Development of a genetic evaluation for mastitis resistance for Canadian dairy cattle

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Abstract

This study is part of a larger project whose overall objective is to develop genetic evaluations for resistance to mastitis and other diseases in Canada. Health data recorded by producers were available from the National Dairy Cattle Health System. Eight diseases are recorded by producers on a voluntary basis: mastitis, displaced abomasum, ketosis, milk fever, retained placenta, metritis, cystic ovaries and lameness. Mastitis is the most recorded disease and with its high frequency, it is the most promising trait to be included in routine genetic evaluation. The overall objective of this study was to investigate if genetic evaluations for mastitis resistance are feasible in Canada. Records from first, second and third lactation Holstein cows were considered in this study. The overall mastitis frequency was 17.0%. Initially a univariate repeatability model was run for mastitis. Subsequently a multivariate repeatability model was run for mastitis and its predictors mean somatic cell score, standard deviation of SCS, excessive test-day somatic cell count, udder depth, fore udder attachment and body condition score. Heritability estimates for mastitis were 0.038 and 0.044 in the univariate and multivariate analyses, respectively. The application of a multivariate model increased the reliability of sire breeding values for mastitis resistance. Pearson correlations between breeding values for mastitis resistance and other routinely evaluated traits were computed, which revealed noticeable favourable relationships to direct herd life and fertility. The present study showed that genetic evaluations for mastitis resistance based on producer-recorded health data are feasible in Canada. Future work is necessary to increase participation and data quality in the Canadian health recording system.

Keywords: mastitis, genetic evaluation, Canadian Holsteins

Introduction

Health traits are of increasing importance to dairy producers. In the Scandinavian countries, direct selection for improved disease resistance has been carried out for more than 30 years (Philipsson and Lindhé, 2003). In these countries, veterinary treatments are recorded, as all treatments involving antibiotics and hormones have to be made primarily by a veterinarian. As veterinarians have extensive knowledge in disease diagnoses, a large number of different health disorders are recorded, e.g. the Norwegian disease code includes 67

different diagnoses (Østerås et al., 2007). Recently, a similar disease recording system has been established in Austria (Egger-Danner et al., 2010).

In Canada, a national dairy cattle health and disease data management system was started in 2007. The main objectives of this initiative are to provide information to dairy producers and their veterinarians for herd management and to establish a national genetic evaluation system for genetic selection for disease resistance. In contrast to the Scandinavian and Austrian approaches, the Canadian recording is done by producers. Eight diseases that are known to affect herd profitability are recorded by producers on a voluntary basis: 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 Ontario and Western Canada; Valacta for Quebec and Atlantic Canada). Additionally, health data from 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 the Canadian Dairy Network (Guelph, Ontario).

The feasibility of using producer recorded health data for genetic evaluations for disease resistance in Canada has been shown previously by Neuenschwander et al. (2011) and Koeck et al. (2012b). In this study the first results of a routine genetic evaluation for mastitis resistance in Canadian Holsteins are presented.

Material and Methods

Data

Health database

Health data from April 2007 to December 2011 were obtained from the Canadian Dairy Network (Guelph, Ontario). Summary of current data in the database is given in Table 1. The database consisted of 475,939 health events from 221,550 cows, of which 95.5% were from Holstein, 2.3% from Ayrshire and 1.8% from Jersey. A total of 6,024 herds were represented. Recording of mastitis was done in the majority of herds (87%), followed by displaced abomasum (65%) and retained placenta (60%). Only 17% of herds had records for all eight health categories.

The number of reported disease cases per year and month has shown a continuous increase from 2007 to 2010 and stabilized in the year 2011 (Figure 1). In contrast, the total number of herds recording health data remained almost unchanged in the last 4 years (Figure 2). In 2011, 4,033 herds recorded health data, which accounts for 42% of all herds under milk recording.

Table 1. Summary statistics of the health traits database.

Health category	Health event	% of disease cases	% of herds
Mastitis	Mastitis	41.0	87
Displaced abomasum	Displaced abomasum	5.1	65
Ketosis	Ketosis	3.2	38
Milk fever	Milk fever	3.8	49
Retained placenta	Retained placenta	8.6	60
Metritis	Acute metritis	5.7	37
	Purulent discharge	3.9	21
	Endometritis	1.5	11
	Chronic metritis	2.6	23
Cystic ovaries	Cystic ovaries	12.2	46
Lameness	Lameness	12.0	54
	Foot rot, laminitis, sole ulcer and other claw disorders	0.4	7

Figure 1. Number of reported disease cases per year and month (dashed line represents delay in data delivery).

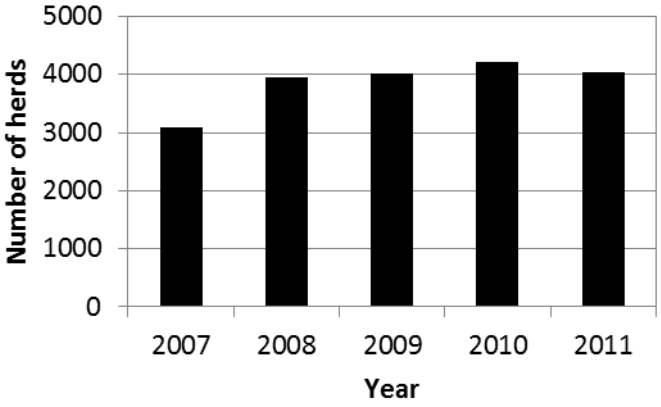

Figure 2. Number of herds recording health data per year.

Data validation and editing

In order to ensure that all cows were from herds with reliable mastitis recording, only herds having at least two recorded mastitis cases within the study period were considered. The first and last mastitis case had to be at least 180 d apart for not removing a herd from the analysis, otherwise it would be considered to have health recording for just a short period of time. In addition, a minimum mastitis frequency of 5% per herd and per year was applied to ensure continuous data recording. After all the described editing to assure reliable documentation and recording, 48% of all herds were excluded.

Holstein is the most common dairy cattle breed in Canada (constituting up to 90% of the dairy cows) and, therefore, almost all health records were from Holstein cows. For this reason, analyses were carried out for this breed only. Only records from first, second and third lactation cows were considered.

Trait definition

Mastitis was defined as a binary trait (0 = no mastitis, 1 = mastitis) based on whether or not the cow had at least one mastitis case in the period from calving to 305 d after calving. Three traits derived from SCC were considered as mastitis indicators based on a previous study in Canadian Holstein cows (Koeck et al., 2012a): mean SCS in early lactation (**SCS_{150}**), standard deviation of SCS (**SCS_{SD}**) and excessive test-day SCC (**$TD_{>500}$**). SCS_{150} was the mean of monthly test-day SCS from 5 to 150 DIM. SCS were calculated from SCC as follows: $SCS = \log_2(SCC/100{,}000) + 3$. SCS_{SD} was the standard deviation of monthly test-day SCS from 5 to 305 DIM. $TD_{>500}$ was scored as "1" or "0", based on whether or not the cow had at least one SCC test-day above 500,000 cells/mL within 305 DIM. Udder depth (**UD**), fore udder attachment (**FUA**) and body condition score (**BCS**) were routinely recorded by professional type classifiers. Only first classifications within 365 DIM were analyzed, reclassification records were not considered. For UD, FUA and BCS only information from first lactation cows was available. Summary statistics of the analyzed data is given in Table 2.

Table 2. Summary of statistics for the data set used.

Trait	Description of trait	Number of records	Mean
Mastitis, %	Cows with at least one mastitis case within 305 d after calving	210,559	17.0
SCS_{150}, $\log_2$	Mean SCS in early lactation (5 to 150 DIM)	203,789	2.2
SCS_{SD}, $\log_2$	Standard deviation of SCS during lactation	196,794	1.1
$TD_{>500}$, %	Cows with at least one SCC test-day above 500,000 cells/mL within 305 DIM	204,107	26.9
UD, cm	Udder depth Measurement from hock to floor of the udder	78,827	10.32
FUA	Fore udder attachment 1 = extremely weak to 9 = extremely strong	78,827	5.02
BCS	Body condition score 1 = very thin to 5 = very fat	78,827	2.81

Pedigree

The sire pedigree file was generated by tracing the pedigrees of sires and maternal grandsires back as far as possible. The sire pedigree file had 7,490 males, including the 6,238 sires with daughters in the dataset.

Model

Linear sire models were fitted using the AI-REML procedure in the DMU package (Madsen and Jensen, 2008). Initially a univariate sire model was run for mastitis. Subsequently a multivariate sire model was run for mastitis, SCS_{150}, SCS_{SD}, $TD_{>500}$, UD, FUA and BCS. In matrix notation, the model was:

$$\mathbf{y} = \mathbf{X\beta} + \mathbf{Z_h h} + \mathbf{Z_s s} + \mathbf{W_p p} + \mathbf{e}$$

where **y** is a vector of observations for mastitis, SCS_{150}, SCS_{SD}, $TD_{>500}$, UD, FUA and BCS; **β** is a vector of systematic effects, including fixed effects of herd-round-classifier for UD and FUA, parity for mastitis, SCS_{150}, SCS_{SD} and $TD_{>500}$, age at calving-stage of lactation for UD, FUA and BCS and year-season of calving for mastitis, SCS_{150}, SCS_{SD} and $TD>_{500}$; **h** is a vector of random herd-year of calving effects for mastitis, SCS_{150}, SCS_{SD} and $TD_{>500}$; **s** is a vector of random sire effects; **p** is a vector of permanent environmental effects for mastitis, SCS_{150}, SCS_{SD} and $TD_{>500}$; **e** is a vector of random residuals; and **X**, $\mathbf{Z_h}$, $\mathbf{Z_s}$, and $\mathbf{W_p}$ are the corresponding incidence matrices.

Age at first calving had 16 classes, in which <22 and >35 months were the first and last class, respectively, and other classes were single months. Stage of lactation was coded in approximately 30 day intervals (1 = 0 to 30 DIM, 2 = 31 to 60 DIM,…, 10 = 271- 300 DIM, and 11 = 301 to 365 DIM). Four seasons of calving were defined from January to March, April to June, July to September and October to December.

Breeding value estimation

Breeding values of sires with at least 30 daughters for mastitis were obtained from univarite and multivariate analyses as described above. 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 were calculated based on effective daughter contribution (**EDC**). The EDC software of Sullivan (2010) was used.

Pearson correlations of sire RBV for mastitis with official breeding values of other routinely evaluated traits were computed.

Results and Discussion

The overall mastitis frequency was 17.0%. The frequency increased with parity and was 12.9, 18.6 and 22.2% in first, second and third lactation cows, respectively.

Genetic parameters

Heritability estimates and genetic correlations for all traits are given in Table 3. Heritability estimates for mastitis were 0.038 and 0.044 in the univariate and multivariate analyses, respectively. Heritabilities for the mastitis predictors SCS_{150}, SCS_{SD}, $TD_{>500}$, UD, FUA and BCS were 0.11, 0.03, 0.06, 0.42, 0.21 and 0.18, respectively. Mastitis was strongly correlated with SCS_{150}, SCS_{SD} and $TD_{>500}$ with estimates of 0.78, 0.82 and 0.92, respectively. Moderate genetic correlations of -0.44, -0.31 and -0.33 were found between mastitis and UD, FUA and BCS, respectively.

Table 3. Heritabilities (on the diagonal) and genetic correlations (above the diagonal) for mastitis, mean SCS in early lactation (SCS_{150}), standard deviation of SCS (SCS_{SD}), presence of at least one SCC test-day above 500,000 cells/mL ($TD_{>500}$), udder depth (UD), fore udder attachment (FUA) and body condition score (BCS).

	Mastitis	SCS_{150}	SCS_{SD}	$TD_{>500}$	UD	FUA	BCS
Mastitis	0.04	0.78	0.82	0.92	-0.44	-0.31	-0.33
SCS_{150}		0.11	0.50	0.90	-0.35	-0.25	-0.10
SCS_{SD}			0.03	0.79	-0.39	-0.28	-0.28
$TD_{>500}$				0.06	-0.35	-0.25	-0.25
UD					0.42	0.79	0.01
FUA						0.21	0.19
BCS							0.18

Breeding values

A total of 935 sires had at least 30 daughters with information for mastitis. However, the number of young bulls with a RBV for mastitis resistance is quite small (Figure 3).

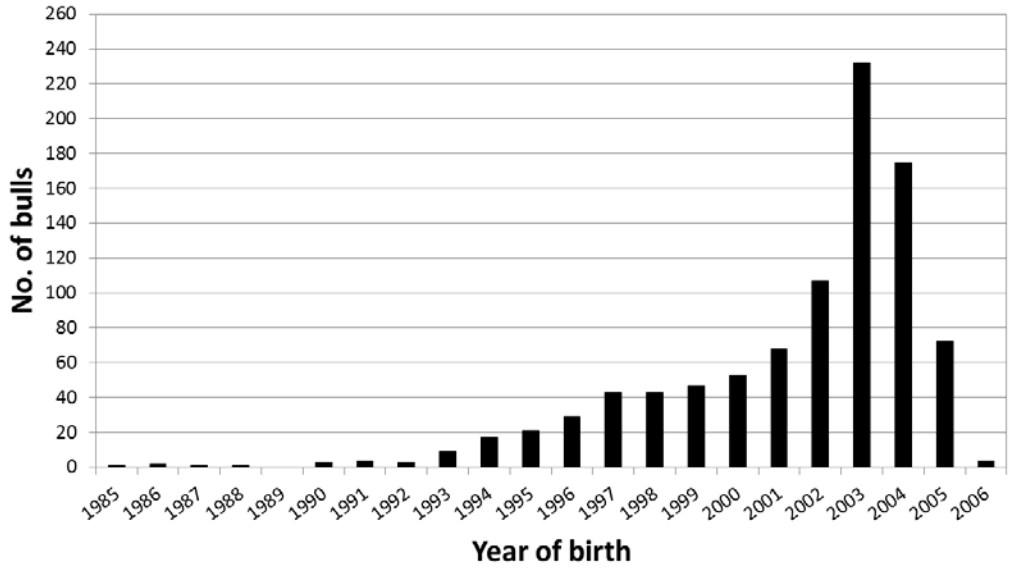

Figure 3. Year of birth of bulls with at least 30 daughters (N=935 sires).

RBVs of sires with at least 30 daughters are presented in Figure 4. Despite the low heritability of mastitis, large differences between daughter groups were observed. The percentage of diseased daughters varied between 8 and 33% among the 10 sires with the best and worst RBV for mastitis resistance. In other words, for the worst bulls, 1 out of 3

daughters had a mastitis case whereas only 1 out of 12 daughters of the best sires was affected by mastitis.

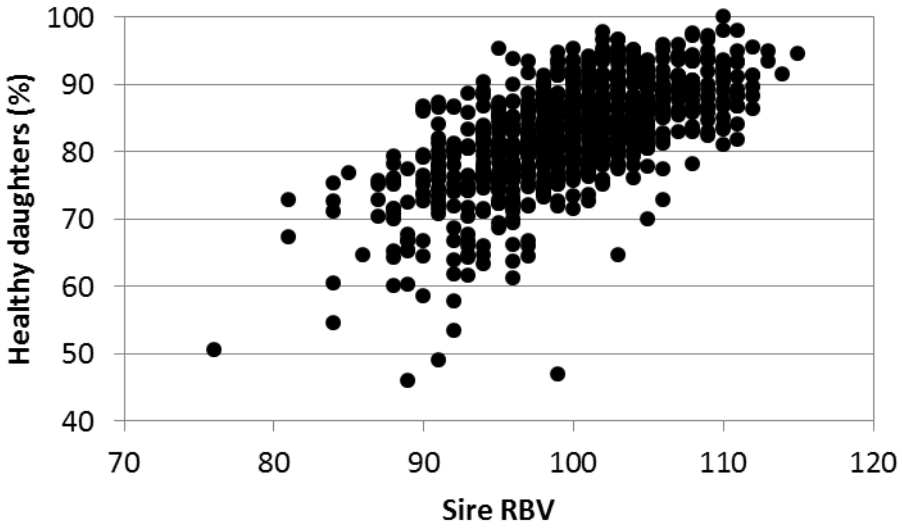

Figure 4. Percentage of healthy daughters according to the relative breeding value (RBV) of mastitis resistance of sires with at least 30 daughters (N=935 sires) from multivariate analysis.

Reliability

The application of a multivariate model increased the reliability of sire RBV for mastitis considerably (Figure 5). For a newly proven sire with 51 to 100 daughters, there was a gain of 22 points in reliability compared to a univariate model.

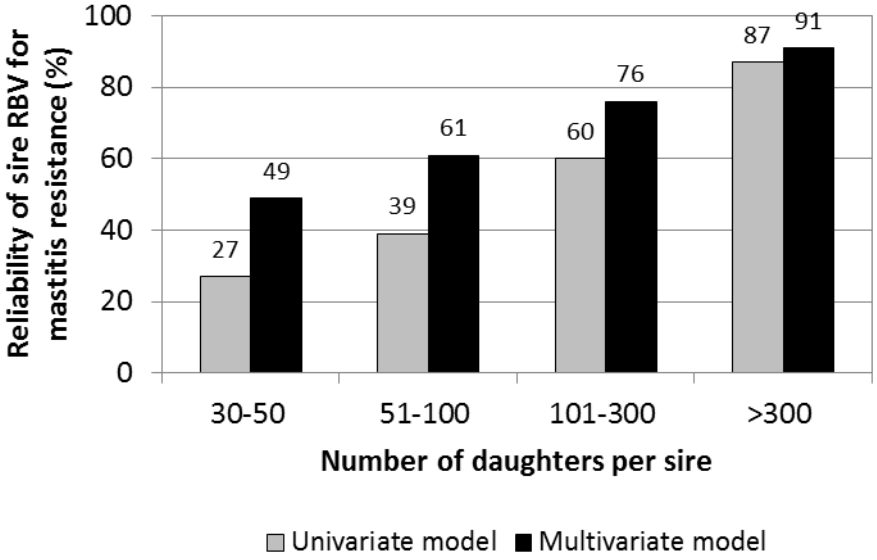

Figure 5. Reliability of sire RBV for mastitis resistance for sires with at least 30 daughters (N=935) from univariate and multivariate analyses.

Correlations with other routinely evaluated traits

Correlations of sire RBV for mastitis resistance with other routinely evaluated traits are shown in Table 4. 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. Positive associations were found between mastitis and fertility and longevity. This means that selection for mastitis resistance would inevitably lead to selection for cattle with improved fertility and longer herd life.

Table 4. Pearson correlations between RBV of sires with at least 30 daughters for mastitis resistance from multivariate analysis and other routinely evaluated traits.[1]

Trait	Mastitis resistance (N=935 sires)
LPI	0.07*
LPI – Production	-0.16***
LPI – Durability	0.26***
LPI – Health & Fertility	0.36***
Milk yield	-0.19***
Protein yield	-0.20***
Fat yield	-0.07*
Herd life	0.41***
Direct herd life	0.35***
Somatic cell score	-0.61***
Calving to first service	0.22***
56-d non-return rate (cows)	0.12***
Number of services (cows)	0.16***
First service to conception (cows)	0.19***
Days open	0.23***
Overall Conformation	0.16***
Overall Mammary System	0.17***
Overall Feet and Legs	0.10**
Angularity	-0.18***

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

Conclusions

The present study showed that genetic evaluations for mastitis resistance based on producer-recorded health data are feasible in Canada. Future work is necessary to increase participation and data quality in the Canadian health recording system.

Acknowledgments

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List of References

Egger-Danner C., W. Obritzhauser, B. Fuerst-Waltl, B. Grassauer, R. Janacek, F. Schallerl, C. Litzllachner, A. Koeck, M. Mayerhofer, M. Miesenberger, G. Schoder, F. Sturmlechner, A. Wagner, and K. Zottl. 2010. Registration of direct health traits in Austria – Experience review. Proc. ICAR 37th Annual Meeting, Riga, Latvia, 69-77.

Kelton, D. F., K. D. Lissemore, and R. E. Martin. 1998. Recommendations for recording and calculating the incidence of selected clinical diseases of dairy cattle. J. Dairy Sci. 81:2502-2509.

Koeck, A., F. Miglior, D. F. Kelton, and F. S. Schenkel. 2012a. Alternative somatic cell count traits to improve mastitis resistance in Canadian Holsteins. J. Dairy Sci. 95:432-439.

Koeck, A., F. Miglior, D. F. Kelton, and F. S. Schenkel. 2012b. Health recording in Canadian Holsteins – data and genetic parameters. J. Dairy Sci. (accepted for publication).

Madsen, P., and J. Jensen. 2008. An User's Guide to DMU. A package for analyzing multivariate mixed models. Version 6, release 4.7. Danish Institute of Agricultural Sciences, Tjele, Denmark.

Neuenschwander, T. F.-O., F. Miglior, J. Jamrozik, O. Berke, D. F. Kelton, and L. Schaeffer. 2011. Genetic parameters for producer-recorded health data in Canadian Holstein cattle. Animal (accepted for publication).

Østerås, O., H. Solbu, A. O Refsdal, T. Roalkvam, O. Filseth, and A. Minsaas. 2007. Results and evaluation of thirty years of health recordings in the Norwegian dairy cattle population. J. Dairy Sci. 90:4483-4497.

Philipsson, J., and B. Lindhé. 2003. Experiences of including reproduction and health traits in Scandinavian dairy cattle breeding programmes. Livest. Prod. Sci. 83:99-112.

Sullivan, P. 2010. Description of Usage for crEDC_5e.c. Canadian Dairy Network, Guelph, Canada.