Preliminary Results from a Genetic Analysis of Clinical Mastitis Data for Holstein cattle in Czech Republic

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Abstract

Cases of mastitis from 22 812 lactations of 10 294 cows were recorded on 7 farms in the Czech Republic from 2000 to 2012. The number of clinical mastitis (CM) cases per lactation (CM1), the number of days of CM per lactation (CM2) and CM considered as an all-or-none trait (CM3) with values of 0 (no CM case) and 1 (at least 1 CM case) were analyzed with linear animal models. Bivariate linear animal models were used for estimation of genetic correlation between CM traits and lactation mean somatic cell score (SCS) or 305-d milk yield (MY305). Factors included in the model of choice were parity, effect of herd, year of calving period, calving season, permanent environmental effect of the cow, and additive genetic effect of the cow. Estimated heritability for CM traits were in the range (0.9 – 0.10). Permanent environmental effects accounted for approximately two-third of the phenotypic variance. Heritability estimates for lactation mean SCS(305) and 305-d milk yield were 0.23 and 0.24, respectively, and genetic correlations of SCS(305) and MY305 with of CM traits were 0.22±0.062, 0.23±0.064, 0.29±0.086, 0.80±0.037, 0.79±0.040 and 0.83±0.038, respectively. Spearman rank correlations between breeding values for different CM trait definitions and SCS(305) for 139 sires with reliability of breeding value over 50% in the analyzed dataset were in the range (0.53 – 0.77). Genetic evaluation of CM cases in Czech Holsteins could be carried out including data from all parities using linear animal model. Regarding the selection character CM, our analysis showed that can be used by any of the analyzed characters. The limiting factors will likely availability of data on mastitis.

Keywords: mastitis, somatic cell score, genetic evaluation, genetic parameters, Holstein cattle

Introduction

Mastitis is the most common and costly disease in dairy cattle (Halasa *et al.*, 2007). Improved animal health is getting increasingly important worldwide. The most effective method is using of the direct measures of health or disease but they must have to be included in recording, evaluation and selection schemes. Unfortunately, experience with direct udder health data is still limited in Czech Republic. In the Czech Republic, SCS(305) has been mainly used as an indicator for the udder health. Furthermore, breeding values have been calculated for linear type traits including udder conformation since 1999. What concerns clinical mastitis (CM), registration of every CM occurrence has been obligatory on all dairy farms since 1997, but mainly due to the evidence of used pharmaceuticals. Each treatment with antibiotics and affected quarters must be recorded on farm. Resulting records are not transferred to the central database and their availability is low.

The objective of the present study was to analyze data on CM and other traits recorded on Czech dairy farms to determine their suitability for breeding value estimation for mastitis resistance.

Materials and Methods

Animal and traits definition

Data on mastitis incidence were collected from 7 Holstein herds between 2000 and 2012. The observation length on these farms is given in Table 1. The farms were not randomly chosen from the national population but rather were those willing to participate in the study. They were of different sizes and from distinct regions but used management, feeding, and housing systems commonly applied to dairy herds in the Czech Republic. On all farms, straw was used for bedding and cows were fed a balanced TMR and milked twice a day.

Records collected on farms included cow identification, data of beginning CM treatment, date of the end of CM (i.e. the last day that milk form a treated cow was discarded), and identification of a treated quarter. Detection of CM was done by farmers on the basis of visual or perceptible signs of the udder or milk. However, a detected mastitis case was recorded only if it was treated with antibiotics prescribed by veterinarian. Thus, CM was defined as a veterinary-treated udder disease. The remaining data required for genetic evaluation of CM (birth date, calving data, parity, length of lactation, culling data, cumulative milk yield for lactation, average lactation somatic cell count (SCC) etc.) together with pedigree file were made available from the national database for progeny testing. The number of cows and lactation in the analyzed dataset after data editing are shown in Table 1. Cows were daughters of 1424 sires; the number of daughter per sire was between 1 and 227, with a median of 6.

The traits of interest were the number of CM cases per lactation (CM1), the number of days of CM per lactation (CM2) and CM considered as an all-or-none trait (CM3) with values of 0 (no CM case) and 1 (at least 1 CM case). A new case of CM for the same cow was indicated when the period between the end of the previous case and the next occurrence was at least 5 d. The frequency of cows with CM as a function of the day of lactation is shown for all parity classes in Figure 1.The distribution of cows over the number of CM cases per lactation is shown in Table 2.

Further analyzed traits were the 305-d milk yield (MY305) and average lactation somatic cell count (SCC). Somatic cell count was not analyzed directly but was first transformed to somatic cell score (SCS305) according to the following formula:

$$SCS(305) = \log_2\left(\frac{SCC}{100{,}000}\right) + 3$$

Table 1. Distribution of cows and lactation over herds.

Herd	Data collection period	Average herd size[1] (cows)	Cows (n)	Lactation (n) in sum	Mastitis cases (n)
1	2000-2012	900	4 006	9 038	6 072
2	2002-2012	500	1 665	4 032	1 819
3	2000-2012	150	556	1 184	1 282
4	2004-2012	150	397	843	506
5	2000-2012	200	760	1 708	1 109
6	2000-2012	150	619	1 428	1 752
7	2000-2012	500	2 291	4 579	5 066
Total			10 294	22 812	17 606

[1] Approximate average number of cows per herd per year

Table 2. Distribution (relative frequency, %) of the number of clinical mastitis (CM) cases per lactation in the investigated dataset (n=22,812).

	Parity				
CM cases (n)	1	2	3	≥4	All
0	29.5	17.7	8.3	5.6	61.1
1	8.3	6.0	3.9	2.9	21.1
2	3.0	2.6	1.8	1.4	8.9
3	1.1	1.3	0.9	0.8	4.1
4	0.5	0.7	0.5	0.4	2.1
5	0.2	0.3	0.3	0.2	1.1
≥6	0.3	0.5	0.3	0.4	1.5

Table 3. Number of observations, means, standard deviations (SD), minima and maxima of CM traits, SCS and milk production.

Trait	Observations	Mean	SD	Min	Max
CM1[1]	8863	1.99	1.62	1	18
CM2[1]	8843	11.52	12.14	1	163
CM3	22 812	0.39	0.49	0	1
MY(305)	22 501	9 202	2 096	856	16 990
SCS(305)	15 209	3.64	1.13	0.88	6.60

[1] only lactation with CM cases

CM1 = number of CM cases per lactation; CM2 = the number of days in CM per lactation; CM3 = CM considered as an all-or-none trait with values of 0 (no CM case) and 1 (at least 1 CM case); MY(305) = 305-d milk yield; SCS(305) = average SCS;

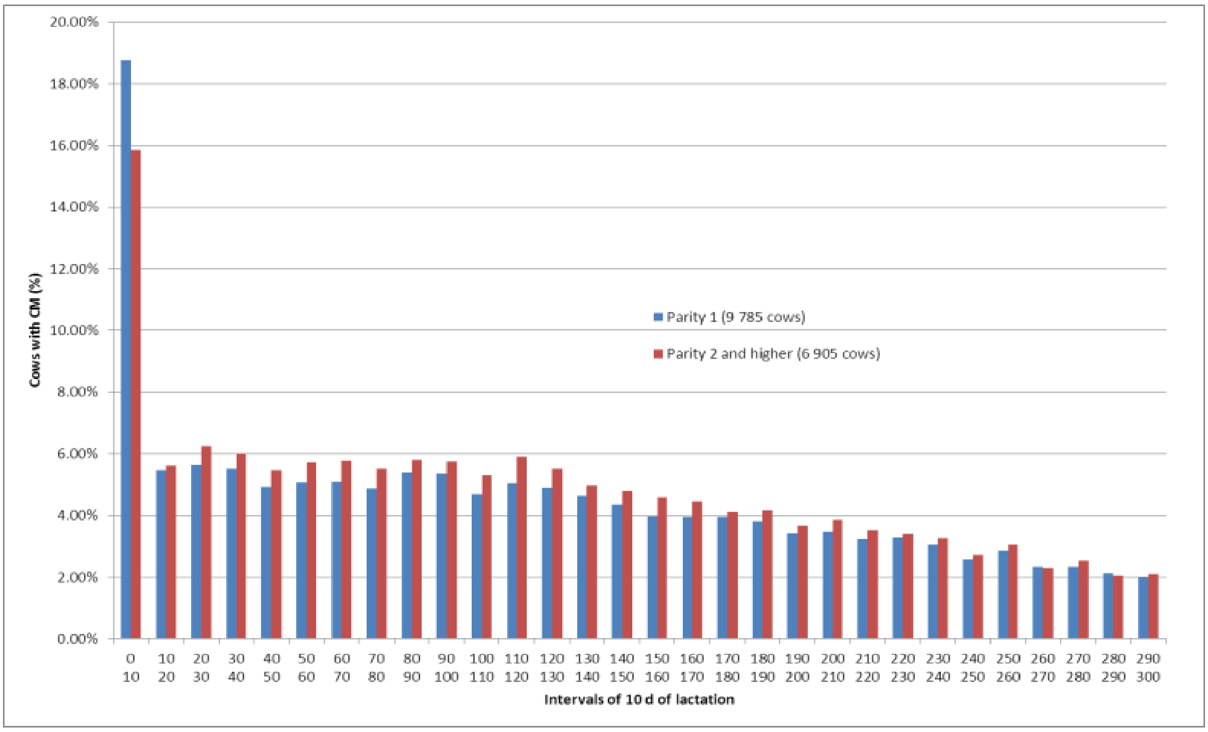

Figure 1. Frequency of cows with clinical mastitis (CM) as a function of the 10 d interval of days of lactation.

Statistical methods

The following linear traits animal model was used for the estimation of genetic parameters between the analyzed CM traits, production traits, SCS.

Model equation:

$$y_{ijklmn} = parity_i + herd_j + year_k + season_l + pe_m + a_m + e_{ijklmn},$$

where y_{ijklmn} are number of CM classes, the number of days of CM per lactation or CM considered as an all-or-none trait with values of 0 (no CM case) and 1 (at least 1 CM case); $parity_i$ is the effect of parity class *I* (4 levels); $herd_j$ is the effect of herd *j* (7 levels); $year_k$ is the effect of calving year *k* (12 levels); $season_l$ is the effect of calving season (4 levels); pe_m is the permanent environmental effect of the cow *m*; a_m is the additive genetic effect of the cow *m*; and e_{ijklmn} is the residual effect. The pedigree file contained 25 359 records. Data were analyzed using the DMU package (Madsen and Jensen, 2010).

Estimated genetic parameters were used in the prediction of breeding values for CM traits using the same equation of linear animal model as well as the same dataset. The breeding values were predicted for CM traits and SCS(305) using four univariate animal models and three bivariate animal models combining particular CM traits with SCS(305). Spearman rank correlations between breeding values for different CM trait definitions and SCS(305) for 139 sires with reliability of breeding value over 50% in the analyzed dataset.

Results

Genetic parameters

Variance components and their standard errors and estimates of genetic parameters (proportion of the total phenotypic variance and correlations) for three analyzed CM traits are shown in Table 4. For the all CM trait, the additive genetic variances were significant. The permanent environmental effect of the cow accounted for approximately two-thirds of the additive variance for CM1 and CM3 while for CM2 the permanent environmental effect of the cow accounted for three quarters of additive variance. The residual variance made up 86% of total variance for CM3 and up 83% for CM1 and CM2. The heritability was 0.10 for CM1 and CM2 and 0.09 for CM3, mastitis considered as an all-or-none trait. It is consistent with Wolf *et al.* (2010) that estimates heritability for CM in the range 0.11 to 0.13 when CM was defined as number of mastitis cases per lactation. The estimates of heritability for SCS(305) and for MY305 were 0.23 and 0.25, respectively. The estimates for lactation SCS are usually given lower than our findings (Carlen et al. 2004; Buch et al. 2011). The estimated heritability for milk production is consistent for example with Carlen *et al.* (2004).

Heritability estimates for mastitis defined as an all-or-none traits have generally been low, especially from linear model analysis, where Heringstad *et al.* (2000) reported values from 0.02 to 0.03. Defining CM as binary traits can underestimate the cow susceptibility to CM because there is no distinction among cows with 1 versus multiple CM cases. Including multiple CM cases in the evaluation and handling CM in different parities as a repeatable trait can increase variation among cows.

Estimates of correlations and their standard errors are shown in Table 5. There were high positive genetic correlations among CM traits (0.90-0.97). High genetic correlations occurred also between SCS(305) and the CM traits. They were positive in the range 0.79-0.83. The genetic correlations between milk production and CM traits showed values in the range 0.22-0.23. There were also positive correlations caused by permanent environmental effect among CM traits (0.71-0.94). The permanent environmental correlations between CM traits and SCS(305) were positive and significant (0.28-0.52) while the permanent environmental correlations between CM traits and MY(305) were partly negative (-0.05-0.15) or near to zero. Again, the highest residual correlations occurred among CM traits and between CM traits and SCS(305).

Table 4. Variance components and their standard errors (in parentheses) estimated for the number of clinical mastitis (CM) cases per lactation, the number of days of CM per lactation or CM considered as an all-or-none trait with values of 0 (no CM case) and 1 (at least 1 CM case).

	CM1[1]	CM2[1]	CM3[1]
Variance estimate			
Additive genetic	0.188 (0.020)	8.119 (0.912)	0.019 (0.002)
Permanent environment	0.131 (0.020)	6.350 (0.913)	0.012 (0.002)
Residual	1.492 (0.018)	68.235 (0.814)	0.193 (0.002)
Proportion of the total phenotypic variance			
Additive genetic	0.10	0.10	0.09
Permanent environment	0.07	0.08	0.05
Residual	0.82	0.83	0.86

[1] CM1 = number of CM cases per lactation; CM2 = the number of days in CM per lactation; CM3 = CM considered as an all-or-none trait with values of 0 (no CM case) and 1 (at least 1 CM case); MY(305) = 305-d milk yield; SCS(305) = average SCS;
The all variances are significant P<0.001

Table 5. Estimates of correlations between CM traits, SCS and milk production including their standard errors (in parenthesis).

Trait	CM1	CM2	CM3
Additive genetic correlations			
CM1		0.90 (0.016)**	0.97 (0.014)**
CM2			0.93 (0.025)**
MY(305)	0.23 (0.062) **	0.24 (0.063) **	0.29 (0.086) **
SCS(305)	0.80 (0.037)**	0.79 (0.040)**	0.83 (0.038)**
Permanent environmental correlations			
CM1		0.94 (0.021)**	0.75(0.056)**
CM2			0.71(0.062)**
MY(305)	0.02 (0.075)	-0.05 (0.073)	0.15 (0.231)
SCS(305)	0.39 (0.104)**	0.28 (0.111)**	0.52 (0.111)**
Residual correlations			
CM1		0.84 (0.002)**	0.64 (0.005)**
CM2			0.54 (0.006)**
MY(305)	-0.12 (0.008)**	-0.10 (0.009)**	-0.15 (0.008)**
SCS(305)	0.31 (0.008)**	0.27 (0.010)**	0.26 (0.017)**

CM1 = number of CM cases per lactation; CM2 = the number of days in CM per lactation; CM3 = CM considered as an all-or-none trait with values of 0 (no CM case) and 1 (at least 1 CM case); MY(305) = 305-d milk yield; SCS(305) = average lactation SCS;
** P<0.001

Positive (unfavorable) genetic correlation between CM traits and milk yield, and the high positive correlation between CM traits and SCS, both observed in our investigation, are in good agreement with correlations CM as binary traits ad milk yield (0.26-0.45) or SCS(305)(0.58-0.86) reported in the literature (Carlén *et al.*, 2004; Hinrichs *et al.*, 2005; Koivula *et al.*, 2005; Negussie *et al.*, 2006; De Haas *et al.*, 2008; Buch *et al.*, 2011). Additive correlations between CM traits and milk yield are on the lower limit of range of the cited results. It is known that the relationship between CM and milk yield is very complex and there are the reciprocal effects between traits (Wu *et al.,* 2008). The mastitis incidence caused the lowering of milk production and at the same time the culling for mastitis occurs with higher frequency in cows with high milk yield.

Breeding value and ranking of sires

The breeding values were estimated for CM traits (CM1, CM2 and CM3) and SCS(305) separately by univariate model and by bivariate models that combined CM trait and SCS(305). Spearman rank correlation estimates between sire breeding values obtained for different CM traits are summarized in Table 6. Only sires with daughters in the investigated dataset were included in the analysis. The correlation coefficient among breeding values for CM traits were high, for univariate model (over 0.81) as well as for bivariate model (over 0.88). Although there were relatively high correlation coefficients between the breeding values for CM trait and SCS(305), some changes in the ranking of sire may be expected.

Table 6. Spearman rank correlations between breeding values for different CM trait definitions and SCS(305) for 139 sires with reliability of breeding value over 50% in the analyzed dataset ; The range of sire breeding values for several model absolute and expressed in standard deviation (SD).

Pair of traits and model			Spearman's rank correlation	Traits and model combination	Range of breeding values	
					Absolute value	In SD
CM1	x	CM2	0.87	CM1	0.34	4.99
CM1	x	CM3	0.84	CM2	2.13 d	5.85
CM2	x	CM3	0.81	CM3	0.10	4.95
CM1scs	x	CM2scs	0.92	CM1scs	0.34	5.04
CM1scs	x	CM3scs	0.88	CM2scs	2.14 d	5.64
CM2scs	x	CM3scs	0.88	CM3scs	0.10	5.11
CM1	x	SCS(305)	0.53	SCS(305)	0.37	5.27
CM2	x	SCS(305)	0.55			
CM3	x	SCS(305)	0.59			
CM1scs	x	SCS(305)	0.70			
CM2scs	x	SCS(305)	0.71			
CM3scs	x	SCS(305)	0.77			

CM1 = number of CM cases per lactation; CM2 = the number of days in CM per lactation; CM3 = CM considered as an all-or-none trait with values of 0 (no CM case) and 1 (at least 1 CM case);; SCS(305)=average SCS – breeding value estimated in univariate model
CM1scs, CM2scs, CM3scs – breeding value estimated in bivariate models including CM traits and SCS(305)

It is clear that the bulls selected on the basis of direct breeding values for one of the CM trait are different than those selected according breeding value for SCS. The reason is that the genetic correlation between CM traits and SCS (305) is lower than one. The range of sire breeding values predicted were 0.34 for CM1 trait, 0.10 for CM3 trait and 2.14 days for CM2 trait, regardless if it was the uni or bivariate model. Thus, using the best instead of the worst sire could decrease the number of CM case per lactation in daughters by about 0.34 or 0.10 depending on trait.

Conclusion

The data on CM collected on Czech dairy farms appear to be suitable for genetic evaluation of CM susceptibility. The later may by described by the number of CM cases per lactation, the number of days in CM per lactation or CM considered as an all-or-none trait. All of this CM traits showed heritability of 0.10 and therefore be improved by selection. A linear animal model including the permanent environmental effect of the cow is recommended for genetic evaluation of the Czech Holstein.

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