

Genomic and conventional breeding values for clinical mastitis

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Conventional and genomic breeding values for clinical mastitis were estimated, based on a dataset of 15,905 cows (36,250 lactations) from 10 farms, calving years from 1996 to 2014. The number of genotyped bulls was 2647 and 799 of them had offspring among the surveyed cows. Pedigree consisted of 64,306 individuals. Analyzed trait was defined as the number of incidence of clinical mastitis per standard lactation. Parity was limited from 1 to 7. The highest proportion of mastitis disease was observed in early lactation and decreased with month of lactation, while there was an upswing of diseases with parity. Genetic trend for cows showed a deteriorating tendency for clinical mastitis. From 1992 to 2010 there was a rise in the relative values of breeding values from 88 % to 112 % (worsening). Relative breeding values of these bulls were on average above 100 %. The correlations between classical genomic breeding values and the values were high: 93 % for the whole sample, 81 % to 48 young genomic bulls without daughters born in years 2011 and 2012.

Keywords: mastitis, genetic value, genomic value, Holstein cattle

1 Introduction

Among health traits, priority is on genetic improvement of clinical mastitis (CM). This is due to the obvious effect of CM on involuntary dairy cow disposal and detrimental effect of CM on dairy farming profitability and economy (e. g. Halasa et al., 2007, Wolfová et al. 2006, Sagedhi-Sefidmazgi et al., 2011). Genetic selection programs are focusing on reducing diseases and improving functional traits (Zwald et al. 2006). 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, routinely recording of clinical mastitis is not implemented in many countries whereas it is well-established in the Nordic countries since more than 40 years (Carlén, 2008). Also, experience with direct udder health data is still limited in the Czech Republic. In the Czech Republic, breeding values for somatic cell scores, estimated by test-day animal model with random regression, 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. Concerning 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 heritabilities for clinical mastitis traits were estimated in the range of 0.09 to 0.10 by Zavadilová et al. (2015) using datasets from 7 Czech Holstein dairy farms.

The objective of this study was to estimate breeding values for clinical mastitis traits: conventional and genomic.

2 Material and methods

Data on clinical mastitis incidence were collected from 10 Holstein herds between 1996 and 2014. The farms were not randomly chosen from the nationally recorded population but rather were those willing to participate in the study. They varied in size and were from distinct regions but all used management, feeding, and housing systems commonly applied to dairy herds in the Czech Republic. Straw was used for bedding on all farms, and all cows were fed a balanced total mixed ration (TMR) and milked twice a day.

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Dataset included 15,905 Holstein cows on 1st to 7th parity (36,250 lactations), daughters of 1,817 sires. The number of genotyped bulls was 2647 and 799 of them had offspring among the surveyed cows.

Records collected on farms included cow identification, date on the beginning of each CM treatment, date at the end of each CM incident (i.e. the last day that milk from a treated cow was discarded), and identification of treated quarters. Farmer detection of CM was accomplished by visual examination of the udder or milk. However, a mastitis case was recorded only if it was treated with antibiotics prescribed by a veterinarian. Thus, CM was defined as a veterinary-treated udder disease.

Traits of interest for each cow were the number of CM cases per lactation. A new case of CM for the same cow was indicated when the period between the end of the previous case and the beginning of the next occurrence was at least 5 days.

The following linear animal model was used to estimate conventional (GV) as well as genomic (GBV) breeding values:

$$y_{ijklmn} = \text{parity}_i + \text{herd}_j + \text{year}_k + \text{season}_l + pe_m + a_n + e_{ijklmn},$$

where,

- y_{ijklmn} is the number of CM cases per lactation,
- parity_i is the effect of parity class i (4 levels, first, second, third, fourth and higher parity)
- herd_j is the effect of herd j (10 levels);
- year_k is the effect of calving year k (18 levels)
- season_l is the effect of calving season (4 levels, January – March; April – June; July – September; October - December)
- pe_m is the *random* permanent environmental effect on cow traits across m sequential lactations;
- a_k *random* additive genetic effect of cow m
- e_{ijklmn} is the *random* residual effect

Pedigree consisted of 64,306 individuals. Genomic breeding values were estimated by single step genomic BLUP using the pedigree-based relationship matrix augmented by the genomic relationship matrix. Single nucleotide polymorphism (SNP) markers from the Illumina BovineSNP50 BeadChipV2 (Illumina Inc., San Diego, USA) were available for 2,647 sires. The 799 genotyped sires had offspring among the surveyed cows. Data were analyzed using the DMU package (Madsen and Jensen, 2010). The heritability for clinical mastitis traits was 0.10 by Zavadilová et al. (2015).

Demanded breeding value (BV as well as GBV) for clinical mastitis incidence should be located at the bottom of the BV scale. The lower BV the lower the incidence of mastitis is. Based on the presented file, relative breeding values (RBV) were calculated using the average for bulls born in 1995. Required RBV (high resistance to mastitis) are less than 100 %.

3 Results and discussion

In subsequent years, we recorded 30 %–40 % of lactations with greater or lesser incidence of clinical mastitis, see Figure 1. Downward trend in the average number of disease per lactation on the first and on all lactations is desired and positive development in udder health.

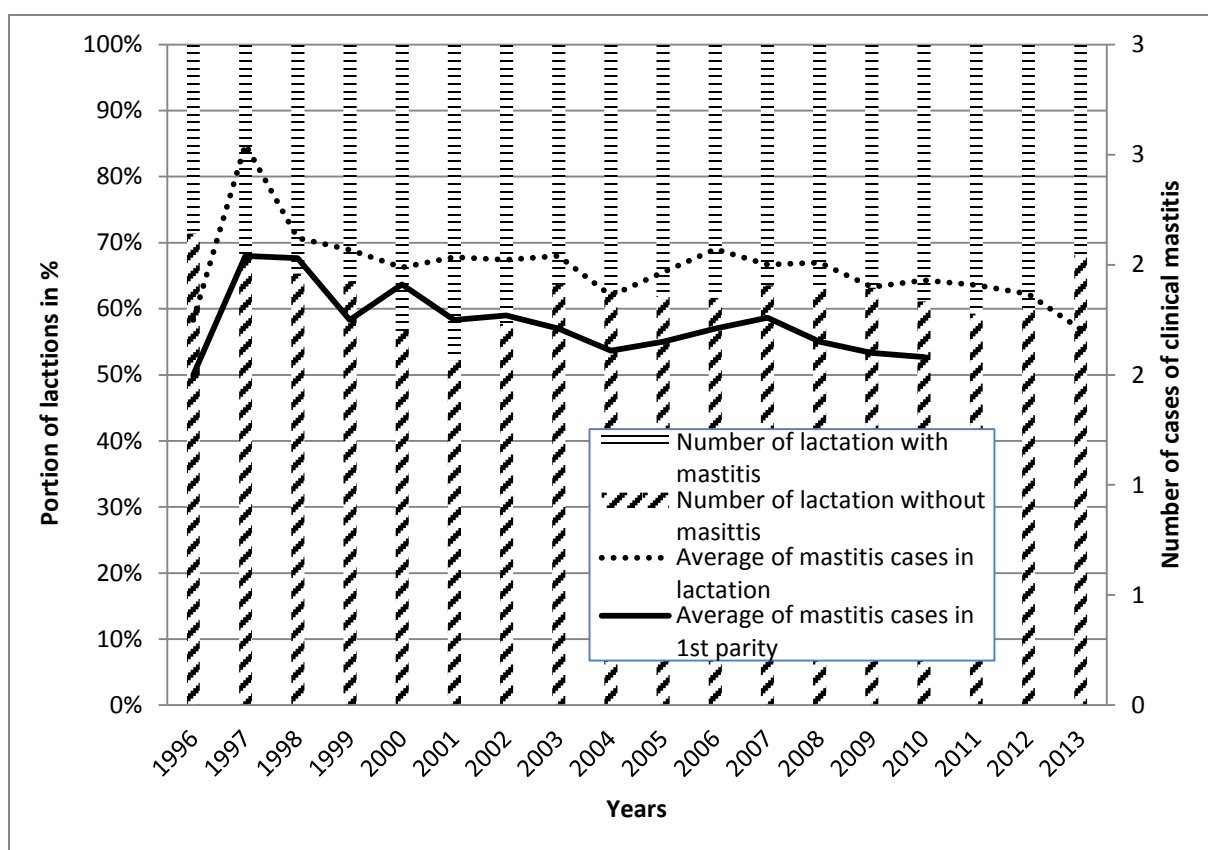


Figure 1 Percentage of healthy lactation and lactation with clinical mastitis during the years of monitoring

During lactation, the highest number recorded cases of clinical mastitis was found in early lactation. For breeding against clinical mastitis incidence, the first 100 days of lactation seems to be very important. It is obvious that the highest proportion of the disease is in the early lactation see Figure 2, then this number decreased with continued lactation. At the same time, there was a rise of clinical mastitis ratio with parity except the first month of the second lactation, where the value was lower than in the first lactation.

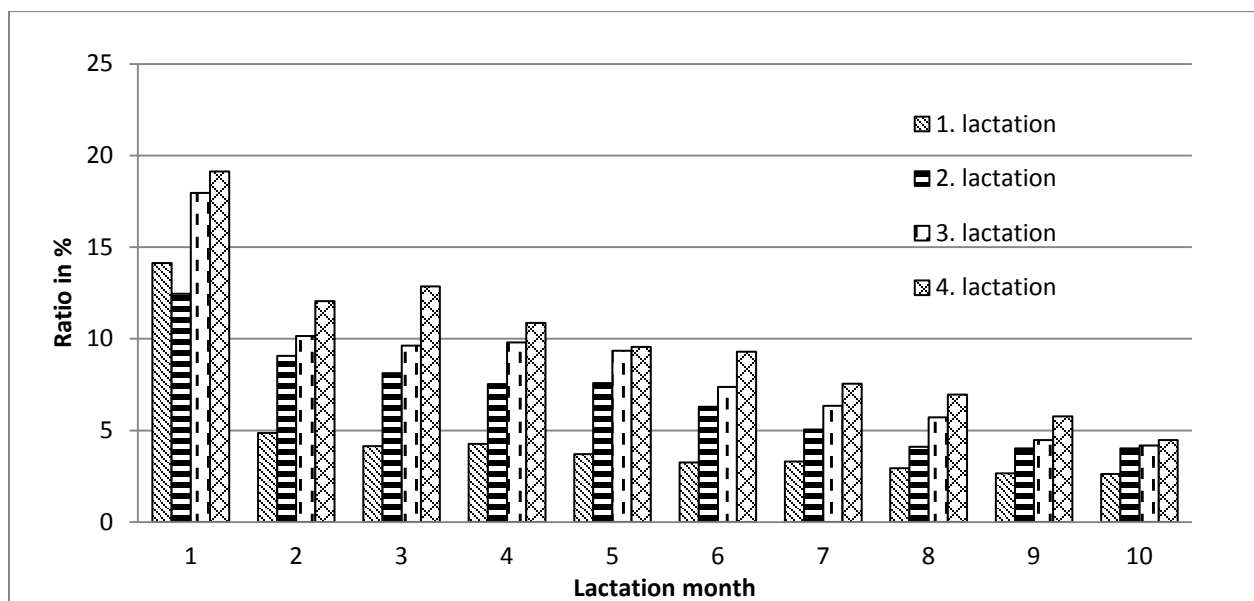


Figure 2 The proportion of clinical mastitis by month and lactation

Genetic trend for cows, see Figure 3 showed that the genetic value of clinical mastitis per lactation increased with the years, which is a negative phenomenon.

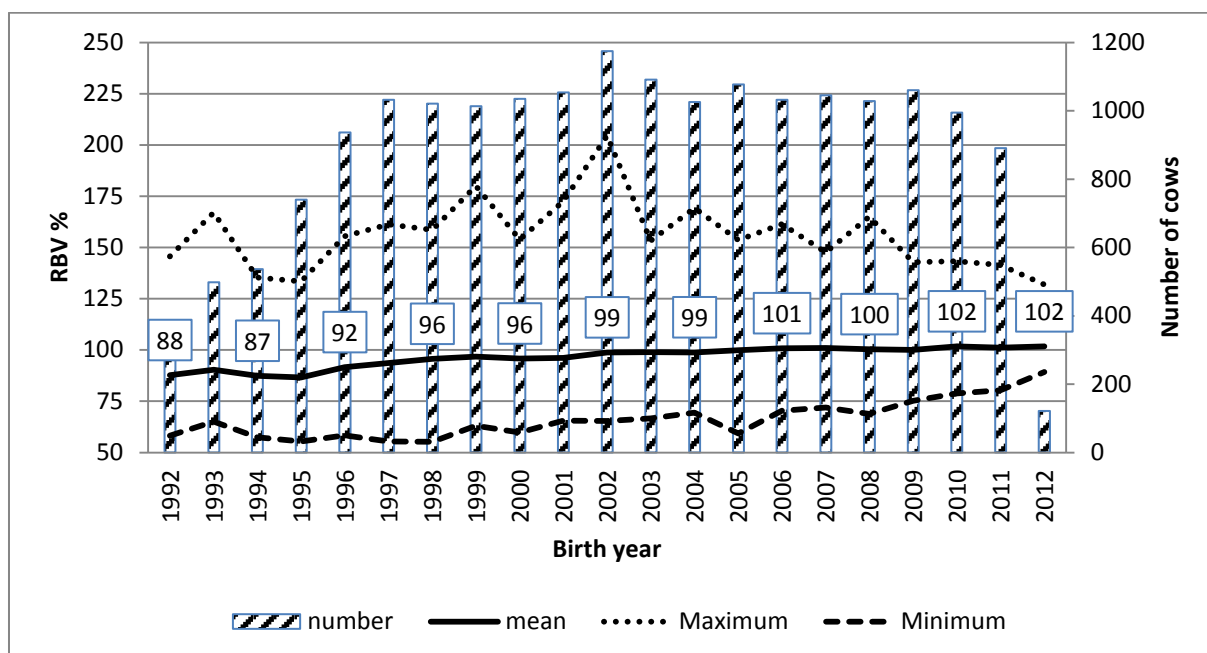


Figure 3 Genetic trend for clinical mastitis, RBV by year of birth, cows

From 1992 to 2010 there was an increase RBV from 88 % to 112 %. Whether it was due to the fact that the bulls were slightly worse (higher RBV) for clinical mastitis than cows monitored, see Figure 4, the genetic trend for clinical mastitis RBV by year of birth, bulls, or is it worsening due to selection for other traits, e.g., milk performance, we can only speculate.

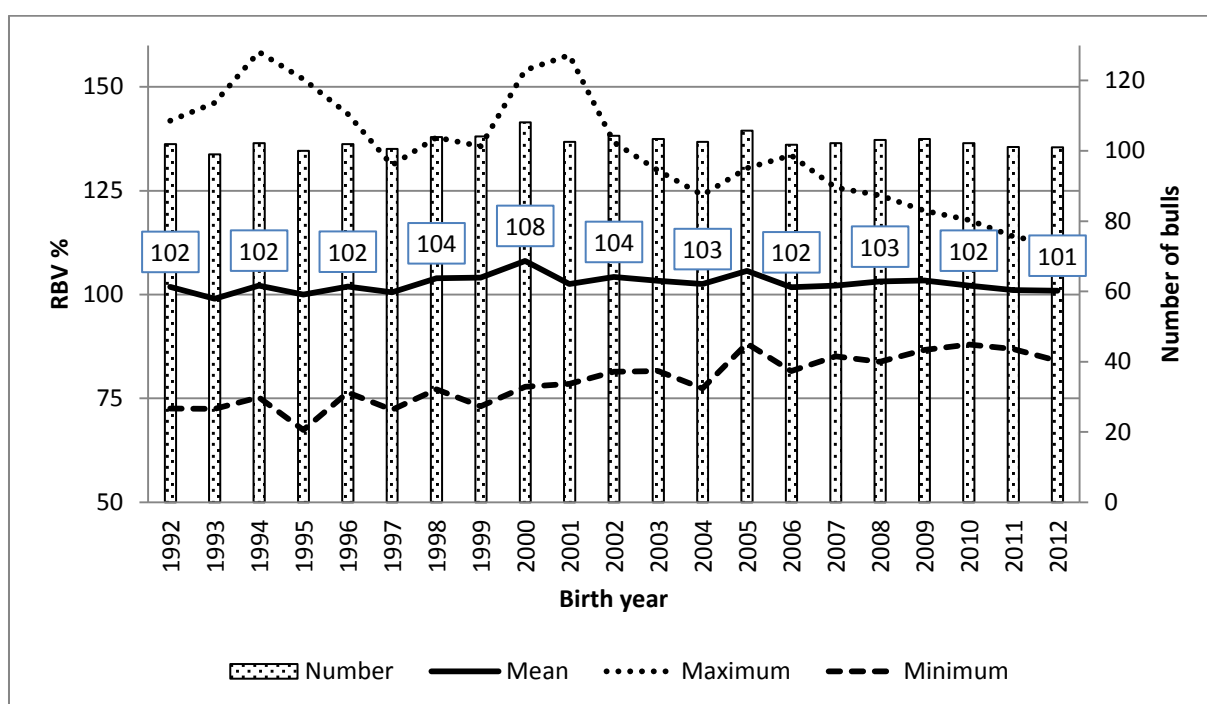


Figure 4 The genetic trend for clinical mastitis RBV by year of birth, bulls

In any case, this deterioration is slow but steady. Relative breeding values of bulls on average are slightly above 100 %. The highest average was achieved in 2000 (108 %). Analyzed dataset of Holstein cows was rather random selection from the Holstein population. Nevertheless, we can assume that breeding of Holsteins cattle is focused on high quality high performance, exterior and good reproduction. Yet we see a deterioration of the genetic basis of cows for clinical mastitis. We can expect the future improvement of sires breeding values for mastitis incidence, because a direct selection on the incidence of mastitis in many populations of Holsteins has already started.

As an example for the selection of cows by RBV for clinical mastitis, a selection of heifers calved in 2012 is presented. RBVs of these heifers (1,030 animals) ranged between 78.8 % and 143.3 %, see Figure 5. Heifers with desired values of RBV are on the left side of the figure, most of them showed RBV in the range of 95–100 %.

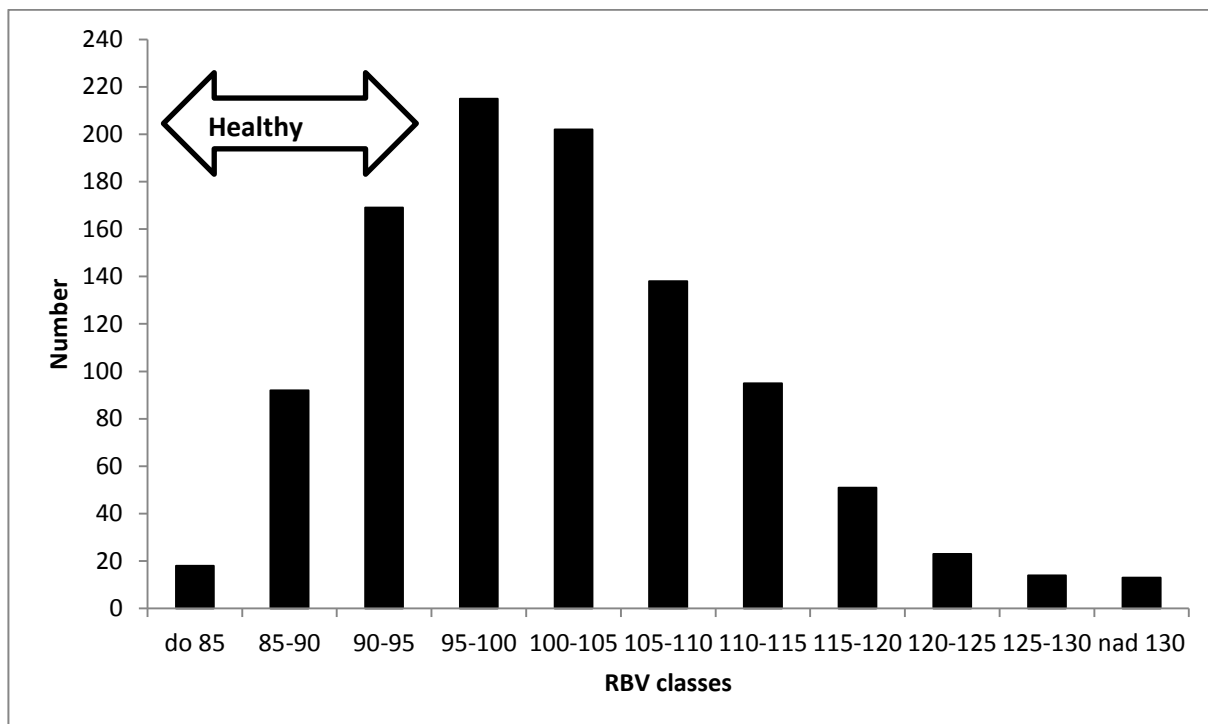


Figure 5 The number of heifers according of RBV for clinical mastitis

The most common value was 102 % and the average was 101.6 %. According to evaluated RBV, the selection of cows with greater or lesser genetic predisposition to clinical mastitis could be undertaken. Reliabilities of presented RBV were in the range from 11 % to 36 %, the most frequent value of 20 %–30 %.

Correlations between classical breeding values (BV) and genomic breeding values (GBV) were strong: 93% for the whole dataset, 90 % for all bulls, 87 % for genomic bulls, 98 % for genomic bulls with more than 20 daughters, 81 % for 48 young genomic bulls without daughters. On average, the relative genomic breeding values (RGBV) (100.4 ± 10.44) and RBV (102.6 ± 9.50) were almost identical. Conventional breeding values showed tendency to be higher than genomic estimates, up to 100 % values RGBV. Genomic reliability was much higher than conventional (54.7 ± 20.1 vs. 33.96 ± 13.47). If we focus on the young bulls with no progeny, i.e., 48 bulls born between 2011 and 2012, we find that genomic breeding values were generally lower than conventional RBV. When comparing the first ten selected out of the 10 bulls with the best RGBV then it would be chosen by RBV only the first seven, the remaining three are in 26th place by RBV.

4 Conclusions

Presented analyzes indicate that breeding for disease resistance to mastitis is possible even in the Czech Republic. Breeding value for clinical mastitis should be used for selection of breeding animals despite a limited number of data. We can distinguish individuals with positive and negative genetic

basis for this character with sufficient accuracy. It is obvious that an enlargement of the file size increases the estimation accuracy.

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