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Genetic Evaluation of Clinical Mastitis Traits in Holstein Cattle

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ABSTRACT

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The results obtained from different models for predicting breeding values for clinical mastitis (CM) in Holstein cattle were compared. CM was recorded in 30 882 lactations of 12 793 cows in 8 herds from 1996 to 2016. CM was considered either as an all-or-none binary trait (0 – absence of mastitis; 1 – at least one case of CM per lactation) or as the number of cases. CM is recorded in the first 150 days of lactation or throughout the entire course of lactation. Breeding values were predicted with a single-trait repeatability model and with a bivariate animal model, where CM during the 1st lactation and CM during the 2nd and later lactations were considered as two different traits. Estimated heritability ranged from 0.06 for CM as a 0/1 trait during the first 150 days of lactation in the repeatability model to 0.12 for the number of CM cases during the 1st lactation in the bivariate model. Ranking of the sires with 15 or more daughters and of the cows was performed according to their breeding values, and Spearman correlation coefficients were calculated. Rank correlations of breeding values from the repeatability and bivariate models were stronger for the same parts of lactation (150 vs 305 days; 0.88–0.96) and for the repeatability model and the bivariate model for the 2nd and later lactations (0.95–0.98). Trends of average male and female breeding values according to their birth year were used to assess genetic changes in the population. The average breeding values declined slowly for cows born since 2003 but stayed above neutral value, thus indicating permanent genetic deterioration of mastitis resistance.

Keywords: udder health; mastitis resistance; genetic parameters; genetic trend

Clinical mastitis (CM) is commonly reported as one of the most widespread and costly diseases of dairy herds. Udder diseases also belong to the most prevalent causes of involuntary culling of dairy cows in the Czech Republic (Kvapilik et al. 2016). Despite providing the best environment in terms of nutrition, herd management, treatment, housing and technology, CM is present in most dairy herds. The incidence of CM across studies differs according to the trait definition (binary trait or a count of cases per lactation), the origin of records (farmers or veterinarians; field or population study), and the stage and rank of lactation (reduced vs whole lactation; only the first lactation or the first and later lactations). The lactational incidence of CM mostly ranged between 10–25% as reported for example Heringstad et al. (2005), Zwald et al. (2006), Koeck et al. (2010b), Mrode et al. (2012), Govignon-Gion et al. (2016), and others. The frequency of CM is usually higher in later lactations compared to that in the first lactation. Therefore the trait should not be considered to be the same across lactations (Heringstad et al. 2005).

Heritability of CM is low; its value depends on the trait and the method of estimation. CM is usually defined either as an all-or-none binary trait

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according to whether it was absent or present in the evaluated lactation or as the number of cases per lactation. Heritability estimates vary between 0.01 from a linear model, encompassing the binary trait and later lactations (Carlen et al. 2004) to 0.15 from a threshold model, encompassing the binary trait and final stage of first lactations (Zwald et al. 2006). The threshold model is theoretically appropriate for the evaluation of the binary CM trait, but the linear approach was preferred in different studies (Govignon-Gion et al. 2016; Jamrozik et al. 2016; Zavadilova et al. 2017) and also in the routine evaluation.

A very important question is the standard definition of CM, which would ensure comparability and international prediction of breeding values for this trait. A widely used definition is that of Kelton et al. (1998), who stated a cow is considered to have CM if she has visually abnormal milk secretion which might be accompanied by signs of inflammation of the udder tissue. Abnormal milk in a different quarter or in the same quarter following at least 8 days of normal milk was considered a new case.

When genetic selection focused on health traits in Nordic countries, it was shown that mastitis resistance could be improved (Heringstad et al. 2000). The genetic evaluation of Czech dairy cattle is currently aimed at indicator traits genetically associated with CM. The Czech total merit index for Holstein includes the somatic cell score (SCS) and udder conformation traits. As stated by Mrode et al. (2012), the less than complete genetic correlation of CM with SCS implies that we could achieve additional genetic gain by the use of direct CM records. The direct CM evaluation is currently unavailable in the Czech Republic due to the missing national database. However, there is an experimental dataset at the Institute of Animal Science in Prague, which has been used for many previous investigations (Wolf et al. 2010; Zavadilova et al. 2015, 2017). We used the same dataset and focused on the time aspect and the proper definition of CM which could be considered either as one or as two different traits in the first and later parities. The objective of the present study was to predict the breeding values for CM defined either as an all-or-none binary trait or as the number of cases recorded in different lactation periods (the first 150 days in milk vs whole lactations) with the support of two different models (a repeatability linear model vs a bivariate model) and to compare the obtained results.

MATERIAL AND METHODS

The data were collected from 1996 to 2016 on eight Czech farms willing to cooperate in CM data recording. The farms were from different regions, their average size ranged between 150–1000 cows per year, and average milk yield was about 9200 kg of milk per cow and lactation. The farms used technologies (management, feeding, housing) commonly applied in the Czech Republic. The cows were milked twice per day. The detection of CM was done by farmers on the basis of visually abnormal milk secretion and/or the signs of udder inflammation. However, only veterinary-treated cases were recorded for further evaluation. A new case of CM was defined when the period between the end of previous case and the next occurrence was at least 8 days. We had the records of CM from 30 882 lactations of 12 793 cows. The data structure is described in Table 1. CM was considered as (1) an all-or-none binary trait with values of 0 (no CM case) and 1 (at least 1 CM case per lactation) or (2) the number of CM cases per lactation. Both traits were recorded either in the first 150 days in milk (CM1_150, CM2_150) or in the whole lactation period (CM1_305, CM2_305).

Table 1. Structure of evaluated data

	No. of lactations	LIR (%)	No. of CM cases	Average No. of cases per affected lactation	
				150 days	305 days
All lactations	30 882	38.69	22 351	1.57	1.87
1st lactation	12 793	30.93	6 266	1.38	1.58
2nd lactation	8 830	38.61	6 409	1.59	1.88
3rd lactation	5 298	45.18	4 917	1.67	2.05
4th and later	3 691	55.26	2 189	1.73	2.17

CM = clinical mastitis, LIR = lactational incidence rates (number of affected lactations/number of lactations at risk × 100)

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Breeding values were predicted with the following models: (1) a single-trait repeatability linear animal model (BVs) and (2) a bivariate linear animal model, where CM traits in the 1st (BVt1) and in later lactations (BVt2) were considered as two different traits.

The equation for the single-trait repeatability model consisted of the following effects:

$$y_{ijklmn} = l_i + h_j + y_k + s_l + pe_m + a_m + e_{ijklmn}$$

The equations for the bivariate model were:

$$y_{ijklm} = h_i + y_j + s_k + \beta_1 \times aac_{ijklm} + \beta_2 \times aac^2_{ijklm} + a_l + e_{ijklm}$$

$$y_{ijklmn} = l_i + h_j + y_k + s_l + pe_m + a_m + e_{ijklmn}$$

where:

y_{ijklmn} = recorded CM trait
l_i = effect of the order of lactation i (4 levels; 1, 2, 3, 4 and later)
$h_{i(j)}$ = effect of the herd of calving $i(j)$ (8 levels)
$y_{j(k)}$ = effect of the year of calving $j(k)$ (20 levels)
$s_{k(l)}$ = effect of calving season $k(l)$ (4 levels)
aac_{ijklmn} = fixed linear regression of the age at first calving
aac^2_{ijklmn} = fixed quadratic regression of age at first calving (from 500 to 1400 days)
β_1, β_2 = corresponding partial regression coefficients
pe_m = random permanent environmental effect of the cow m
a_m = random additive genetic effect of the cow m (pedigree included 26 575 animals)
e_{ijklmn} = residual effect.

The effect of the herd had 8 subclasses with average size 3860 lactations (min = 197; max = 12 821). The effect of the season of calving was divided into 4 subclasses (January–March, April–June, July–September, October–December) with average size 7720 lactations (min = 6827; max = 8125). The effect of the year of calving had 20 subclasses with average size 1544 lactations (min = 104; max = 2414).

The average information restricted maximum likelihood (AI-REML) was used for variances and covariances estimation as implemented in the DMU package (Madsen and Jensen 2010).

Estimated breeding values (EBVs) for sires with 15 or more daughters (262 sires) and for cows from both models were ranked, and Spearman correlation coefficients were calculated.

Trends of average male and female breeding values according to their birth year were used to assess genetic changes in the population.

RESULTS AND DISCUSSION

We applied the linear models for CM traits evaluation, though the data does not fulfil the assumption of normal distribution. Some studies (Heringstad et al. 2005; Zwald et al. 2006; Koeck et al. 2010b) preferred threshold models, as they can account for the binary nature of the CM data. However, the linear models are usually used for routine CM evaluation (Jamrozik et al. 2013; Govignon-Gion et al. 2016), because they are fast and easier to implement. Koeck et al. (2010a) performed a complex comparison of different models and showed that linear models are robust toward departures from normality and perform equally well as threshold models for genetic evaluation of CM.

Genetic parameters. Estimated genetic parameters are summarised in Table 2. Their values are consistent with our previous results (Zavadilova et al. 2015) obtained in the same population but at a different time period (from 2000 to 2012) but are higher than values in Zavadilova et al. (2017) for the time period 1996–2014. Estimated heritability for CM traits ranged from 0.06 for CM as a 0/1 trait for the first 150 days of lactation with the repeatability model to 0.12 for the number of CM cases during the 1st lactation with the bivariate model. Heritability was slightly higher in the bivariate model, during the 2nd and later lactations, for CM recorded as the number of cases and for CM recorded during the whole lactation period. Our estimates are similar to those from other studies, although at the higher end of the range. This fact could be due to the higher incidence and hence higher variability of CM in our population. As stated by Heringstad et al. (2000), the heritability estimates for all-or-none traits are functions of incidence, and differences in estimates between studies may be caused by real differences between population and countries. Mrode et al. (2012) estimated the genetic parameters for mastitis, which was considered as a binary trait or as the number of cases. According to those authors, the estimates of heritability increased with lactation number, at 0.05, 0.07, and 0.09 for mastitis as a binary trait during the 1st, 2nd, and 3rd lactations, respectively, with similar corresponding heritability at 0.06, 0.07, and 0.13 for mastitis as the number of cases. Additionally, Pritchard et al. (2013) found that the heritability of mastitis increased with parity, with estimates 0.04, 0.05, and 0.10 in parities 1,

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2, and 3, respectively for mastitis as a binary trait obtained from multivariate analysis across parities. Jamrozik et al. (2013) compared mastitis treated as a binary, and they estimated heritability to be 0.03 for the 1st lactations and 0.05 for later lactations. In contrast to previous studies, Carlen et al. (2004), Heringstad et al. (2005), and Negussie et al. (2006) found higher heritability in the 1st lactation than in the 2nd or 3rd lactation. Negussie et al. (2006) explains this trend by an increase in residual variance and a decrease in genetic variance over lactation. Lower heritability could also be partly explained by selection carried out in the 1st parity. Heringstad et al. (2004) pointed to larger genetic changes in the 1st lactation due to the selection on focusing on CM resistance during the period from 15 days before to 120 days after first calving.

Genetic parameters for different lactation segments were estimated by Zwald et al. (2006), who found increasing heritability estimates as lactation progressed. In contrast to those findings, Zavadilova et al. (2017) found higher heritability in the first 100 days of lactation compared to later periods. Additionally, Koeck et al. (2010b) found slightly higher heritability of CM in an earlier interval that ranged from 10 days prior to 50 days after calving (0.06) compared to the interval from 10 days prior to 150 days after calving (0.05). The same authors suggested that most of the genetic variation in CM is found in early lactation, when the cows face high physiological demands.

Genetic correlations between the 1st and later lactations in our study ranged from 0.67 for CM as a binary trait recorded in the first 150 days of lactation to 0.80 for the same trait recorded during the whole lactation period (Table 2). Again, the genetic parameter is higher when the whole lactation period is taken into account. Generally, genetic correlations tend to be the highest between the 2nd and 3rd lactations and the lowest between

Table 2. Variance components and their standard errors (in parentheses) estimated for the clinical mastitis (CM) traits with repeatability model breeding values (BVs), for the 1st lactation with the bivariate model BVt1 and for the 2nd and later lactations with the bivariate model BVt2

	CM1_150	CM1_305	CM2_150	CM2_305
BVs				
Variance component estimates				
Additive genetic	0.011 (0.0014)	0.017 (0.0018)	0.051 (0.0058)	0.130 (0.0131)
Permanent environment	0.008 (0.0016)	0.012 (0.0019)	0.032 (0.0061)	0.097 (0.0129)
Variances as proportions of total phenotypic variance				
Heritability	0.06	0.08	0.07	0.09
Repeatability	0.10	0.13	0.11	0.15
BVt1				
Variance component estimates				
Additive genetic	0.011 (0.0020)	0.018 (0.0027)	0.035 (0.0057)	0.109 (0.0130)
Variances as proportions of total phenotypic variance				
Heritability	0.07	0.09	0.08	0.12
Genetic correlation between 1st and later lactations	0.67 (0.088)	0.80 (0.066)	0.68 (0.077)	0.78 (0.054)
BVt2				
Variance component estimates				
Additive genetic	0.016 (0.0022)	0.023 (0.0027)	0.090 (0.0110)	0.219 (0.0232)
Permanent environment	0.013 (0.0026)	0.014 (0.0029)	0.068 (0.0117)	0.154 (0.0234)
Variances as proportions of total phenotypic variance				
Heritability	0.08	0.10	0.10	0.11
Repeatability	0.14	0.16	0.17	0.19

CM1_150 = all-or-none binary trait with values of 0 (no CM case) and 1 (at least 1 CM case) in the first 150 days in milk, CM1_305 = all-or-none binary trait with values of 0 (no CM case) and 1 (at least 1 CM case) in the whole lactation period, CM2_150 = number of CM cases in the first 150 days in milk, CM2_305 = number of CM cases in the whole lactation period

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the 1st and 3rd lactations. Carlen et al. (2004) stated that the genetic correlations of CM across the first 3 lactations were above 0.7. Zwald et al. (2006) estimated the genetic correlations as 0.46 (1st and 2nd lactation), 0.49 (2nd and 3rd lactation), and 0.42 (1st and 3rd lactation). Negussie et al. (2006) obtained higher genetic correlations for CM: 0.86 (1st and 2nd lactation), 0.95 (2nd and 3rd lactation), and 0.75 (1st and 3rd lactation). Mrode et al. (2012) reported values of 0.55 (1st and 2nd lactation), 0.89 (2nd and 3rd lactation), and 0.48 (1st and 3rd lactation) for mastitis as a binary trait and of 0.62 (1st and 2nd lactation), 0.85 (2nd and 3rd lactation) and 0.42 (1st and 3rd lactation) for mastitis as the number of cases. Jamrozik et al. (2013) found that the genetic correlation between the first and later lactations was 0.59. Our estimates of genetic correlations between the first and later lactations were higher, reflecting a higher incidence of CM in the evaluated population. To summarise, genetic correlations are the highest between the 2nd and 3rd lactations and the lowest between the 1st and 3rd lactations, which indicates that the 1st and later lactations are genetically different traits and that the multitrait model, which allows these traits to be treated as different but correlated traits, would be justifiable.

Rank correlations between breeding values. Rank correlations between sires or cows with estimated BVs (single-trait repeatability model) and BVt1 and BVt2 (bivariate model) are shown in Figure 1. All correlations were higher than 0.70. Re-ranking among the top ten sires due to CM traits and due to the employed models was substantial, which shows that the employed models are not interchangeable.

The strongest rank correlations were found between sires with BVs for CM incidence in the same stages of lactation (0.88–0.98) compared to sires with BVs for CM in different stages of lactation

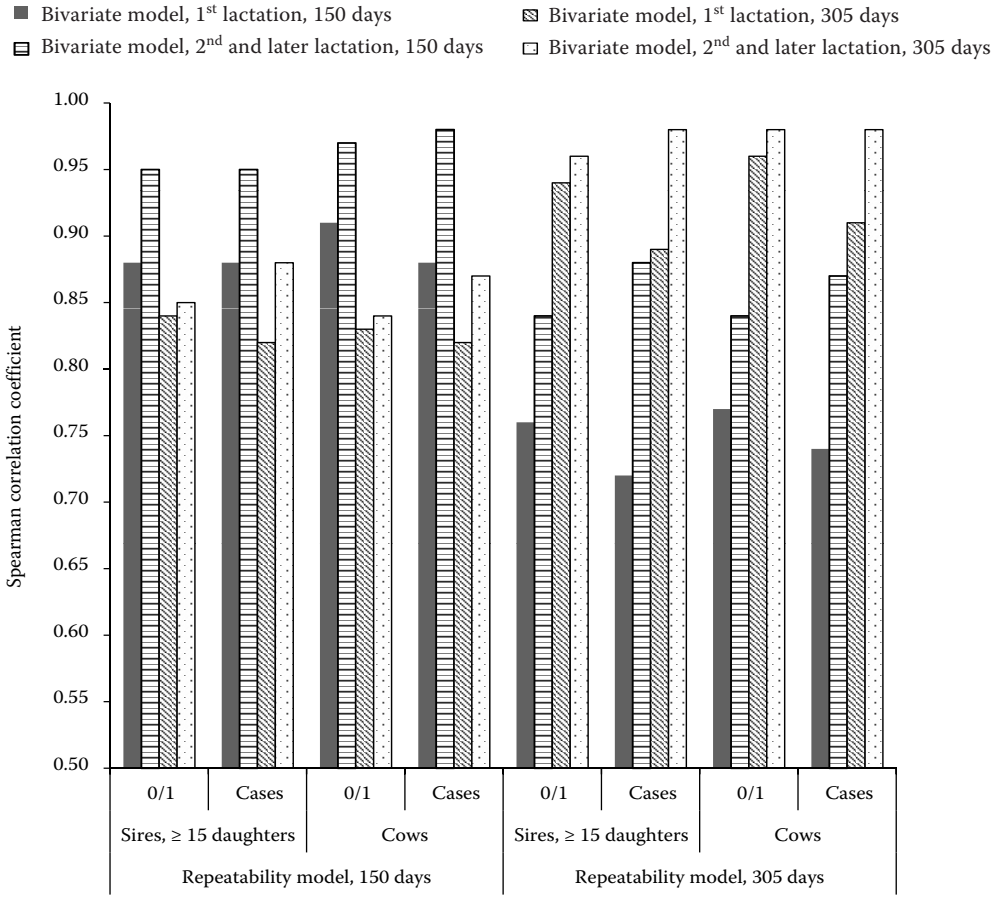

Figure 1. Rank correlations between animals (sires or cows) with breeding values predicted with the repeatability or bivariate model for clinical mastitis (CM) defined as a bivariate 0/1 trait or as the number of cases in the first 150 days in milk or the whole lactation period

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(0.78–0.88). This result reflects the genetic correlation between CM incidence in 150 days in milk and during the whole lactation period. Different studies estimated breeding values for CM traits in the reduced part of lactation to avoid the bias due to culling cows (Carlen et al. 2004; Heringstad et al. 2005; Negussie et al. 2006; Koeck et al. 2010b). However, the reduction of the evaluated period may lead to a loss of information. According to Carlen et al. (2004), approximately 60–65% of all CM cases occur within the first 150 days of lactation, although most cases of mastitis occur in the first half of lactation, Wolf et al. (2010) documented that approximately 10% of cows that were healthy until 150 days in milk (DIM) suffered from CM later. To avoid the loss of information, Heringstad et al. (2004) and Zwald et al. (2006) suggested dividing lactations into shorter intervals. Heringstad et al. (2004) reported the advantages of shorter intervals in the possibility of taking multiple episodes of CM and their time aspects into account. This type of model also reduces the bias from culling cows, and incomplete lactations in different stages of progress can be included in the analysis. The estimates of genetic correlations between different lactation stages ranged from 0.37 to 0.73 in Heringstad et al. (2004) for early lactation in Norwegian Red cows and from 0.26 to 0.64 in the study of Zwald et al. (2006) for US Holstein cows, who also claimed that mastitis in early lactation has a low correlation with mastitis during mid or late lactation. In contrast to those studies, Koeck et al. (2010b) found the genetic correlation of liability to CM between two intervals in the early part of lactation to be close to unity. Additionally, Zavadilova et al. (2017)

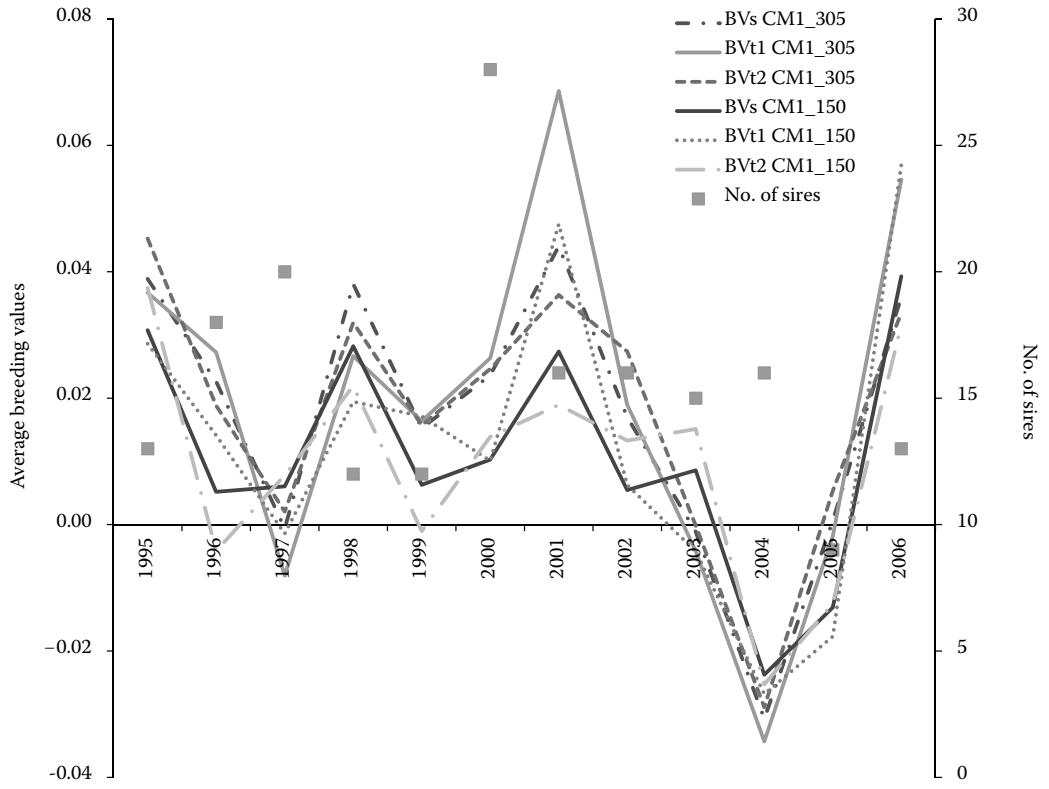

Figure 2. Genetic trends of clinical mastitis (CM) as a binary trait in Holstein sires with at least 15 daughters according to their birth year with the number of sires per year on the secondary axis

BVs CM1_305 – repeatability model, CM as a binary trait recorded during the whole lactation period; BVt1 CM1_305 – bivariate model, CM as a binary trait recorded in the whole 1st lactation; BVt2 CM1_305 – bivariate model, CM as a binary trait recorded in the whole 2nd and later lactations; BVs CM1_150 – repeatability model, CM as a binary trait recorded in the first 150 days in milk; BVt1 CM1_150 – bivariate model, CM as a binary trait recorded in the first 150 days in milk of the 1st lactation; BVt1 CM1_150 – bivariate model, CM as a binary trait recorded in the first 150 days in milk of the 2nd and later lactations

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found genetic correlations between the first 100 days of lactation and the whole lactation period to be close to 1, which suggests that records of CM in the first part of lactation could successfully replace data from the whole lactation period.

Our rank correlations were also stronger between sires with BVs and BVt2 for CM during the 2nd and later lactations (0.95–0.98) compared to BVs and BVt1 for CM during the 1st lactation (0.88–0.96), which reflects genetic differences between the 1st and later lactations.

Rank correlations between sires were also stronger when breeding values were predicted for CM1 (binary trait) compared to CM2 (number of cases) in the first 150 DIM. However, defining CM as a binary trait can underestimate the susceptibility of cows to CM because there is no distinction among cows with 1 versus multiple CM cases (Wolf et al. 2010).

Genetic trends. The genetic trends based on average EBVs of sires and cows for CM as a binary trait according to their birth year are plotted in Figures 2–3. The genetic trends for both categories varied between years. The values are also affected by small numbers of sires per year. In cows, these values reflect, to a certain degree, the process of Holstein cattle breeding. As summarised by Miglior et al. (2017), selection indices in major dairy countries showed great changes in recent decades, when emphasis turned from production traits towards fertility and health, as selection for milk production had negative effects on both. We can see the same trend in the Czech Republic. Selection and breeding of Holstein was originally focused on production traits, with the average milk yield per cow doubling between 1990 and 2010 (from 4301 kg to 8912 kg of milk per lactation). The composite selection index (SIH)

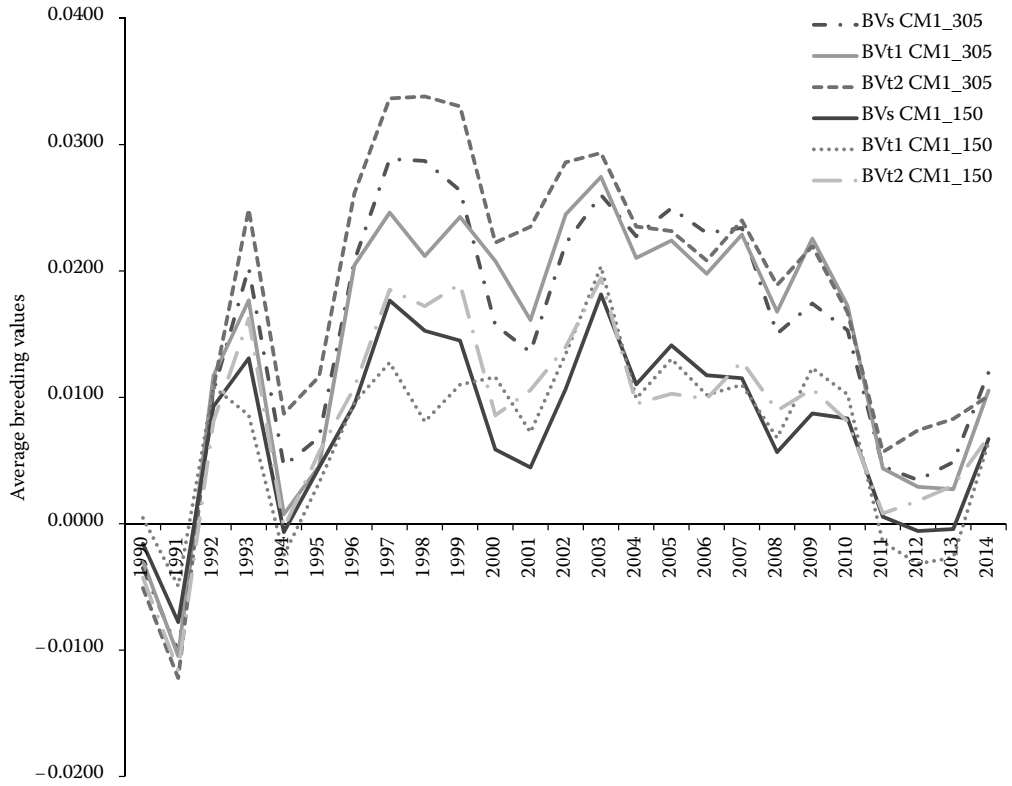

Figure 3. Genetic trends of clinical mastitis (CM) as a binary trait in Holstein cows according to their birth year
BVs CM1_305 – repeatability model, CM as a binary trait recorded in the whole lactation period; BVt1 CM1_305 – bivariate model, CM as a binary trait recorded in the whole 1st lactation; BVt2 CM1_305 – bivariate model, CM as a binary trait recorded in the whole 2nd and later lactations; BVs CM1_150 – repeatability model, CM as a binary trait recorded in the first 150 days in milk; BVt1 CM1_150 – bivariate model, CM as a binary trait recorded in the first 150 days in milk of the 1st lactation; BVt1 CM1_150 – bivariate model, CM as a binary trait recorded in the first 150 days in milk of the 2nd and later lactations

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was introduced in 2004 and consisted of the production (65%), fertility (10%), and exterior (25%) of the cattle. Somatic cells were integrated into the index in 2006, with 5% of the weighting, and the weighting of production was reduced. Another important change in weightings in favour of functional traits came in 2008, with production reduced to 49%; exterior traits 25%; daughters' fertility 12%; functional longevity 7%; and udder health 7%, as described in the "Breeding program of Holstein cattle" in March 2012. The average EBVs for CM traits declined slowly to neutral values for cows born after 2003, which could be related to the extension of breeding objectives. Although CM traits are not included in the selection index, their EBVs may reflect the presence of genetically correlated indicator traits, such as SCS and udder type traits. However, the EBVs averages stay above the neutral value, which means the permanent deterioration of genetic disposition for resistance to CM. Govignon-Gion et al. (2016) described a similar trend in Holstein, where mastitis resistance declined rapidly in 1990 as a result of strong selection for production. The implementation of somatic cell count (SCC) evaluation in 1997 and its inclusion in the total merit index in 2001 had a favourable, but not sufficient effect on mastitis, as the genetic correlation between SCC and CM is far from being complete. As mentioned by Heringstad et al. (2000), SCC and CM are both an indication of udder health, though they are genetically different traits. High SCC reflects better subclinical cases of mastitis, but their measurements in test-day intervals cannot capture short-term, acute cases of CM. In contrast, CM traits ignore subclinical cases of mastitis. The selection for CM acts on all biological processes that improve mastitis resistance. In contrast, the low value of SCC may indicate both the resistance and susceptibility of a cow to mastitis, as somatic cells play an important role in udder defence mechanisms. Therefore, the combination of information on SCC and CM helps increase the accuracy of evaluation (Negussie et al. 2006) and efficiency of selection for udder health (Carlen et al. 2004).

On the other hand, studies from Nordic countries, where the selection for health traits is well-developed and long-term, have shown that genetic selection results in favourable genetic trends. For example, Eriksson et al. (2017) described the genetic trends of health traits in Swedish Red cows with the 1st and 2nd lactations between 1990 and 2007 and found neutral to favourable genetic trends for CM. Heringstad et al. (2004) reported that the trend for CM in Norwegian Red sires was relatively flat in the beginning, with little or no genetic change from 1976 to 1986 but a decreasing trend for CM afterwards, with favourable genetic change. The first breeding values for CM were calculated in 1978 in Norway and in 1984 in Sweden. CM traits are included in the total merit indices in both countries as a part of the udder health index together with SCC.

CONCLUSION

The presented procedures for the evaluation of breeding values for CM traits are not interchangeable. The evaluation of CM traits based on the first 150 days of lactation is possible without the substantial loss of variation. Prediction of breeding values with the support of a bivariate model better reflects the different genetic nature of the 1st lactation compared to later lactations. Including CM among breeding objectives would enable better targeted and more precise selection of Czech Holstein for CM resistance without a reduction in the rate of progress for production traits.

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