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Predictive ability of genomic breeding values for corkscrew claw in Norwegian Red

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ABSTRACT: The aim was to predict genomic breeding values (GEBV) for corkscrew claw (CSC) in Norwegian Red and to investigate whether including historical data from a correlated trait improved the predictive ability of GEBV. Corkscrew claw, the most prevalent claw disorder in Norway, has since 2004 been recorded by claw trimmers. Hoof quality (HQ), a feet and leg conformation trait recorded by breeding advisors, is a highly correlated trait to CSC. A total of 2,114 sires were included in the analyses, of which 1,074 had daughters with CSC records. A 10-fold cross-validation was used to assess predictive ability of GEBV for CSC, using daughter yield deviation as response variable. The mean predictive correlation of GEBV for CSC was 0.29 in univariate analysis, and when including HQ as a correlated trait the predictive ability increased slightly to 0.32.
Keywords: dairy cow; genomic breeding value; claw health; corkscrew claw

Introduction

Corkscrew claw (CSC) is the most prevalent claw disorder in Norway (Ødegård et al. (2013)) and will be included in the routine genetic evaluation of Norwegian Red in 2014. Recording claw health at claw trimming started in 2004 with 9 disorders, including CSC, being reported to the Norwegian Dairy Herd Recording System. Hoof quality (HQ) is a feet and leg conformation trait recorded on first parity cows by breeding advisors. Corkscrew claw from claw trimming and HQ from conformation scores are supposed to measure the same trait and an estimated genetic correlation of -0.86 between these 2 traits confirm this (Ødegård et al. (2014)). The measurement of CSC at claw trimming is probably more accurate and therefore the preferred trait to use in genetic evaluation of sires.

Accuracy of genomic breeding values (GEBV) for the feet and leg conformation traits included in the routine genetic evaluation in Norway range from 0.60 (rear leg rear view) to 0.71 (foot angle), and for HQ it was 0.65 (Svendsen et al. (2013)). There are limited historical data available for CSC, and the reference population is therefore smaller than for other traits. To still predict GEBV for CSC one may include HQ as a correlated trait to increase the number of animals in the reference population.

The aim was to perform a first genomic analysis of claw health in Norwegian Red and to compare the predictive ability of GEBV for CSC from univariate and bivariate analyses whit HQ included as a correlated trait.

Materials and Methods

An imputed 25K/54K SNP dataset, which after standard editing contained 48,249 SNP, for a total of 3,768 Norwegian Red AI sires was available. Only sires with both genotype and daughters with CSC, HQ or both traits were included in the analyses. Records of CSC obtained at claw trimming from 2004 to September 2013 were used. Data editing for CSC was as described in Ødegård et al. (2013). In addition, only sires with at least 30 daughters with claw health records were included in the analyses. A cow was defined as healthy (0) or affected (1) for CSC in each lactation with at least 1 record from claw trimming. Hoof quality from conformation scores was available from 1996 onwards. The editing was performed as described in Ødegård et al. (2014). This trait was measured on first parity cows and scored linearly on a scale from 1 to 9, where 9 was the optimum value.

A univariate analysis of CSC was performed on 271,796 records from daughters of 1,074 sires. Further, 2 bivariate analyses of CSC and HQ were performed including either HQ data from 1996 to 2013 (HQ96) with records from 298,189 daughters of 2,214 sires, or HQ data from 2004 to 2013 (HQ04) (same time period as the CSC data) including 157,334 daughters of 1,263 sires. The pedigree of the sires was traced back as far as possible and included for the univariate and the 2 bivariate models; HQ04 and HQ96, 15,003, 17,118 and 22,343 animals, respectively.

Estimated breeding values (EBV) were obtained by linear sire models using DMU (Madsen and Jensen (2010)). The models included the same effects as in Ødegård et al. (2013) and Ødegård et al. (2014).

A 10-fold cross-validation was performed to assess predictive ability of GEBV for CSC from the univariate and bivariate models. The 1,074 sires with daughter information on CSC were randomly assigned to 10 groups, including 107 or 108 sires. In the cross-validation 1 group was used as validation set and the remaining 9 constituted the reference population. Daughter yield deviation (DYD) was used as response variable for genomic predictions. The DYD were calculated from EBV predicted separately for each of the 10 reference populations used in the cross-validation. Genomic breeding values were estimated by GBLUP (Meuwissen et al. (2001)) using DMUAI in DMU (Madsen and Jensen (2010)). The analyses were weighted by number of daughters with records on CSC and HQ, to account for different amount of

information per sire. The inverse G-matrix used in prediction of GEBV was obtained using the G-matrix package (Su and Madsen, 2012). Predictive ability was calculated as the correlation between GEBV and DYD, where DYD was calculated from EBV estimated using the full dataset. An additional validation set including the youngest sires (born in 2007 or 2008) with CSC records was analyzed, and its predictive ability was compared to the 10-fold cross-validation. This validation set included 171 sires, and the reference population (sires born before 2007) used in the univariate model and the 2 bivariate models; HQ04 and HQ96, had 903, 1,046 and 1,869 sires, respectively.

Results and Discussion

Results from the cross-validation are given in Table 1. The mean predictive correlation of GEBV for CSC from the univariate model was 0.29. By including HQ96 as a correlated trait the mean predictive correlation of GEBV for CSC increased slightly to 0.32. In the bivariate model including HQ04 the mean predictive correlation of GEBV for CSC did not change compared to the univariate model. The standard deviation (SD) decreased in the 2 bivariate models compared to the univariate model. In spite of the strong genetic correlation between CSC and HQ (Ødegård et al. 2014) and a reference population more than twice as large in the bivariate model with HQ96, the bivariate analysis did not improve predictive ability much.

Table 1. Predictive ability of genomic breeding values (GEBV) for corkscrew claw (CSC) from a 10-fold cross-validation. Correlation between GEBV and daughter yield deviation from univariate analyses of CSC from claw trimming and CSC together with hoof quality (HQ) from conformations scores from 2004 (CSCHQ04) or HQ from 1996 (CSCHQ96).

Validation set	Univariate model	Bivariate model (HQ from 2004)	Bivariate model (HQ from 1996)
1	0.19	0.23	0.23
2	0.19	0.20	0.23
3	0.44	0.43	0.42
4	0.13	0.15	0.22
5	0.31	0.33	0.41
6	0.28	0.31	0.34
7	0.33	0.28	0.31
8	0.45	0.35	0.42
9	0.32	0.36	0.36
10	0.28	0.28	0.26
Average	0.29	0.29	0.32
SD	0.10	0.08	0.08

The predictive correlation of GEBV for CSC in the 10 validation sets ranged from 0.19 to 0.45 for the univariate model, and from 0.23 to 0.42 for the bivariate model with HQ96. The differences between validation sets could be due to different amount of information on the validation sires or their relationship with the reference population. By using 10-fold cross-validation some sires in the validation sets may be older bulls having sons with information in the reference population, and thereby gaining a lot of information compared to young bulls with less data.

When sires born in 2007 and 2008 were used for validation the predictive correlation of GEBV for CSC was 0.29 in the univariate model. This result was equal to the mean predictive correlation found in the 10-fold cross-validation. When including HQ04 as a correlated trait the predictive ability of GEBV for CSC did not change compare to the univariate model, whereas including HQ96 the predictive correlation of GEBV for CSC increased to 0.35. This was above the mean, but within the range of correlations found in the cross-validation of the bivariate models.

Corkscrew claw is a novel trait recorded since 2004, hence the size of the reference population become smaller than for other traits. However, the predictive ability of GEBV for CSC was in the same range as the accuracies of GEBV for other health traits of Norwegian Red. Svendsen et al. (2013) found correlations between GEBV and EBV ranging from 0.16 (stillbirth, direct) to 0.77 (slaughter classification) for Norwegian Red. Their results showed correlations around 0.6 for milk production traits, whereas health and fertility traits had correlations ranging from 0.2 to 0.4. Similar results were found by Haugaard et al. (2014) who estimated accuracy of GEBV for 4 fertility related disorders in Norwegian Red ranging from 0.17 to 0.65; and by Luan et al. (2009) who found low accuracies of health traits (mastitis and calving ease) and higher accuracies for the production traits (milk, protein and fat).

To obtain better predictive ability of GEBV for CSC more animals in the reference population and increasing amount of claw health data would be beneficial. This could be obtained by genotyping cows and motivate farmers to report claw health status in their herds. The number of claw health records increase every year but daughter groups per sire are still small, and few cows have both CSC and HQ recorded.

Conclusion

The predictive correlation of GEBV for CSC was 0.29 when including information only for CSC recorded at claw trimming. Although including HQ from conformation scores as a correlated trait more than doubled the size of the reference population the increase in predictive ability of GEBV for CSC was marginal. Similar results were found both in 10-fold cross-validation and for a validation set including the youngest bulls.

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References

Haugaard, K., M. Svendsen, and B. Heringstad. 2014. Proc 10th WCGALP.

Luan, T., J. A. Woolliams, S. Lien, et al. 2009. *Genetics* 183:1119-1126.

Madsen, P., and J. Jensen. 2010. University of Aarhus, Faculty Agricultural Science (DJF), Dept. of Genetics and Biotechnology, Research Center Foulum, Tjele Denmark.

Meuwissen, T. H. E., B. J. Hayes, and M. E. Goddard. 2001. *Genetics* 157:1819-1829.

Su, G., and P. Madsen. 2012. Departments of Genetics and Biotechnology, Aarhus University.

Svendsen, M., B. Heringstad, and T. R. Solberg. 2013. Husdyrforsøksmøte. (In Norwegian).

Ødegård, C., M. Svendsen, and B. Heringstad. 2013. *J. Dairy Sci.* 96:7274-7283.

Ødegård, C., M. Svendsen, and B. Heringstad. 2014. *J. Dairy Sci.* (submitted).