomasum using data set 2. For milk BHBA model [1] was used, whereas the model for the metabolic diseases was as follows:

$$\mathbf{y} = \mathbf{X\beta} + \mathbf{Z_h h} + \mathbf{Z_a a} + \mathbf{e}, \qquad [2]$$

where **y** is a vector of observations; **β** is a vector of systematic effects, including fixed effects of age at calving and season of calving; **h** is a vector of random herd of calving effects; **a** is a vector of random animal additive genetic effects; **e** is a vector of random residuals; and **X**, $\mathbf{Z_h}$, and $\mathbf{Z_a}$ are the corresponding incidence matrices. Herd of calving effects and residuals were assumed to be correlated among traits. Classes for age at first calving and season of calving were formed in the same way as for the model [1].

Results and Discussion

Genetic Parameters for Milk BHBA. Heritability estimates for milk BHBA increased with DIM, from 0.13 to 0.29 (Table 5). In agreement with our results, van der Drift *et al*. (2012) found a heritability of 0.16 for milk BHBA in dairy cows between 5 and 60 DIM.

The genetic correlations between milk BHBA were higher between adjacent DIM intervals and decreased as intervals were further apart (Table 5).

Milk BHBA and Metabolic Diseases. Phenotypic associations of milk BHBA at the first test-day with metabolic diseases are shown in Figure 2. The frequency of clinical ketosis was the highest among cows tested

positive for hyperketonemia (10.8%), followed by cows classified as suspect (5.4%) and negative (2.3%). There was also a slightly higher frequency of displaced abomasum among positive tested cows compared to negative tested cows (4% versus 2.5%).

Estimates of heritability and genetic and phenotypic correlations for all traits are given in Table 6. Heritability for milk BHBA at the first test-day was 0.13. Heritability estimates for clinical ketosis and displaced abomasum were 0.03 and 0.05, respectively, and in agreement with previous studies in Canadian Holsteins (Neuenschwander *et al*. 2012; Koeck *et al*., 2012).

Milk BHBA was moderately genetically correlated with clinical ketosis (0.50), whereas the genetic correlation with displaced abomasum was lower (0.21). The genetic correlation estimates had large standard errors and were not statistically significant.

Metabolic diseases were highly genetically correlated (0.63). Although the estimate was not statistically significant, a similar result was obtained by Neuenschwander *et al*. (2012).

Conclusions

- Routine genetic evaluation for mastitis resistance will be officially implemented in August 2014.
- An index for Mastitis Resistance was developed that includes both the clinical mastitis traits (CM-F and CM-L) and the official SCS evaluation.
- Milk BHBA in early first lactation is a heritable trait, with heritability estimates ranging from 0.13 to 0.29 across DIM.
- Estimation of genetic correlations as more data accumulates in the future is warranted to confirm the correlations found between milk BHBA and metabolic disease traits in Canadian Holsteins.
- Milk BHBA can be routinely analyzed in milk samples on test-days, and, therefore, provide a potential tool for breeding cows with a lower susceptibility to hyperketonemia

Acknowledgements

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Table 1. Response to selection per year for various combinations of Mastitis Resistance index.

Weights			**Genetic gain per year (RBV points)**		
CM-F[1]	**CM-L[2]**	**SCS**	**CM-F**	**CM-L**	**SCS**
1/3	1/3	1/3	0.14	0.19	0.44
0.5	0.5	0	0.13	0.18	0.24
0	0	1	0.13	0.17	0.63
1	0	0	0.15	0.12	0.21
0	1	0	0.11	0.23	0.25
1/6	3/6	2/6	0.13	0.20	0.44
0.5	0	0.5	0.15	0.16	0.50

[1]Clinical mastitis in first lactation (CM-F)
[2]Clinical mastitis in later lactations (CM-L)

Table 2. Correlations among genetic evaluations related to mastitis based on Holstein sires with a minimum reliability of 45% for either clinical mastitis in first lactation (CM-F) or clinical mastitis in later lactations (CM-L).

Trait	**CM-F**	**CM-L**	**SCS**
MR[1]	0.87	0.92	-0.79
CM-F		0.74	-0.48
CM-L			-0.62

[1]MR = 1/3 CM-F + 1/3 CM-L + 1/3 SCS

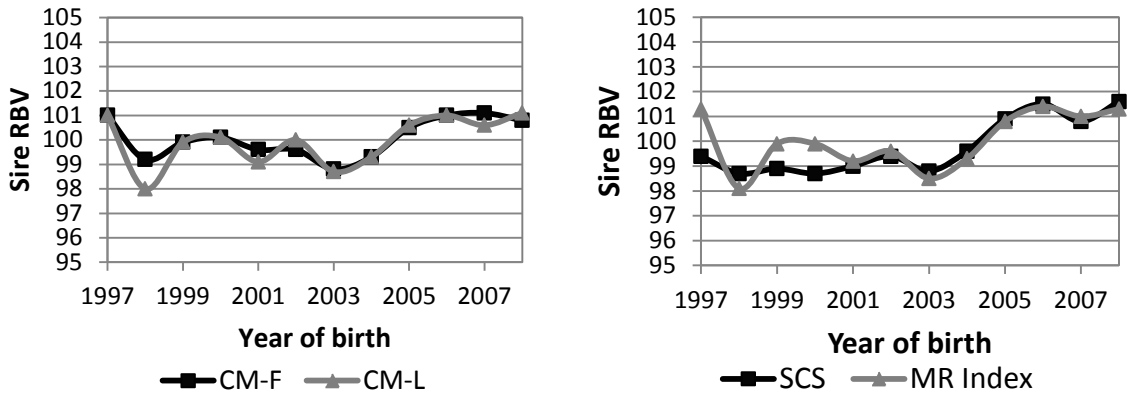

Figure 1. Genetic trend for clinical mastitis in first (CM-F) and later lactations (CM-L) and SCS and Mastitis Resistance Index (MR Index).

Table 3. Summary statistics for milk BHBA at different DIM.

Trait	DIM	Records, no.	Mean	SD
$BHBA_1$, mmol/L	5-20	20,845	0.115	0.085
$BHBA_2$, mmol/L	21-40	26,871	0.094	0.079
$BHBA_3$, mmol/L	41-60	27,404	0.075	0.055
$BHBA_4$, mmol/L	61-80	27,233	0.068	0.045
$BHBA_5$, mmol/L	81-100	26,811	0.067	0.041

Table 4. Summary statistics for milk BHBA at the first test-day (5-40 DIM), clinical ketosis (KET) and displaced abomasum (DA).

Trait	Records, no.	Mean	SD
BHBA, mmol/L	43,714	0.104	0.083
KET frequency, %	3,437	3.608	-
DA frequency, %	6,894	2.742	-

Table 5. Heritabilities (on the diagonal) and genetic correlations (above the diagonal) with standard errors (SE) in parentheses for milk BHBA at 1) 5-20 DIM, 2) 21-40 DIM, 3) 41-60 DIM, 4) 61-80 DIM and 5) 81-100 DIM.

Trait	$BHBA_1$	$BHBA_2$	$BHBA_3$	$BHBA_4$	$BHBA_5$
$BHBA_1$	0.13 (0.02)	0.96 (0.02)	0.84 (0.04)	0.75 (0.05)	0.67 (0.06)
$BHBA_2$		0.13 (0.01)	0.99 (0.01)	0.85 (0.04)	0.77 (0.05)
$BHBA_3$			0.16 (0.02)	0.98 (0.01)	0.96 (0.02)
$BHBA_4$				0.22 (0.02)	0.99 (0.01)
$BHBA_5$					0.29 (0.02)

Table 6. Heritabilities (on the diagonal) and genetic correlations (above the diagonal) with standard errors (SE) in parentheses for milk BHBA at the first test-day (5-40 DIM), clinical ketosis (KET) and displaced abomasum (DA).

Trait	BHBA	KET	DA
BHBA	0.13 (0.01)	0.50 (0.26)	0.21 (0.16)
KET		0.03 (0.03)	0.63 (0.43)
DA			0.05 (0.02)

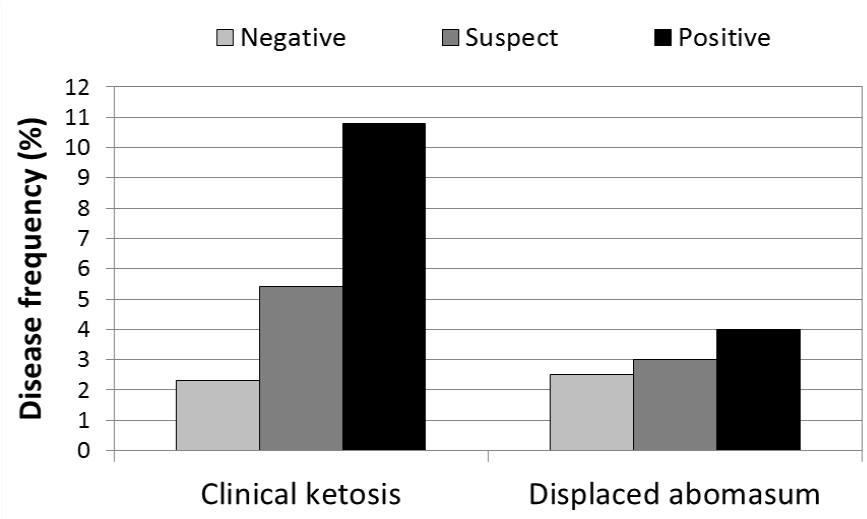

Figure 2. Frequency of clinical ketosis and displaced abomasum of first lactation cows with a negative (milk BHBA < 0.15 mmol/L), suspect (0.15 ≤ milk BHBA < 0.20 mmol/L) or positive (milk BHBA ≥ 0.20 mmol/L) test result for hyperketonemia at the first test-day (5-40 DIM).