Genetic and Genomic Evaluation of Mastitis Resistance in Canada

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Abstract

A nation-wide health recording system for dairy cattle was started in Canada in 2007. Eight diseases are recorded by producers on a voluntary basis, including mastitis, displaced abomasum, ketosis, milk fever, retained placenta, metritis, cystic ovaries and lameness. Mastitis is the most frequent and most recorded disease, which highlights the economic importance of this trait. A routine genetic evaluation system for mastitis resistance will be officially implemented in December 2013 for Holstein, Ayrshire and Jersey breeds. The model for estimation of breeding values for mastitis resistance is a multiple-trait linear animal model including mastitis, mean SCS in early lactation, standard deviation of SCS, excessive test-day SCC, fore udder attachment, udder depth and body condition score. EBVs for mastitis resistance are published as relative breeding values with a mean of 100 and a standard deviation of 5, where higher values are desirable.

Key words: mastitis resistance, genetic parameters, genetic evaluation

Introduction

In Canada, a national dairy cattle health and disease data management system was started in 2007. Eight diseases that are known to affect herd profitability are recorded by producers on a voluntary basis, namely mastitis, displaced abomasum, ketosis, milk fever, retained placenta, metritis, cystic ovaries and lameness. Producers were provided with disease definitions, adapted from work by Kelton *et al.* (1998), as a guide for identification and recording of the diseases. Health data is recorded by producers using on-farm herd management software or record books. Data are collected by milk recording technicians at each test day herd visit and forwarded to the DHI association for the region (CanWest DHI for Western Canada and Ontario; Valacta for Atlantic Canada and Quebec). Additionally, health data from Quebec producers participating in the "Dossier Santé Animale/Animal Health Record" (DS@HR) program is collected and forwarded to the DHI database by their veterinarians. All data are stored in the national database at Canadian Dairy Network (CDN). Currently, about 40% of all herds enrolled on milk recording participate in the health recording system (Koeck *et al.*, 2012b).

The feasibility of using producer recorded health data for genetic evaluation of disease resistance in Canada has been shown previously (Neuenschwander *et al.*, 2012; Koeck *et al.*, 2012b).

Of the eight targeted diseases, mastitis is the most frequent and most recorded in Canada on a voluntary basis (Koeck *et al.*, 2012b), which reflects the high economic importance of this trait. The focus of this paper is the implementation of a routine genetic evaluation system for mastitis resistance in Canada.

Materials and Methods

Data

Mastitis records from April 2007 to May 2013 were obtained from Canadian Dairy Network (CDN). In order to ensure that all cows were from herds with reliable mastitis recording, only herds with a minimum mastitis frequency of 5% per year were considered for estimation of variance components. Holstein is the most common dairy cattle breed in Canada (constituting over 90% of the dairy population) and, therefore, almost all mastitis records were from Holsteins. For this reason, variance

component estimation was carried out for this breed only. Only records from first to fifth lactation cows were considered.

An animal pedigree file was generated by tracing the pedigrees of cows with data seven generations back.

Definition of traits

A detailed analysis of mastitis and its predictors is given by Koeck *et al.* (2012a,c) and Loker *et al.* (2012). Based on this research, the new genetic evaluation system for mastitis resistance includes the following traits (11 traits in total):

Mastitis and SCS indicator traits from first and second and later lactations:

- Mastitis (**MAST**)
  Scored as 0 (no case) or 1 (at least one case) in the period from calving to 150 d after calving.
- Mean somatic cell score in early lactation (**SCS_{150}**)
  Mean of monthly test-day SCS from 5 to 150 DIM.
- Standard deviation of somatic cell score (**SCS_{SD}**)
  Standard deviation of monthly test-day SCS from 5 to 150 DIM.
- Excessive test-day somatic cell count (**$SCS_{>500}$**)
  Scored as 0 or 1 based on whether or not the cow had at least one SCC test-day higher than 500,000 cells/mL within the first 150 DIM.

First and later lactation mastitis and SCS traits are treated as different but correlated traits.

Type traits from first lactation cows (from first classifications within 365 DIM):

- Fore udder attachment (**FUA**), linear trait 1 to 9
- Udder depth (**UD**), measured trait
- Body condition score (**BCS**), measured trait

Two data sets were created. The first data set includes only SCS and type trait records from cows with records for mastitis resistance (**reduced data set**). The second data set includes all data available for SCS and type traits (**full data set**). Summary statistics of the data used are given in Table 1.

Genetic evaluation model

The model for estimation of breeding values for mastitis resistance is a multiple-trait linear animal model. Single-trait models are the same for MAST, SCS_{150}, SCS_{SD} and $SCS_{>500}$ in the first lactation, and for UD, FUA and BCS. Models for mastitis and SCS traits in later lactations are the same as for the first lactation data; the permanent environmental effect (**PE**) was included for later lactation traits to account for repeated observations on a cow. Example models for MAST in later lactations and UD, in a simplified scalar notation can be presented as:

MAST = H + YS + ASP + HY + A + PE + E

UD = HRC + AST + A + E,

where the fixed effects were:

H: herd, YS: year-season, ASP: age-season-parity, HRC: herd-round-classifier, AST: age-stage-time of classification,

and the random effects were:

HY: herd-year, A: animal additive genetic, PE: permanent environmental, E: residual.

In matrix notation, the model can be written as

$$\mathbf{y} = \mathbf{X}\,\mathbf{b} + \mathbf{Z}_1\,\mathbf{h} + \mathbf{Z}_2\,\mathbf{a} + \mathbf{Z}_3\,\mathbf{p} + \mathbf{e}$$

where **y** is a vector of observations (traits within parities within cows), **b** is a vector of all fixed effects, **h** is a vector of HY effects, **a** is a vector of animal additive genetic effects (A), **p** is a vector of PE effects, **e** is a vector of residuals, **X** and $\mathbf{Z}_i$ (i =1,.., 3) are respective incidence matrices.

Model assumptions were that

$[\mathbf{h}' \ \mathbf{a}' \ \mathbf{p}' \ \mathbf{e}']' \sim N[\mathbf{0}, \mathbf{V}]$ with $\mathbf{V} = \sum_{i=1}^{4} + \mathbf{V}_i$,

where

$\mathbf{V}_1 = \mathbf{I} \otimes \mathbf{H}$, **I** is an identity matrix, **H** is a covariance (8x8) matrix for HY effects;
$\mathbf{V}_2 = \mathbf{A} \otimes \mathbf{G}$, **A** is an additive relationship matrix, **G** is a genetic covariance (11x11) matrix;
$\mathbf{V}_3 = \mathbf{I} \otimes \mathbf{P}$, **P** is a covariance (4x4) matrix for PE effect;
$\mathbf{V}_4 = \sum_{i=1}^{N} + \mathbf{E}_i$, $\mathbf{E}_i$ is a residual covariance matrix (of order up to 7x7, depending on how many traits were missing) for either first or later lactations, N is the total number of records. Residuals for mastitis and SCS indicator traits were assumed correlated within each lactation and uncorrelated across lactations. Similarly, non-zero residual correlations were allowed for all conformation traits. All other residual correlations were equal to 0. Also, residual co-variances between type and health traits were set to zero because the traits of the two data sets were recorded from two separate systems, and any residuals were assumed to be independent.

Relative Breeding Values

Estimated breeding values were standardized to relative breeding values (**RBV**) with a mean of 100 and a standard deviation of 5 and reversed in sign. Thus, higher RBVs indicate sires with daughters more resistant to mastitis.

Reliabilities of sire RBVs for mastitis resistance were calculated based on effective daughter contribution (EDC). The EDC software of Sullivan (2010) was used.

Genomic Evaluation Method

GBLUP methodology as used officially by CDN for all traits (Van Doormaal *et al.*, 2009) was applied to estimate genomic evaluations for mastitis resistance. Progeny proven sires reaching the minimum requirements for publication of an official RBV for mastitis resistance were used as the reference population for estimation of SNP effects. Direct Genomic Values (DGV) were blended with RBV (or Parent Average), weighted by the relative Reliability of each value, to produce published genomic RBV for bulls.

Results and Discussion

The frequency of mastitis increased with parity and was 8.9 and 14.9% in first and later lactation cows, respectively.

Genetic parameters

Estimates of heritability for MAST were 0.03 and 0.05 for first and later lactations, respectively (Table 2). Heritability for SCS traits ranged from 0.02 (SD of SCS) to 0.17 (average SCS). Conformation traits were moderately heritable, from 0.26 (BCS) to 0.50 (UD). Mastitis in first lactation was a different trait that mastitis in older cows (genetic correlation = 0.59) and had relatively high genetic correlations with SCS traits (from 0.51 to 0.71, and from 0.60 to 0.78 for first and later lactations, respectively). Genetic correlations between MAST and conformation based indicator traits were moderate and stronger for first lactation (from -0.34 for BSC to -0.52 for UD) compared with later parities (from -0.09 for FUA to -0.27 for UD).

Genetic evaluations

The current data available for genetic evaluation yielded roughly 750 and 1,410 sires that have at least 30 daughters with information for mastitis resistance in first lactation and later lactations, respectively. However, the number of younger progeny proven bulls with an RBV for mastitis resistance is relatively small (Figure 1).

RBVs of sires with at least 30 daughters are presented in Figure 2. Despite the low heritability of mastitis, large differences between daughter groups were observed. The percentage of diseased daughters varied between 3% and 21% among the 10 sires with the best and worst RBV for mastitis resistance in first lactation cows. In higher lactation cows, the percentage of diseased daughters

varied between 9% and 28% among the 10 sires with the best and worst RBV.

The use of historical data for SCS and type traits increased the reliability of sire RBVs for mastitis resistance slightly, especially for sires with a low number of daughters (Figure 3).

Relationships with other traits

Correlations of sire RBV for mastitis resistance with other routinely evaluated traits are shown in Table 3. Routinely evaluated traits in Canada, with the exception of SCS, are scored to have a higher breeding value being favorable. Higher milk yield was genetically linked with more mastitis cases. Desirable, positive associations were found between mastitis resistance with both fertility and longevity. This means that selection for mastitis resistance would inevitably lead to selection for cattle with improved fertility and longer herd life.

Conclusions

- Routine genetic evaluation for mastitis resistance will be officially implemented in December 2013 for Holstein, Ayrshire and Jersey breeds.
- Due to insufficient mastitis data for breeds other than Holstein, genetic parameters estimated for Holstein will be used for the other breeds.

Acknowledgements

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Table 1. Descriptive statistics of data used.

Trait[1]		Reduced data set		Full data set	
		Number of records	**Mean**	**Number of records**	**Mean**
First Lactation	**MAST, %**	174,142	8.92	174,142	8.92
	SCS150	162,400	2.15	3,408,360	2.07
	SCSSD	162,400	0.99	3,408,360	1.00
	TD>500, %	162,400	15.17	3,408,360	14.94
Later Lactations	**MAST, %**	314,253	14.91	314,253	14.91
	SCS150	290,491	2.37	5,539,425	2.38
	SCSSD	290,491	1.12	5,539,425	1.13
	TD>500, %	290,491	24.65	5,539,425	24.71
Conformation	**UD**	151,964	10.45	2,509,631	10.57
	FUA	151,964	5.02	2,509,631	5.09
	BCS	151,964	2.81	1,016,945	2.79

[1] MAST = Mastitis, SCS150 = Mean somatic cell score in early lactation (<150), SCSSD = Standard deviation of somatic cell score, TD>500 = Excessive test-day somatic cell count, UD = Udder Depth, FUA = Fore Udder Attachment, BCS = Body Condition Score.

Table 2. Heritabilities (in bold on the diagonal) and genetic correlations (above diagonal) for mastitis and its indicators.[1,2]

Lactation/Trait		First lactation				Later lactations				Conformation		
		MAST	SCS150	SCSSD	TD>500	MAST	SCS150	SCSSD	TD>500	UD	FUA	BCS
First Lactation	MAST	**0.03**	0.55	0.51	0.72	0.59	0.54	0.50	0.59	-0.52	-0.46	-0.34
	SCS150		**0.13**	0.15	0.78	0.55	0.76	0.45	0.69	-0.32	-0.27	-0.29
	SCSSD			**0.02**	0.52	0.45	0.29	0.60	0.43	-0.44	-0.23	-0.15
	TD>500				**0.04**	0.65	0.74	0.63	0.76	-0.50	-0.36	-0.32
Later Lactations	MAST					**0.05**	0.74	0.69	0.78	-0.27	-0.09	-0.23
	SCS150						**0.17**	0.64	0.91	-0.26	-0.08	-0.27
	SCSSD							**0.03**	0.74	-0.30	-0.06	-0.12
	TD>500								**0.09**	-0.28	-0.11	-0.31
Conformation	UD									**0.50**	0.71	0.10
	FUA										**0.33**	0.22
	BCS											**0.16**

[1] MAST = Mastitis, SCS150 = Mean somatic cell score in early lactation (<150), SCSSD = Standard deviation of somatic cell score, TD>500 = Excessive test-day somatic cell count, UD = Udder Depth, FUA = Fore Udder Attachment, BCS = Body Condition Score.
[2] Based on research by Jamrozik *et al.* (2013).

Table 3. Pearson correlations between RBVs of sires with at least 30 daughters for mastitis resistance in first ($MAST_1$) and later lactations ($MAST_{2+}$) (n=number of sires).

Trait	Reduced data set		Full data set	
	$MAST_1$ (n=750)	**$MAST_{2+}$ (n=1,410)**	**$MAST_1$ (n=750)**	**$MAST_{2+}$ (n=1,410)**
LPI	0.12**	0.17***	0.11**	0.16***
Milk Yield	-0.11**	-0.07*	-0.15***	-0.15***
Protein Yield	-0.13***	-0.06*	-0.17***	-0.14***
Fat Yield	-0.03	0.06*	-0.08*	0.01
Herd Life	0.38***	0.35***	0.44***	0.47***
Direct Herd Life	0.32***	0.30***	0.39***	0.41***
Somatic Cell Score	-0.57***	-0.63***	-0.63***	-0.79***
Calving to First Service	0.20***	0.14***	0.24***	0.18***
56-d Non-Return Rate (cows)	0.13***	0.10***	0.10**	0.13***
Number of Services (cows)	0.13***	0.10***	0.13***	0.13***
First Service to Conception (cows)	0.16***	0.11***	0.16***	0.15***
Days Open	0.21***	0.14***	0.23***	0.19***
Conformation (Overall)	0.13***	0.09**	0.20***	0.12***
Mammary System	0.23***	0.14***	0.29***	0.15***
Feet and Legs	0.06	0.08**	0.08*	0.09**
Angularity	-0.24***	-0.11***	-0.22***	-0.17***

[1] Significant effects: *P<0.05, **P<0.01, ***P<0.001.

Figure 1. Year of birth of bulls with at least 30 daughters for mastitis resistance in first ($MAST_1$) and later lactations ($MAST_{2+}$) (n=number of sires).

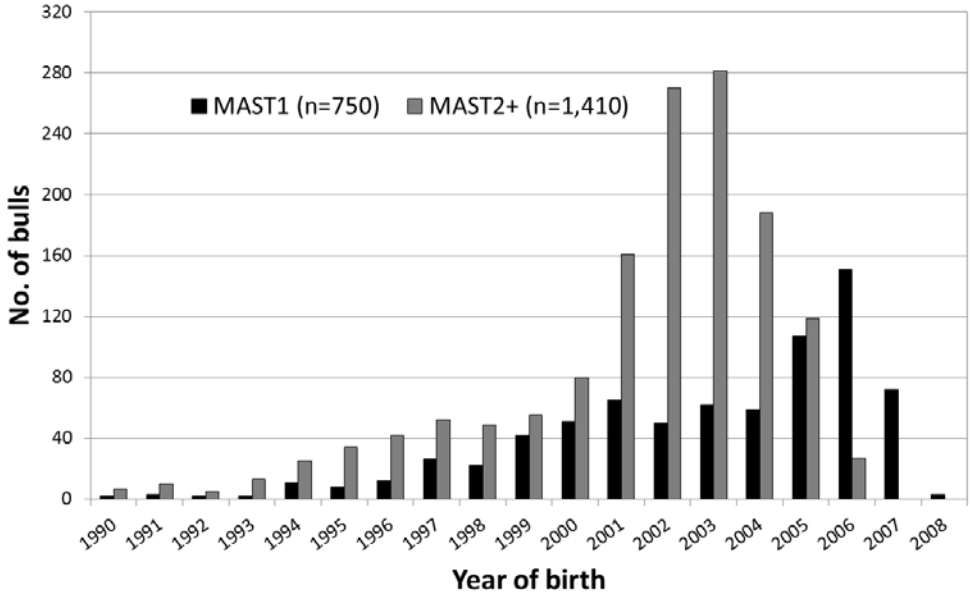
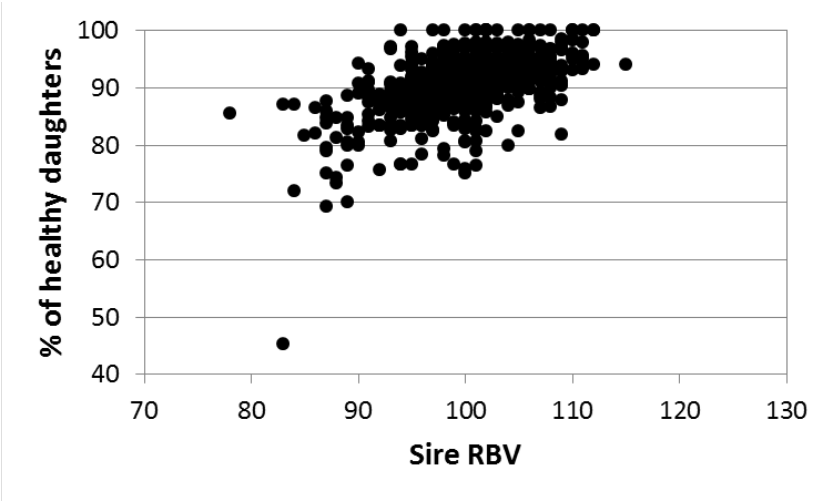


Figure 2. Percentage of healthy daughters according to the relative breeding value (RBV) for mastitis resistance for sires with at least 30 daughters for mastitis resistance in first (a) and later lactations (b) based on the full data set.

a)



b)

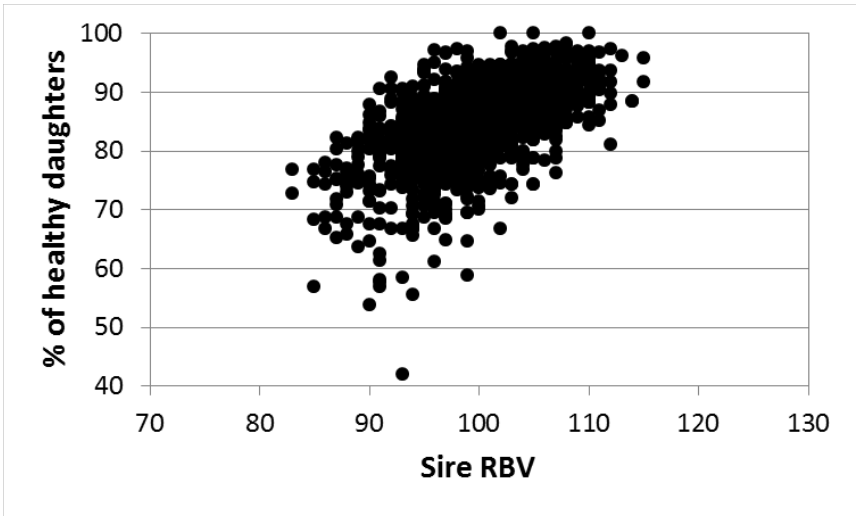
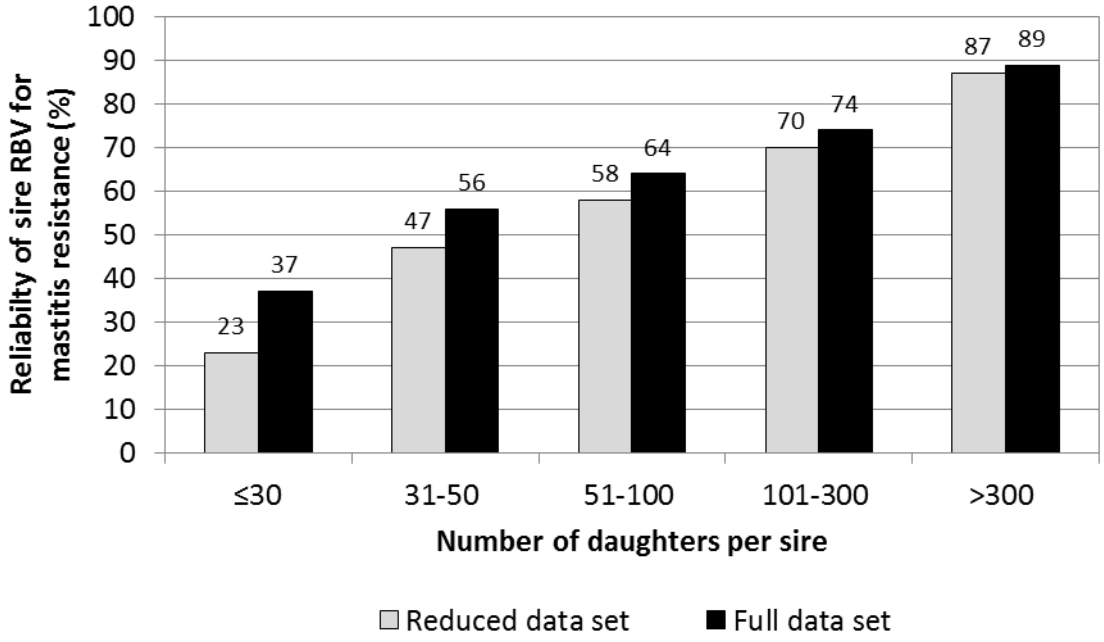


Figure 3. Reliability of sire RBVs for mastitis resistance in first ($MAST_1$) and later lactations ($MAST_{2+}$) .

a) Reliability of sire RBV for mastitis resistance in first lactation cows



b) Reliability of sire RBV for mastitis resistance in later lactation cows