Genomic Evaluation for Clinical Mastitis in Czech Holstein

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Abstract

Genomic breeding values for resistance to clinical mastitis (CM) have been estimated using a single-trait or multi-trait model; the latter comprised besides CM also linear udder traits and somatic cell count (SCC) transformed to somatic cell score (SCS). Dataset included 79,431 Holstein cows and 132,614 lactations with a lactation incidence of clinical mastitis for all lactations 19.91%. Cows calved between 2017 and 2021 in 104 herds. CM was defined as binary trait with 0 (no case) and 1 (at least 1 case) during the lactation, SCC as the average value per lactation. The linear type traits were udder depth, udder width, suspensory ligament, and udder's subjective score in %. The single-step genomic method was employed to predict CM genomic breeding values (GEBV_CM). Linear model equations included the random additive genetic effect of animal and for CM and SCS fixed effects parity and age at calving class, herd-year-season of calving and random effect of the permanent environmental effect of a cow; for linear udder traits herd-year-season of scoring, classifier and linear and quadratic regression on the age at calving and the days in milk. Pedigree involved 208,217 animals. Number of genotyped animals was 35,472; effective animals 35,131; bulls 5,377, cows 14,941 and heifers 15,154. The final number of effective SNPs was 35,338. Variance and covariances included in the multi-trait model GEBV_CM prediction yielded heritabilities 0.22 udder assessment, 0.38 udder depth, 0.19 udder support, 0.16 udder width, 0.11 SCS, 0.04 CM; and genetic correlations between CM and udder assessment -0,30, udder depth -0,41, udder support -0,30, udder width, 0.11 SCS. The mean of GEBV_CM was 0.0047 and 0.0174 for the multi-trait and single-trait models, respectively. For bulls born in 2019 (235), the mean of GEBV_CM was -0.0241 and 0.0059 for the multi-trait and single-trait models, respectively. An increase in the reliability of the breeding value appeared in the multi-trait model compared to the single-trait model. The average reliability of GEBV_CM increased for young genomic bulls (235, born 2019) from 0.22 to 0.45; for genomic heifers (15,154) from 0.27 to 0.50.

Key words: Holstein cattle, clinical mastitis, udder exterior, somatic cell score, multi-trait model

Introduction

Genetic evaluation for clinical mastitis (CM) in dairy cattle aimed to increase the resistance to udder diseases. CM negatively affects cow's production, reproduction and welfare. Hence CM deteriorates the cows' life and the farm's economy. Nevertheless, CM exhibits a genetically-related variation, and although the heritability of CM traits is low (to 10%) (Martin et al. 2018), selection against udder disease is applicable. For example, Heringstad et al. (2001) confirmed the positive effect of selection on the CM genetic trend in Norway. The primary condition of CM genetic evaluation is udder disease monitoring. It is currently being pursued, for example, in the USA, Canada, Austria, Germany, Australia and the Czech Republic, where the national cattle health monitoring system, "The Diary of Diseases and Medication", has been implemented (Kasna et al. 2017). The linear models are regularly used for routine estimates of CM, although CM is often binary, and a threshold model provides somewhat higher heritability estimates (Carlen et al. 2006).

The somatic cell scores and udder exterior traits are often used as auxiliary traits for CM,

for example, the udder depth, fore udder attachment, and body condition score. (Jamrozik et al. 2013; (Govignon-Gion et al. 2016).

In the Czech Republic, CM genetic parameters and breeding values were estimated. First, the data on CM from cooperating farms were used (Zavadilova et al. 2015; 2016) and Kasna et al. (2018). The data later used was from the national monitoring system (Zavadilova et al. 2020).

This study aimed to employ a genomic multi-trait model with somatic cell score and udder exterior traits in the genomic evaluation of clinical mastitis in Czech Holstein cattle using the data on CM from the national monitoring system.

Materials and Methods

Data

Dataset included 79,431 Holstein cows and 132,614 lactations with a lactation incidence of clinical mastitis for all lactations at 19.91%. Cows calved between 2017 and 2021 in 104 herds. Farmers collected CM records and registered voluntarily in the national cattle health monitoring system called "The Diary of Diseases and Medication" (Kasna et al. 2017). This recording system was implemented in August 2018 after a one-year trial. It consists of an online health recording form for farmers and a simplified key of diagnoses based on the International Committee for Animal Recording (ICAR) recommendations.

Traits definition

CM was defined as a binary trait with 0 (no case) and 1 (at least 1 case) during the lactation (to 305 days in milk); SCC was calculated as the average value per lactation (number of lactations was 132,614).

Average somatic cell count in lactation (SCC) was transformed to somatic cell score (SCS) according to the following formula:

$$SCS305 = \log_2\left(\frac{SCC}{100\ 000}\right) + 3$$

The linear type traits included were udder depth, udder width, suspensory ligament, and udder's subjective score in %. The basic statistics of them are in Table 1. Those traits were selected based on genetic correlations with CM (see Table 2).

Table 1. Statistics of udder exterior traits (65 545 animals)

Trait	Mean± SD	Type traits score 1	Type traits score 9
Suspensory ligament	5.10± 1.307	Weak	Extremely strong
Udder depth	5.94± 1.258	Below hock	Shallow
Udder width	5.62± 1.249	Narrow	Wide
Udder's subjective score in %	79.75± 3.805	50	90

Heritabilities and genetic correlation estimates employed in the genomic breeding values for CM (GEBV_CM) prediction are presented in Table 2. They were estimated in the separate analysis using a small dataset of 13,794 Holstein cows and 18,570 lactations, a dataset edited with a focus on data structure in terms of suitability for estimating genetic parameters, e.g. the number of daughters per sire.

Table 2. Heritability (h^2) of analysed traits and their genetic correlations with clinical mastitis (r_g)

	h^2	r_g
Udder's subjective score in %.	0.22	-0.30
Udder depth	0.38	-0.41
Suspensory ligament	0.19	-0.30
Udder width	0.16	0.37
Somatic Cell Score	0.11	0.93
Clinical Mastitis	0.04	

Model description

Linear animal model equations included random additive genetic effects (208,217 animals). For CM and SCS, fixed effects parity and age at calving class, herd-year-season of calving and random effect of the permanent environmental effect of a cow were used (79,431 Holstein cows). For linear udder traits, herd-year-season of scoring, classifier and linear and quadratic regression on the age at

scoring and the days in milk at scoring were employed. Pedigree involved 208,217 animals.

The single-step genomic method (Aguilar et al. 2010, Christensen and Lund, 2010) was employed to predict CM genomic breeding values (GEBV_CM). Animals were genotyped using the Illumina BovineSNP50 Bead chip (Illumina, San Diego, CA, USA).

Number of genotyped animals was 35,472; bulls 5,377, cows 14,941 and heifers 15,154. The total number of effective SNPs used in calculating the G matrix was 35,338, with 35,131 effective animals.

The relative breeding values in % (RGEBV_CM) were calculated using a reference level derived from sires born in 2010 (mean=100) and SD=12. RGEBV_CM over 100 means a favourable value for a CM, i.e. high resistance to clinical mastitis.

A genomic and conventional prediction of CM breeding values was performed by single-trait and multi-trait models based on the same database, trait definition, and statistical model equations.

Results & Discussion

The heritability of the analysed traits, including their genetic correlations with CM, correspond to commonly published values (Pérez-Cabal and Charfeddine, 2013), except for the genetic correlation between SCS and CM. That genetic correlation was very high; previously estimated (Zavadilova et al. 2015, 2020) were lower (0.70-0.85) than that presented now, at least by 10 p. p. and more regardless of the data sets. Jamrozik et al. (2013) found much lower genetic correlations among the mean somatic cell scores in early lactation and CM, especially for the first parity (0.55). Similarly, Govignon-Gion et al. (2016) and Pérez-Cabal and Charfeddine (2013) report a lower genetic correlation (0.70; 0.76-0.85) than we found between these two traits. We speculate that the high value of the presented genetic correlation (0.93) between SCS and CM was caused by the structure of the data set used for the estimation of genetic parameters. Due to achieving an optimal structure for estimating genetic parameters, the final dataset was small and included only three years of CM monitoring. Genetic parameters used in CM genomic evaluation will need to be re-estimated as soon as possible.

The overall incidence of clinical mastitis 19.91% in data sets used for GEBV_CM prediction was similar to Govignon-Gion et al. (2016) incidence (19.3%) for the third parity of the Holstein breed. They reported lower CM incidence in the first and second parity, but they suspect underreporting by farmers. Martin et al. (2018) summed up the findings of several studies. They concluded that the CM incidence averaged over all lactations is around 20 % depending on the part of lactation, parity, breed and recording system. Zavadilova et al. (2015) found a twofold CM incidence (38.8%), analysing a dataset from long-term monitoring of seven herds. We suppose a higher CM incidence was due to the different data monitoring and the limited number of herds.

The mean of GEBV_CM was 0.0047 and 0.0174 for the multi-trait and single-trait models, respectively. For bulls born in 2019 (235), the mean of GEBV_CM was -0.0241 and 0.0059 for the multi-trait and single-trait models, respectively. Genetic trends compared between the single-trait and multi-trait models were similar (see Figure 1) for bulls or cows. Genetic trends were expressed in RGEBV_CM; therefore, the higher values were desirable. Genetic trends showed that resistance to clinical mastitis is improving in the Czech Holstein cow population, probably through long-term udder health selection by a genetic and genomic evaluation by the test-day model with random regression on the somatic cells count in milk. Compared to our results, Zavadilova et al. (2016) and Kasna et al. (2018) reported a worsening genetic trend for resistance to clinical mastitis of Holstein cows until about 2002, followed by a gradual improvement caused probably by including SCS and other functional traits in the composite selection index of Czech Holstein cattle. As Govignon-Gion et

al. (2016) stated, GEBV_CM predicted with the multi-trait model including SCS are a valuable tool at least counterbalance the negative correlated response on mastitis resistance due to selection on production traits.

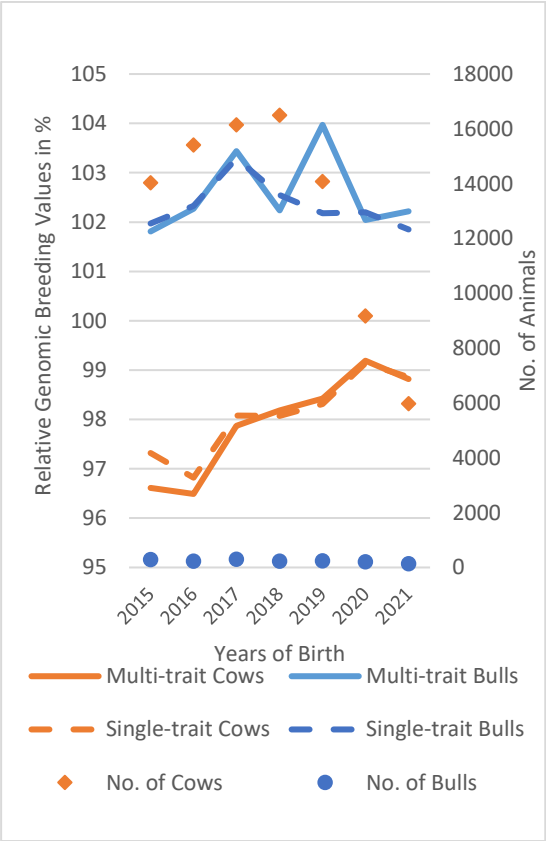

Figure 1. Genetic trends for the single-trait and multi-trait models

An increase in the reliability of the breeding values appeared in the multi-trait model compared to the single-trait model. The average reliability of GEBV_CM increased for young genomic bulls (235, born 2019, see Table 3) from 0.22 to 0.45; for genomic heifers (15,154, see Table 4) from 0.27 to 0.50. The increase of the average reliabilities of conventional breeding values was lower than those of genomic breeding values for young bulls and heifers.

Table 3. The average reliability of genomic breeding values for CM for genotyped young bulls (235)

Model	Mean ±SD	25pct	75pct
Multi-trait genomic	0.45± 0.059	0.42	0.48
Multi-trait conventional	0.19± 0.082	0.13	0.23
Single-trait genomic	0.22± 0.052	0.19	0.25
Single-trait conventional	0.08± 0.047	0.05	0.10

25pct - 25th percentile; 75pct - 75th percentile

Table 4. The average reliability of genomic breeding values for CM for genotyped heifers (15,154)

Model	Mean ±SD	25pct	75pct
Multi-trait genomic	0.50± 0.046	0.47	0.53
Multi-trait conventional	0.26± 0.086	0.20	0.32
Single-trait genomic	0.27± 0.050	0.24	0.30
Single-trait conventional	0.12± 0.059	0.08	0.15

25pct - 25th percentile; 75pct - 75th percentile

Figure 2 showed the average reliability of GEBV_CM for bulls and cows when the single-trait or multi-trait model was used. The increase in the average reliabilities due to employing the multi-trait model is evident**.**

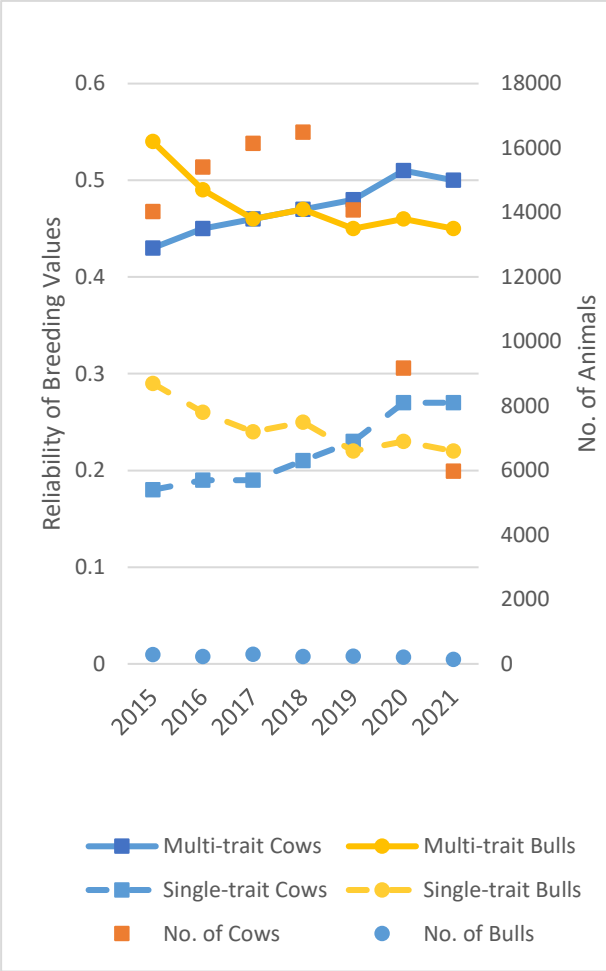

Figure 2. Average reliabilities for single-trait and multi-trait models

Conclusions

Genetic evaluation for mastitis resistance by multitrait model employing the CM, somatic cell score and the udder type traits led to higher reliability of breeding values than the single trait model. These findings are essential for the genetic and genomic evaluation of CM and have a practical impact on genetic selection for increasing clinical mastitis resistance in Czech Holstein cattle.

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