GENOMIC BREEDING VALUES FOR CLAW DISEASES/DISORDERS IN CZECH HOLSTEIN COWS

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Abstract

Genomic breeding values (GEBV) were predicted for claw diseases/disorders in Holstein cows. The data sets included 6,498, 6,641 and 16,208 cows for the three groups of analysed disorders. The analysed traits were infectious diseases (ID), including digital and interdigital dermatitis and interdigital phlegmon, and non-infectious diseases (NID), including ulcers, white line disease, horn fissures, and double sole and overall claw disease (OCD), comprising all recorded disorders. Claw diseases/disorders were defined as 0/1 occurrence per lactation. Linear animal models were employed for prediction of conventional breeding values (BV) and genomic breeding values (GEBV), including the random additive genetic effect of animal and the permanent environmental effect of cow and fixed effects of parity, herd, year and month of calving. Both high and intermediate weights (80% and 50%, respectively) of genomic information were employed for GEBV50 and GEBV80 prediction. The estimated heritability for ID was 3.47%, whereas that for NID 4.61% and for OCD was 2.29%. Approximate genetic correlations among claw diseases/disorders traits ranged from 19% (ID x NID) to 81% (NID x OCD). The correlations between predicted BV and GEBV50 (84–99%) were higher than those between BV and GEBV80 (70–98%). Reliability of breeding values was low for each claw disease/disorder (on average, 3.7 to 14.8%) and increased with the weight of genomic information employed.

Keywords: dairy cattle, foot and claw disorders, heritability, genomic breeding values, Holstein breed

INTRODUCTION

Claw diseases/disorders are possible candidates for improvement by selection due to their negative influence on production, reproduction and culling of cows; the welfare of the animals; and the economic success of farms (Egger-Danner *et al.*, 2013; van der Spek, 2015; Heringstad *et al.*, 2018; Alvergnas *et al.*, 2019). Low incidence of claw diseases/disorders can be accomplished by management practices, but genetic changes in animals by selection are advantageous because positive changes are transmitted between generations. Sufficient genetic variability as a condition of successful genetic selection was confirmed in cases by Buch *et al.* (2011), Chapinal *et al.* (2013) and Pérez-Cabal and Charfeddine (2015). In the Czech Republic, the analysis of genetic parameters has been done by Zavadilová *et al.* (2018). The economic importance of claw diseases as breeding objectives was analysed by Krupová *et al.* (2018).

A single-step procedure for genomic evaluation was developed by Misztal *et al.* (2009), Christensen and Lund (2010) and Legarra and Ducrocq (2012), combining all sources of information on target animals to directly predict genomic breeding values. This procedure directly predicts genomic values through consideration of production records and pedigree databases along with genomic information. Přibyl *et al.* (2012) tested the single-step procedure for the genetic prediction of production traits in Czech Holstein cattle.

The aim of this study was to predict genomic breeding values for claw diseases/disorders recorded in the Czech Republic and to compare resulting conventional and genomic breeding values when high and intermediate weights (80% and 50%) of genomic information are employed.

MATERIALS AND METHODS

Data Description and Editing

The raw data set consists of 49,305 lactations of 40,611 cows with 19,888 diagnoses recorded from 89 farms. Data were obtained by the national cattle health monitoring system "The Diary of Diseases and Medication" (The Diary) (Kašná *et al.*, 2017). In the Czech Republic, this recording system was implemented in August 2018 after a one year trial period. It consists of on-line health recording form for farmers and a simplified key for diagnoses based on ICAR recommendations (ICAR Claw Health Atlas (Egger-Danner *et al.*, 2015)). Records of claw diseases/disorders were gathered during both regular and emergency visits of trimmers to the farms.

The SAS software package, version 9.4 (SAS, 2012) was used to perform data editing and calculation of correlations and basic statistics. Only cows with 75% or greater Holstein breed were included. Three groups of claw disorders were defined: infectious diseases (ID), including digital and interdigital dermatitis and interdigital phlegmon; non-infectious diseases (NID) including ulcers, white line disease, horn fissures, and double sole; and overall claw disease (OCD). These categories comprised all recorded claw disease and disorders plus lameness.

The incidence of claw diseases/disorders is reported in Tab. I.

For each of the three analysed groups of diseases/disorders a separate dataset was created because of differences in monitoring of claw disease among herds. For each particular trait, a herd was omitted when the lactation incidence rate (LIR) of the trait was less than 2%.

$$\text{LIR(\%)} = \text{number of affected lactations} \times$$
$$\times\ 100/\text{number of lactations.} \tag{1}$$

The final numbers of herds assigned for analysis was 13 (ID), 14 (NID) and 35 (OCD). The increase in the number of herds selected for analysis of OCD was caused by counting of lameness (26% of records of OCD) that together with ID and NID records comprised OCD. After editing, the data sets included 6,498, 6,641 and 16,208 cows for the three groups of analysed disorders. The descriptive statistics for the dataset are reported in Tab. II.

Linear Model for Data Analysis

A univariate linear animal model was employed to estimate heritability and subsequent prediction of breeding values for foot and claw diseases/disorders. The model equation was:

$$y_{ijklm} = \text{parity}_i + \text{herd}_j + \text{month-year}_k +$$
$$+\ \text{pe}_l + a_m + e_{ijklm}, \tag{2}$$

where y_{ijklm} is the analysed trait: ID, NID, OCD defined as 0/1 occurrence per lactation, in period from calving to 305 days in milk (DIM); parity_i is the effect of parity class i (5 levels, first, second, third, fourth, five and higher parity); herd_j is the effect of

I: *The number of claw diseases/disorders, total and most frequent diseases/disorders (Holstein cows)*

Trait/Diagnosis	No. of records	No. of cows	Ratio of cow with 1 record	Maximum no. of records per cow
ID in total	1101	902	83%	6
Digital/interdigital dermatitis	581	464	81%	6
Interdigital phlegmon	465	411	89%	5
NID in total	1678	999	67%	11
Ulcers	1600	975	70%	11
OCD in total	4110	2561	71%	15
Lameness	1087	811	83%	6

II: *The descriptive statistics for the datasets*

Trait	No. of cows with data	No. of lactations	LIR*	No. of sires of cows with data
Infectious diseases	6 498	7 272	8.24%	810
Non-infectious disorders	6 641	7 481	11.76%	859
Overall claw disorders	16 208	18 385	10.00%	1 641

*lactation incidence rate

herd j (13 (ID), 14 (NID) and 35 (OCD) levels); month-year$_k$ is the effect of calving month-year k (8 levels); pe$_l$ is the random permanent environmental effect on a cow; a$_m$ is the random additive genetic effect of cow m; and e$_{ijklm}$ is the random residual effect.

The model equation was the same for each foot and claw diseases/disorders trait, for both conventional as well as genomic prediction.

For prediction of genomic breeding values, a single-step procedure was applied (Aguilar *et al.*, 2010, Christensen and Lund, 2010). A genomic relationship matrix G was calculated according to deviations from the averages of observed allele frequencies and standardized using division by the average value of the diagonal of G, so that average of diagonal elements = 1 (Forni *et al.*, 2011), and transformed so that the elements of an additive pedigree relationship matrix for genotyped animals A22 and elements of G have the same average (Vitezica *et al.*, 2011). Two weights, 80% and 50%, of the genomic relationship were employed. Resulting predictions included conventional breeding values (BV), genomic breeding values with 50% genomic relationship included (GEBV50) and those with 80% genomic relationship included (GEBV80). The relative breeding values in % for BV, GEBV50 and GEBV80 were calculated using a reference level derived from sires born in 2010 (mean) and SD = 12. Higher relative breeding values mean a higher required value for a trait, for example, higher resistance to particular claw disease/disorder. The reliability of each breeding value was calculated using the standard error of prediction and additive variance for particular traits.

The pedigree file contained 25,446 (ID), 36,092 (NID), and 49,700 (OCD) records (4 generations). The genotyped animals were chosen according to pedigree. A detailed account of the allocation of genotyped animals is presented in Tab. III.

The genotypic data were edited both by animal and by loci. Animals with genotype call rates < 95% were excluded from further evaluation. SNPs were discarded if more than 5% of SNP calls were missing. The procedure used for selecting SNPs was described by Přibyl *et al.* (2012). The Illumina BovineSNP50 BeadChip V2 (Illumina Inc., San Diego, USA) was used for preparation of a genomic relationship matrix (G). Initial no. of SNP 54 609. The effective no. of SNP was 39 537.

Data were analysed using the DMU package (Madsen and Jensen, 2010). Genetic correlations between traits were approximated using

correlations between predicted breeding values using Proc corr in Software packages SAS, version 9.4 (2012, SAS).

RESULTS AND DISCUSSION

Monitoring of Claw Diseases/Disorders

Because of the relatively short period of data collection (8 months) the database of health traits was small. There were substantial differences between farms in their approaches to monitoring herd health. Omitting herds with low LIR, we obtained our data from farms that employ regular health monitoring. The ID trait was mostly represented by dermatitis and necrobacillosis and NID by ulcers (see Tab. I). A sizeable proportion of OCD records (26%) were included due to lameness (see Tab. I). Lameness is very general disorder with a number of different causes. It is an indicator of claw and leg problems and is a reasonably proper part of OCD. We conclude that such diagnoses as lameness, dermatitis digitalis and interdigitalis, necrobacillosis and ulcers are most important for the genetic evaluation of health traits in the Czech Republic. Pérez-Cabal and Charfeddine (2015) stated that six infectious and non-infectious claw disorders are monitored in Spanish Holstein cows: dermatitis, sole ulcer, white line disease, interdigital hyperplasia, necrobacillosis, and chronic laminitis, and that this same grouping of claw diseases/disorders according their causes was used by van der Spek (2015).

Lactation Incidence Rates for Claw Diseases/Disorders

LIR were similar for each analysed trait (ID 8.24%, NID 11.76%, and OCD 10.00%.) This is less than the 40 to 70% reported in recent studies (Sogstad *et al.*, 2005; Buch *et al.*, 2011; Chapinal *et al.*, 2013; van der Spek, 2015). In Czech Holsteins, Krpálková *et al.* (2019) reported LIRs greater than 50%. In our study, the low values are probably caused by the short period of monitoring, low number of farms involved and inconsistency of recording among farms. Zavadilová *et al.* (2018) reported higher LIRs of 28.61% for ID, 27.15% for NID and 52.56% for overall claw diseases. Both Krpálková *et al.* (2019) and Zavadilová *et al.* (2018) analysed data from the same source, different from the data sources used in the present study.

III: *Number of genotyped animals*

Trait	No. of sires	No. of females	No. of cows with data
Infectious disease	1 444	507	391
Non-infectious disorders	1 602	552	439
Overall claw disorders	1 984	833	626

Variance and Heritability for Claw Diseases/Disorders

The estimated variances and heritabilities for claw disorders are presented in Tab. IV. Heritability for INF was 3.47%, whereas those for NID and OCD were 4.61% and 2.29%, respectively.

These estimates are in agreement with the literature but lower than those estimated by Zavadilová *et al.* (2018) for Czech Holsteins. Buch *et al.* (2011) reported heritabilities between 3 and 5% for particular diseases. Heritability estimates by Chapinal *et al.*, (2013) were 9.2% for infectious diseases and 4.5% for non-infectious diseases. Using a linear model, Pérez-Cabal and Charfeddine (2015) estimated heritability at 5% for overall claw diseases. Zavadilová *et al.* (2018) calculated heritabilities of 13.84% for overall claw diseases/disorders, 12.64% for non-infectious disorders and 9.83% for infectious diseases. In this study, the low values of heritability can be explained by the narrow extent of the dataset and the short time of monitoring for claw diseases/disorders. Estimates of heritability should rise both in percentage value and statistical significance in proportion to increases in the number of monitored herds and with provision of an equal chance for every cow to be monitored during its entire period of lactation.

Breeding Values and their Reliability

The descriptive statistics for breeding values and their reliabilities are presented in Tabs. V, VI and VII.

The impact of genomic information was evident, especially with regards to reliability of breeding values for each analysed trait. For each claw disease/disorder, reliability increased with the amount of genomic information employed. Because this suggestion holds for each trait as well as each group of animals presented in Tabs. V, VI and VII we assumed that the main reason for this phenomenon was the genomic information. The increase in reliability is proportional to the amount of genomic information employed. The increase in reliability due to the amount of genomic information is usually explained by increased accuracy of the relationship matrix. Between analysed claw diseases, the greatest increase occurred for non-infectious disease (8.3% for cows with records). This is less than results typically found in the literature (Aquilar *et al.*, 2010; Přibyl *et al.*, 2012).

Other than this trend in reliability, there is no systematic change in means, standard errors, maximums and minimums for breeding values that could be correlated with increases in genomic information. For infectious claw disease the means for breeding values and their SDs decreased, for non-infectious claw diseases/disorders the means

IV: *Estimates of heritability for claw diseases/disorders*

	Infectious disease	Non-infectious disorders	Overall claw disorders
Additive variance	0.0025 ±0.0011*	0.0035 ±0.0012**	0.0019 ±0.0006**
Variance of permanent environment	0.0119 ±0.0030**	0.0010 ±0.0030	0.0023 ±0.0021*
Residual variance	0.0580 ±0.0029**	0.0714 ±0.0031**	0.0775 ±0.0022**
Heritability	3.47% ±0.068**	4.61% ±0.073**	2.29% ±0.037**

*P < 0.05
**P < 0.01

V: *Descriptive statistics for relative breeding values (%) for infectious claw disease*

Breeding values	No.	Mean	SD	Min.	Max.	Mean of reliability	SD of reliability
			Cows with records				
Conventional	6498	101.3	14.34	28.1	147.9	11.3	3.79
Genomic 50%	6498	99.5	13.67	28.8	142.9	12.4	4.04
Genomic 80%	6498	98.8	13.72	27.8	141.2	13.2	4.19
			Genotyped sires				
Conventional	1444	101.3	11.08	29.5	157.6	7.6	9.59
Genomic 50%	1444	99.5	10.84	29.7	155.3	7.4	10.75
Genomic 80%	1444	98.7	11.47	28.4	155.5	8.4	11.47
			Genotyped cows and heifers				
Conventional	507	102.7	13.41	50.0	141.4	9.1	4.47
Genomic 50%	507	100.7	12.48	52.2	134.6	10.5	5.49
Genomic 80%	507	99.8	12.65	52.7	134.0	12.0	6.14

VI: *Descriptive statistics for relative breeding values (%) for non-infectious claw disease*

Breeding values	No.	Mean	SD	Min.	Max.	Mean of reliability	SD of reliability
Cows with records							
Conventional	6641	94.3	19.83	8.7	177.3	6.5	3.66
Genomic 50%	6641	95.2	19.13	14.0	174.8	12.0	3.91
Genomic 80%	6641	96.1	19.39	14.6	176.0	14.8	4.14
Genotyped sires							
Conventional	1602	93.5	17.33	-11.2	188.8	3.7	10.00
Genomic 50%	1602	94.6	17.22	-2.5	188.6	6.1	11.69
Genomic 80%	1602	95.4	17.96	0.4	191.1	8.4	12.92
Genotyped cows and heifers							
Conventional	552	96.2	13.72	47.7	132.7	4.3	4.56
Genomic 50%	552	96.7	13.51	48.9	132.2	9.5	5.73
Genomic 80%	552	97.3	14.34	46.3	135.5	12.7	6.50

VII: *Descriptive statistics for relative breeding values (%) for overall claw disorders*

Breeding values	No.	Mean	SD	Min.	Max.	Mean of reliability	SD of reliability
Cows with records							
Conventional	16208	104.1	12.26	39.6	153.5	10.9	3.97
Genomic 50%	16208	100.6	11.99	40.3	151.8	11.5	4.11
Genomic 80%	16208	99.1	12.16	40.2	151.8	12.2	4.22
Genotyped sires							
Conventional	1876	103.1	11.37	35.2	159.3	9.3	10.54
Genomic 50%	1876	98.5	12.28	36.4	155.8	9.8	11.51
Genomic 80%	1876	96.5	13.41	36.7	153.8	11.6	12.27
Genotyped cows and heifers							
Conventional	803	104.3	11.53	58.2	138.3	9.3	4.83
Genomic 50%	803	99.9	11.52	56.7	136.5	10.5	5.70
Genomic 80%	803	97.9	12.21	55.4	135.8	12.3	6.26

for breeding values increased but their SDs did not change, and for overall claw diseases the means for breeding values decreased and their SDs increased with amount of genomic information employed; therefore, genomic information influenced each trait according to genetic control of that trait. Differences between infectious and non-infectious claw diseases are obvious. Dissimilarity in OCDs is caused by inclusion of lameness (26%), a trait that is constituted apart from infectious and non-infectious diseases due to it being a very general trait with many causes.

The correlations between BV and GEBV50 (84–99%) were higher than those between BV and GEBV80 (70–98%) as seen in Tab. VIII. Although the majority of correlations between these types of genomic breeding values are 99% the correlations to conventional breeding values are different. Generally, GEBV80 showed lower correlations with BV then GEBV50. In any case, if the number

of animals in a group is high (Tab. VIII, Cows with records) then the correlations between BV and genomic breeding values approach 99%.

Genetic Correlations between Claw Diseases/Disorders

The approximate genetic correlations among claw health traits ranged from 19% (ID x NID) to 81% (NID x OCD), see Tab. IX. Those between infectious and non-infectious claw diseases were low especially based on the breeding values of sires (from 19% to 26%). This is in agreement with the literature when genetic correlations between those traits were estimated directly by multi trait linear models. Genetic correlations between infectious claw diseases and non-infectious disorders were lower than 23% (Buch *et al.*, 2010). A low genetic correlation between infectious diseases and horn lesions (8%) was reported by Chapinal *et al.* (2013). Zavadilová *et al.* (2018) estimated 18%.

VIII: *Correlations between conventional breeding values (BV) and genomic breeding values with 50% (GEBV50) or with 80% (GEBV80) of genomic information employed for analysed claw diseases/disorders*

		No.	BV x GEBV50 (%)	BV x GEBV80 (%)	GEBV50 x GEBV80 (%)
Infectious disease	Cows with records	6498	99	98	99
	Genotyped sires	1444	94	87	98
	Genotyped cows and heifers	507	96	91	99
Non-infectious disease	Cows with records	6641	99	98	99
	Genotyped sires	1602	97	93	99
	Genotyped cows and heifers	552	95	88	99
Overall claw disorders	Cows with records	16208	98	95	99
	Genotyped sires	1876	91	83	98
	Genotyped cows and heifers	803	94	86	98
	Genotyped heifers	177	84	70	98

IX: *Approximation of genetic correlations between analysed claw diseases/disorders using correlations between predicted breeding values*

	Breeding value	No.	ID x OCD (%)	NID x OCD (%)	ID x NID (%)
Sires	Conventional	292	48	66	29
	Genomic 50%	422	49	71	27
	Genomic 80%	498	48	63	19
Cows and heifers	Conventional	896	66	81	46
	Genomic 50%	2470	61	81	40
	Genomic 80%	3024	60	80	36

CONCLUSION

Although our heritability estimates were low, claw health traits showed enough genetic variance to hopefully allow genetic selection of Holsteins cows for high susceptibility to claw disease/disorders. The estimates of breeding values will benefit from utilization of genomic information especially in single-step genomic evaluation.

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