Genomic Evaluation for Foot and Claw Disorders in Czech Holstein

L. Zavadilová[1], E. Kašná[1], J. Kučera[2], S. Šlosárková[3], P. Fleischer[3] and J. Bauer[2]*

[1] *Institute of Animal Science, Přátelství 815, 104 00 Prague 10, Czech Republic*

[2] *Czech Moravian Breeders' Corporation, Inc., Hradištko pod Medníkem, Czech Republic*

[3] *Veterinary Research Institute, Hudcova 296/70, 621 00 Brno, Czech Republic*

Abstract

Genomic breeding values (GEBV) for resistance to foot and claw disorders (CD) have been estimated using a multi-trait model comprising linear type traits and single-step GBLUP. Infectious digital disorders (IDD) included dermatitis digitalis and interdigitalis, interdigital phlegmon, and heel horn erosion; claw horn lesions (CHL) included ulcers, white line disease, horn fissure, and double sole; overall claw disorders (OCD) comprised all the recorded CD. Datasets for IDD, CHL and OCD included 40,859; 25,143; 57,567 Holstein cows and 71,219; 44,265; 100,903 lactations with a lactation incidence rate of 13.3%; 12.5%; 17.0%, respectively. Cows calved between 2017 and 2021 in 46 (IDD), 30 (CHL), and 64 (OCD) herds, respectively. CD traits were binary with 0 (no CD) and 1 (at least one CD) during lactation. Linear type traits were foot angle (IDD, CHL), rear leg set (side view) (CHL), feet & legs score (CHL, OCD), and locomotion (IDD, CHL, OCD). Linear model equations included the random additive genetic effect of animal, and for CD traits, fixed effects of parity and age at calving class, herd-year-season of calving and random effect of the permanent environmental effect of a cow; for linear type traits included fixed effects of herd-year-season of scoring, classifier and linear and quadratic regression on the age at calving and the days of scoring. Pedigree involved 102,862, 72,921, and 130,354 animals. Number of genotyped animals was 12,959; effective SNP 36,520; effective animals 12,672. Variance and covariances in the multi-trait model prediction yielded heritabilities 0.09 foot angle, 0.12 rear leg set (side view), 0.09 feet & legs score, 0.11 locomotion, 0.07 IDD, 0.08 CHL, 0.04 OCD; genetic correlations between IDD and foot angle 0.23, locomotion -0.30, between CHL and foot angle -0.33, locomotion -0.22, rear leg set (side view) 0.21, feet & legs score -0.28, between CHL and locomotion -0.42, feet & legs score -0.27. For young genomic bulls (n=186), average reliability of GEBV: for IDD 0.24 (0.14 to 0.34); for CHL 0.20 (0.10 to 0.27); for OCD 0.26 (0.15 to 0.35).

Keywords: Genomic breeding values, multi-trait linear model, single-step genomic evaluation, foot and claw disorders, exterior, Holstein cow

Introduction

Foot and claw disorders are a foremost welfare problem in dairy cattle (Krpálková et al. 2019). They often caused pain, lameness, decreased production, and reduced reproduction (Charfeddine & Pérez-Cabal 2017). Not surprisingly, they are associated with high costs and have been identified as the third most costly disease in dairy farming after mastitis and fertility problems (Green et al. 2002).

Although improving claw health can be achieved through better herd management, the most important is to change the genotype of cows through selection because it is a permanent solution lasting over generations.

Until recently, the selection for improving claw health in the Czech Republic was attended indirectly by feet and leg type traits in selection indices (Krupová et al. 2019). However, it has been shown that there are low correlations between exterior traits and foot and claw disorders (Van der Waaij et al. 2005), which, therefore, do not allow effective and optimal selection progress in claw health

The direct selection, generally more effective, for claw health traits was enabled because a source of information on the phenotypes of claw diseases appeared in Czechia. In 2017, the national cattle health

monitoring system "The Diary of Diseases and Medication" web application was implemented (Kašná et al. 2017). This recording system consists of farmers' online health recording form and a key of diagnoses based on ICAR recommendations. The arising databases are usable in genetic evaluation for several cattle health traits.

Multi-trait linear mixed models are often employed to estimate genomic breeding value for claw disorders, possibly combining the multiple disorders in one multi-trait analysis (Machioldi et al. 2020). The single-step genomic method proved successful in genetic evaluation (Misztal et al. 2020). In the Czech Republic, it is used in the routine evaluation of many traits in Holstein cattle (Přibyl et al. 2012). We also suggest using it as a proven method for the health traits.

This study aimed to present the genomic breeding value estimation method for foot and claw disorders in Czech Holstein cattle that employed a multi-trait linear model and the single-step genomic BLUP.

Materials and Methods

Data

Datasets for IDD, CHL and OCD consist of 40,859; 25,143; 57,567 Holstein cows and 71,219; 44,265; 100,903 lactations with a lactation incidence rate of 13.3%; 12.5%; 17.0%, respectively. Cows calved between 2017 and 2021 in 46 (IDD), 30 (CHL), and 64 (OCD) herds, respectively.

Holstein Cattle Breeders Association of the Czech Republic and the Czech and Moravian Breeding Corporation provided health traits, linear type traits, and genomic data, including pedigree.

The foot and claw data

Foot and claw disorders (CD) records were gathered by farmers and registered voluntarily in the national cattle health monitoring system "The Diary of Diseases and Medication". The health records are unified with ICAR diagnoses. Three group traits of CD were defined according to the aetiology of disorders: infectious digital disorders (IDD), including digital and interdigital dermatitis; interdigital phlegmon and heel horn erosion; claw horn lesions (CHL), including ulcers, white line disease, horn fissures, and double sole; and overall claw disorders (OCD) comprising all the recorded disorders. Separate analyses were made for each of these CD group traits. Similarly, Buch et al. (2011) analysed the CD disorders according to aetiology.

The linear type

The linear type trait datasets included foot angle, rear leg set (side view), locomotion as scored traits (1 to 9 points), and feet & legs in %. Cows were scored for the exterior in the first parity between the 30^{th} and 210^{th} day in milk. The linear type traits were chosen for adding to the multi-trait genomic evaluation of the specific CD group trait according to the values of genetic correlation to the CD group trait: foot angle (IDD, CHL), rear leg set (side view) (CHL), feet & legs score (CHL, OCD), and locomotion (IDD, CHL, OCD).

Genetic parameters

Genetic parameters for CD and linear type traits have been estimated in separate analyses preceding genomic evaluation.

First, the genetic correlations have been set between linear type traits and CD group traits by bivariate analyses.

Table 1. Heritability and repeatability for CD group traits and linear type traits.

Trait	Heritability	Repeatability
Infectious digital disorders	0.07	0.14
Claw horn lesions	0.08	0.16
Overall claw disorders	0.04	0.22
Rear leg set (side view)	0.12	
Foot angle	0.09	
Locomotion	0.11	
Feet & legs score	0.09	

The variance-covariance matrices were estimated by multi-trait animal model analysis, each formed by one of CD group traits and chosen linear type traits. The heritability and repeatability of analysed traits employed in the genomic analysis are in Table 1. The estimated genetic correlations between CD group traits and linear type traits are in Table 2.

Table 2. Genetic correlations between CD group traits and linear type traits.

Trait	Infectious digital disorders	Claw horn lesions	Overall claw disorders
Rear leg set (side view)		0.21	
Foot angle	0.23	-0.33	
Locomotion	-0.22	-0.30	-0.42
Feet & legs score		-0.28	-0.27

The genomic data and method

Animals were genotyped using the Illumina BovineSNP50 Bead chip (Illumina, San Diego, CA, USA).

For the prediction of genomic breeding values, a single-step procedure was applied (Aguilar et al. 2010; Christensen & Lund, 2010) with 12,959 genomic animals: 5,374 bulls and 5,856 (IDD); 5,439 (CHL); 7,354 (OCD) cows with CD phenotype; a total number of effective SNPs used in the calculation of G matrix was 36,520; effective animals 12,672.

Description of model equations

The following linear animal model was used to estimate genetic parameters and genomic breeding values for CD group traits in multi-trait genomic analysis:

y_{ijklm} = parity_agegroup$_i$ + herd_year_season$_j$ + PE_k + A_l + e_{ijkl},

where y_{ijkl} is the CD group trait: IDD, CHL, OCD, 0/1 occurrence per lactation; parity_agegroup$_i$ is the effect of parity combined with age at calving class (15 levels: first, second, third, fourth, and five and higher parity; 3 classes of age at calving per parity); herd_year_season$_j$ is the combined effect of herd (46 (IDD), 30 (CHL), and 64 (OCD) levels); of calving year (2017-2021 levels) and calving season four levels: January–March, April–June, July–September, and October–December); PE_k is the random permanent environmental effect of cow across parity (40,856 (IDD); 25,143 (CHL); 57,567 (OCD)); A_l is the random additive genetic effect of animal (number of animals in pedigree: 102,862 (IDD); 72,921 (CHL); 130,354 (OCD)), and e_{ijkl} is the random residual effect.

The following linear animal model was used to estimate genetic parameters and genomic breeding values for linear type traits in multi-trait genomic analysis:

y_{ijkl}= herd_year_season$_i$ + classifier$_j$ + β_1 age$_k$ + β_2 age$_k$ + γ_1 dim$_l$ + γ_2 dim$_l$ + A_k + e_{ijkl},

where y_{ijkl} is analysed linear type trait (foot angle, rear leg set (side view), locomotion as scored traits (one to nine points), and feet & legs in %.); herd_year_season$_i$ is the fixed combined effect of herd, year and season of scoring; classifier$_j$ the fixed effect of the classifier. The model included the linear and quadratic regressions on age at calving $\beta_1$age$_k$; $\beta_2$age$_k$ and the linear and quadratic regressions on days in milk at scoring $\gamma_1$dim$_l$; $\gamma_2$dim$_l$; A_k is the random additive genetic effect of animal and e_{ijkl} is the random residual effect.

Software employed

The basic editing and preparation of datasets, processing of results and basic statistical evaluation were carried out by the SAS 9.4 programme) (SAS, 2016. Program package BLUPF90 (Misztal et al. 2018) was used to estimate genetic parameters and genomic breeding values.

Results & Discussion

The heritability of the analysed traits, see Table 1, including their genetic correlations with the type traits, correspond to commonly published values (Heringstad et al. 2018). The heritability of health traits was lower than those chosen linear type traits. The high values of repeatability occurred for the analysed health traits. These findings are following Van der Waaij et al. (2005).

The linear type traits chosen to be included in the multi-trait genomic evaluation with the CD group trait showed at least a genetic correlation over 0.2, see Table 2. The estimated genetic correlations were different between the CD group traits, confirming the etiological differences between the CD group traits. While locomotion was an important indicator for all CD group traits, foot angle showed an opposite relationship with IDD or CHL. These results agree with Chapinal et al. (2013). Genetic correlation between foot angle and IDD indicated that the higher genetic predisposition for IDD is connected with a genetic disposition for steep foot angle, while the higher genetic predisposition for CHL is connected with a genetic predisposition for low foot angle. As Pérez-Cabal and Charfeddine (2016) stated, infectious foot and claw disorders, for example, digital dermatitis, are not strongly affected by the foot exterior. However, our analysis found low to moderate genetic correlations between CD group traits and the type traits, similar to what Chapinal et al. (2013) estimated.

The mean values of breeding values for CD traits and their standard deviation are shown in Table 3. For all analysed CD group traits, the means for young genomic bulls are lower than those for all genomic bulls, which could indicate a positive genetic trend in bulls. The mean values of accuracy of breeding values and their standard deviations are shown in Table 4. The highest accuracy occurred for genomic bulls and cows with health records highlighting the importance of knowing the phenotype. In Figure 1, the accuracy is presented for genotyped animals. The accuracy is higher for genotyped cows than for genotyped bulls, probably due to more information available for cows including the phenotype. The most important is GEBV and its accuracy for young genomic bulls (n=186). Their average reliability of GEBV was for IDD 0.24 (0.14 to 0.34), for CHL 0.20 (0.10 to 0.27), and 0.26 (0.15 to 0.35). If comparing the accuracy of GEBV from the single-trait and multi-trait models, the increase is about two p.p. due to adding the type traits in the multi-trait model. The low effect of the type traits on the increase of the breeding value accuracy agrees with the findings of the small genetic correlations between CD traits and type traits and agrees with Ødegård et al. (2015).

Table 3. Average genomic breeding values for multi-trait model.

Category	No.	Mean	SD
Infectious digital disorders			
All	102,862	0.0033	0.03
Genomic bulls	5,374	-0.0022	0.05
Cows with health phenotype	40,859	0.0047	0.04
Young bulls	186	-0.0133	0.05
Claw horn lesions			
All	72,921	0.0033	0.04
Genomic bulls	5,374	0.0011	0.05
Cows with health phenotype	25,143	-0.0037	0.04
Young bulls	186	-0.0431	0.03
Overall claw disorders			
All	130,354	0.0037	0.03
Genomic bulls	5,374	0.0012	0.04
Cows with health phenotype	57,567	0.0019	0.03
Young bulls	186	-0.0190	0.04

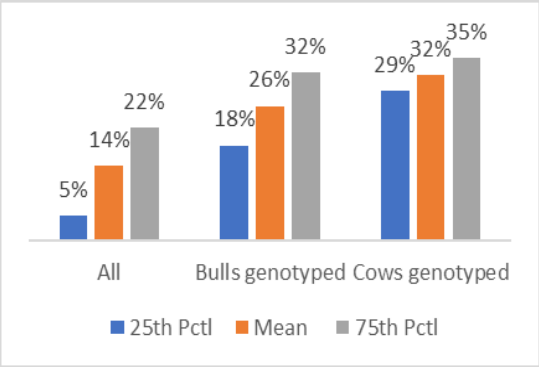

Figure 1. The accuracy of the breeding values for infectious claw disorders

However, we welcome any increase in accuracy of GEBV because the datasets of health phenotypes are small.

Table 4. Average accuracy of genomic breeding values for multi-trait model.

Category	No.	Mean	SD
Infectious digital disorders			
All	102,862	0.14	0.11
Genomic bulls	5,374	0.26	0.12
Cows with health phenotype	40,859	0.26	0.12
Young bulls	186	0.24	0.04
Claw horn lesions			
All	72,921	0.12	0.10
Genomic bulls	5,374	0.21	0.10
Cows with health phenotype	25,143	0.17	0.08
Young bulls	186	0.20	0.03
Overall claw disorders			
All	130,354	0.15	0.11
Genomic bulls	574	0.26	0.12
Cows with health phenotype	57, 567	0.21	0.08
Young bulls	186	0.26	0.04

Conclusions

We conclude that the presented method for genomic evaluation of the foot and claw disorder traits for the Holstein breed in the Czech Republic employing the multi-trait model and single-step BLUP method is feasible for genomic selection for the claw health of cows. The employed method depends closely on the structure and size of the datasets available. We assume the procedure will be adjusted depending on increasing herds and cows with foot and claw disorder records.

Acknowledgements

Supported by the Ministry of Agriculture of the Czech Republic MZE-RO0723. institutional support and project QK1910320.

References

Aguilar. I. Misztal. I. Johnson. D-L. Legarra. A. Tsuruta. S. and Lawlor. T-J. 2010 Hot topic: A unified approach to utilise phenotypic. full pedigree. and genomic information for genetic evaluation of Holstein final score. *J Dairy Sci.* 93(2). 743–752.

Buch. L. H. Sørensen. A. C. Lassen. J. Berg. P. Eriksson. J-Å. Jakobsen. J. H. and Sørensen. M. K. 2011. Hygiene-related and feed-related hoof diseases show different patterns of genetic correlations to clinical mastitis and female fertility. *J Dairy Sci*. 94(3). 1540–1551.

Chapinal. N. Koeck. A. Sewalem A.. Kelton D. F.. Mason. S. Cramer. G. and Miglior. F. 2013. Genetic parameters for hoof lesions and their relationship with feet and leg traits in Canadian Holstein cows. *J Dairy Sci* 96(4). 2596–2604.

Charfeddine. N. and Pérez-Cabal. M-A. 2017. Effect of claw disorders on milk production. fertility. and longevity. and their economic impact in Spanish Holstein cows. *J Dairy Sci* 100 (1). 653-665.

Christensen. O-F. and Lund. M-S. 2010 Genomic prediction when some animals are not genotyped. *Genet Sel Evol*. 42 (2).

Green. L-E. Hedges. V-J. Schukken. Y-H. Blowey. R-W. and Packington. A-J. 2002. The impact of clinical lameness on milk yield of dairy cows. *J. Dairy Sci*. 85(9). 2250-2256.

Heringstad. B. et al. 2018. Invited review: Genetics and claw health: Opportunities to

enhance claw health by genetic selection. J Dairy Sci. 101(6). 4801–4821.

Kašná. E. Zavadilová. L. Krupová. Z. Šlosárková. S. and Fleischer. P. 2017. Breeding values for clinical mastitis in dairy cattle. comparison of several models and traits Proc. of EAAP – 68th Annual Meeting. Tallinn.

Krpálková. L. Cabrera. V-E. Zavadilová. L. and Štípková. M. 2019. The importance of hoof health in dairy production. C*zech J Anim Sci*. 64(3). 107-117.

Krupová. Z. Zavadilová. L. Wolfová. M. Krupa. E. Kašná. E. and Fleischer. P. 2019. Udder and Claw-Related Health Traits in Selection of Czech Holstein Cows. A*nnals of Animal Science*. 19. 647-661.

Malchiodi. F. Jamrozik. J. Christen. A-M.. Fleming. A. Kistemaker. G- J. Richardson. C. Daniel. V. Kelton. D-F. Schenkel. F-S. and Miglior. F. 2020. Symposium review: Multiple-trait single-step genomic evaluation for hoof health. *J Dairy Sci*. 103(6). 5346–5353.

Misztal. I. Lourenco. D. and Legarra. A. 2020. Current status of genomic evaluation. *J Anim Sci*. 98(4). skaa101.

Misztal. I. Tsuruta. S. Lourenco. D. A. L. Masuda. Y. Aguilar. I. et al. 2018. Manual for BLUPF90 family programs. University of Georgia. Available at: http://nce.ads.uga.edu/wiki/doku.php?id=documentation

Ødegård. C. Svendsen. M. and Heringstad. B. 2015. Foot and leg conformation traits have a small effect on genomic predictions of claw disorders in Norwegian Red cows. *J Dairy Sci* 98(6). 4139–4147.

Pérez-Cabal. M. A. and Charfeddine. N. 2016. Short communication: Association of foot and leg conformation and body weight with claw disorders in Spanish Holstein cows. *J Dairy Sci*. 99(11). 9104–9108.

Přibyl. J. Haman. J. Kott. T. Přibylová. J. Šimečková. M. Vostrý. L. and Vondrášek. L. 2012. Single-step prediction of genomic breeding value in a small dairy cattle population with strong import of foreign genes. *Czech J Anim Sci*. 57(4). 151-159.

SAS (2016): Release 9.4 (TS1M1) of the SAS® System for Microsoft® Windows®. SAS Institute. Inc.. Cary. USA.

Van der Waaij. E-H. Holzhauer. M. Ellen. E. Kamphuis. C. and de Jong. G. 2005. Genetic parameters for claw disorders in Dutch dairy cattle and correlations with conformation traits. *J Dairy Sci*. 88(10). 3672-3678.