Genomic Breeding Values for Claw Health in Norwegian Red

C. Ødegård[12], M. Svendsen[1] and B. Heringstad[12]
[1]*Geno Breeding and A. I. Association, P.O. Box 5003, NO-1432 Ås, Norway*
[2] *Department of Animal and Aquacultural Sciences, Norwegian University of Life Sciences, P.O. Box 5003, NO-1432 Ås, Norway*
Email: cecilie.odegard@umb.no

Abstract

The aim was to evaluate reliability of genomic predicted breeding values for claw health in Norwegian Red cows. The following claw disorders recorded at claw trimming were analyzed: Corkscrew claw, infectious claw disorders (including heel horn erosion, dermatitis and interdigital phlegmon), laminitis related claw disorders (including sole ulcer, white line disorder and haemorrhage of sole and white line) and overall claw disorder (including all claw disorders reported at claw trimming). Genomic breeding values were predicted using GBLUP and reliability of genomic prediction was assessed by a 10-fold cross-validation. The mean reliabilities of genomic breeding values ranged from 0.39 to 0.65 for the 4 traits, with standard deviations 0.08 – 0.13. Increased reference population and increased number of daughters with claw health records per sire are needed to improve the reliabilities. However, the reliabilities obtained were high compared to reliabilities reported for genomic predictions of other traits in Norwegian Red.

Key words: claw health, genomic breeding value, dairy cow

Introduction

Claw health is currently in focus among dairy farmers in Norway. Genetic evaluation of claw health for Norwegian Red based on information obtained from claw trimming is therefore under development. Claw health recorded at claw trimming has been reported to the Norwegian Dairy Herd Recording System since 2004. Based on this information Ødegård *et al.* (2013) estimated genetic parameters for 9 single claw disorders and 3 groups of claw disorders and found low to moderate heritabilities, which corresponds well to other studies (e.g. Buch *et al.,* 2011). The estimated genetic correlations suggested grouping of claw disorders into infectious claw disorders and laminitis related claw disorders, which increased the frequency and heritability of claw disorders (Ødegård *et al.,* 2013).

Ødegård *et al.* (2013) showed that genetic evaluation of claw health based on data from claw trimming is possible. Despite limited historical data available, it is of interest to investigate how claw health performs in genomic prediction. The aim of this study was to assess reliability of genomic breeding values for claw disorders in the Norwegian Red population.

Material and Methods

Claw health data reported to the Norwegian Dairy Herd Recording System were used in the analyses. The data set included records between 2004 and February 2013, with a total of 389 251 claw health records from 213 583 cows in 7 252 herds. A total of 2 709 sires had at least one daughter with a claw health record. Based on results from Ødegård *et al.* (2013) 4 claw health traits were chosen: corkscrew claw (CSC), which is the most frequent claw disorder in Norway, and 3 groups of claw disorders: infectious claw disorders (INFEC), laminitis related claw disorders (LAMIN) and overall claw disorder (OVERALL). The group OVERALL included 9 single claw disorders: CSC, heel horn erosion (HH), dermatitis (DE), sole ulcer (SU), white line disorder (WLD), haemorrhage of sole and white line (HSW), interdigital phlegmon (IDP), acute trauma and lameness; INFEC included HH, DE and IDP; and LAMIN included SU, WLD and HSW. Data editing and estimation of breeding values

was performed as described in Ødegård *et al.* (2013). After editing the number of records was 253 318 claw health records from 169 804 cows in 6 612 herds, and 2 033 sires had daughters with claw health records. The frequencies of CSC and groups of claw disorders after editing are shown in Table 1. Each cow was defined as either healthy (0) or diseased (1) per lactation for each of the 4 claw traits. Estimated breeding values (EBV) were obtained by univariate threshold sire models using the RJMC procedure in DMU (Madsen and Jensen, 2010).

An imputed 25K/54K SNP dataset with 48 204 SNP for a total of 3 315 Norwegian Red sires was available. Of these, 2 428 sires had both SNP information and EBV for the claw disorders. For the cross-validation only sires with at least 30 daughters in the dataset were included, in total 959 sires. A 10-fold cross-validation was preformed where the sires were randomly assigned to 10 groups of 96 sires, except the 10th group that included 95 sires. The reference population was the remaining sires not included in a given validation set. Sire EBV from the threshold model were used as response variables in the genomic predictions, and were weighted by number of daughters per sire to account for differences in reliability of EBV. GBLUP (Meuwissen *et al.,* 2001) was used for prediction of genomic breeding values (GEBV).

Table 1. Frequency (%) of corkscrew claw and groups of claw disorders after editing.

Trait	Frequency
Corkscrew claw	10.2
Infectious claw disorders	6.2
Laminitis related claw disorders	7.3
Overall claw disorder	22.4

The model in matrix notation can be written as:

$$\mathbf{y} = \mathbf{1}\mu + \mathbf{Z}\mathbf{s} + \mathbf{e}$$

where $\mathbf{y}$ is a vector of sire EBV, $\mathbf{1}$ is a vector of ones, μ is the population mean, $\mathbf{s}$ is a vector of sire effect to be estimated and $\mathbf{e}$ is a vector of residuals. $\mathbf{Z}$ is the corresponding matrix to $\mathbf{s}$. It was assumed that $\mathbf{s} \sim N(0, \ \mathbf{G}\sigma_s^2)$ and $\mathbf{e} \sim N(0, \ \mathbf{W}\sigma_e^2)$, where $\mathbf{G}$ is the genomic relationship matrix and $\mathbf{W}$ is a diagonal matrix containing weights. The inverse G-matrix was obtained using the G-matrix package (Su and Madsen, 2012). The weights were calculated as number of daughters divided by 100, with maximum value 1. GEBVs were predicted using the DMUAI procedure in DMU (Madsen and Jensen, 2010).

Reliability of GEBV was assessed as the squared correlation between EBV and GEBV divided by the average reliability of EBV for sires in the validation set. The reliabilities of EBV were calculated from effective daughter contribution (EDC) and variance components from the threshold model. This was carried out separately for each of the 10 validation sets for each trait and then average reliabilities of GEBV were calculated.

Results and Discussion

The average reliability of GEBV from cross-validation was 0.39 for CSC, 0.65 for INFEC, 0.56 for LAMIN and 0.46 for OVERALL (Table 2). The SD of the reliabilities were high for all 4 traits (0.08 – 0.13). The average reliability of EBV (959 sires) for CSC, INFEC, LAMIN and OVERALL was 0.79, 0.65, 0.65 and 0.68, respectively, with SD ranging from 0.08 to 0.13 (Table 3). The mean reliability and SD of EBV in each of the 10 validation sets were close to the mean presented in Table 3. Infectious claw disorders and LAMIN which had lowest frequency and heritability had the lowest reliability of EBV.

Table 2. Reliability[1] (rel) of GEBV for corkscrew claw (CSC), infectious claw disorders (INFEC), laminitis related claw disorders (LAMIN) and overall claw disorder (OVERALL) from a 10-fold cross-validation. Mean, standard deviation (SD), minimum (MIN) and maximum (MAX) reliability.

Claw disorder	Mean rel	SD	MIN	MAX
CSC	0.39	0.08	0.21	0.52
INFEC	0.65	0.12	0.49	0.83
LAMIN	0.56	0.13	0.42	0.84
OVERALL	0.46	0.09	0.33	0.62

[1] Reliability of GEBV=squared correlation between EBV and GEBV divided by the average reliability of EBV for sires in the validation set.

Table 3. Reliability of EBV for corkscrew claw (CSC), infectious claw disorders (INFEC), laminitis related claw disorders (LAMIN) and overall claw disorder (OVERALL). Mean, standard deviation (SD), minimum (MIN) and maximum (MAX) reliability of EBV for the 959 sires in the dataset.

Claw disorder	Mean	SD	MIN	MAX
CSC	0.79	0.08	0.63	0.99
INFEC	0.65	0.13	0.44	0.99
LAMIN	0.65	0.13	0.44	0.99
OVERALL	0.68	0.12	0.48	0.99

Eighty-five percent of the 959 sires had less than 100 daughters with claw health records. This is few daughters relative to the daughter groups used for progeny testing of other traits in Norwegian Red. Sires that got their first official proof in 2010 and 2011 had on average 34 and 37 daughters with claw health records, respectively (Ødegård *et al.,* 2013). This limited amount of information per sire makes it challenging to obtain reliable breeding values because claw disorders has low frequencies and heritabilities. The total number of daughters per sire in the dataset varied from 30 to 3 571, showing a large difference in amount of information per sire. Therefore sire EBV was weighted to account for different number of daughters, and reliability was used instead of correlation between EBV and GEBV as a measure of accuracy. Because the reliabilities of EBV were moderate with high SD (Table 3) the results should be interpreted with caution.

We used sire EBV as response variable in the model. Other options are to use daughter yield deviation (DYD) or deregressed proof (DRP) to avoid overestimation of GEBV. Guo *et al.* (2010) concluded that EBV could be used in genomic prediction instead of DYD and that the slight difference in reliability using EBV or DYD depends on heritability and number of daughters per sire.

A 10-fold cross-validation was chosen. Validation using only the youngest sires would imply that either the reference population or the validation set would be too small, as the dataset contained only 959 sires. In applied genomic selection older proven bulls will be in the reference population and the young animals will be in the validation set. With random cross-validation the population structure is not taken into account, key ancestors may be in the validation set which will affect predictability.

To obtain high accuracy of GEBV a large reference population with reliable phenotypic values is needed (e.g. Hayes *et al.,* 2009; Meuwissen *et al.,* 2013). The effective population size and the heritability of the trait will also affect the reliability of GEBV. Norwegian Red has a large effective population size; for these new traits the reference population is small because recording of claw disorders started recently (data available from 2004), and the claw disorder traits have low heritability, all this makes genomic predictions for claw disorders challenging. In spite of this, obtained reliabilities (Table 2) were encouraging and in the upper-range of reliabilities of GEBVs compared to other traits in Norwegian Red (Heringstad *et al.,* 2011). Svendsen *et al.,* 2013 found correlation between GEBV and EBV for feet and leg conformation traits that ranged from 0.60 to 0.71, which includes corkscrew claw recorded on 1st lactating cows by breeding advisors.

Because reliability of GEBV depends on size of the reference population and reliability of the EBV, we chose to include groups of

claw disorders because of their higher frequencies and heritabilities compared to single claw disorders. For efficient breeding for claw health we need to increase the number of records from claw trimming. Implementation of an electronic recording system from 2013 will ease the recording of claw health status, and hopefully encourage to an increased reporting.

Conclusion

The reliabilities of GEBV for CSC, INFEC, LAMIN and OVERALL were moderate to high, with relatively large SD. Few daughters per sire and small reference population makes genomic prediction of claw health challenging. In spite of this the obtained reliabilities were high compared to many other traits in Norwegian Red. To obtain more reliable EBV as well as GEBV for claw health it is crucial that number of claw health records continues to increase.

Acknowledgements

References

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

Guo, G., Lund, M.S., Zhang, Y. & Su, G. 2010. Comparison between genomic prediction using daughter yield deviation and conventional estimated breeding value as response variables. *J. Anim. Breed. Genet. 127,* 423-432.

Hayes, B.J., Bowman, P.J., Chamberlain, A.J. & Goddard, M.E. 2009. Invited review: Genomic selection in dairy cattle: progress and challenges. *J. Dairy Sci. 92,* 433-443.

Heringstad, B., Su, G., Solberg, T.R., Guldbrandtsen, B., Svendsen, M. & Lund, M.S. 2011. Genomic predictions based on a joint reference population for Scandinavian red breeds. *EAAP,* Stavanger.

Madsen, P. & Jensen, J. 2010. *A User's Guide to DMU. A package for analysing multivariate mixed models.* Version 6, release 5.0., University of Aarhus, Faculty Agricultural Science (DJF), Dept of Genetics and Biotechnology, Research Center Foulum, Tjele, Denmark.

Meuwissen, T.H.E., Hayes, B.J. & Goddard, M.E. 2001. Prediction of total genetic value using genome-wide dense marker maps. *Genetics 157,* 1819-1829.

Meuwissen, T., Hayes, B. & Goddard, M. 2013. Accelerating improvement of livestock with genomic selection. *Annu. Rev. Anim. Biosci. 1,* 221-237.

Su, G. & Madsen, P. 2012. *User's Guide for Gmatrix. A program for computing relationship matrix.* Department of Genetics and Biotechnology, Aarhus University.

Svendsen, M., Heringstad, B. & Solberg, T.R. 2013. Bruk av genomisk avlsverdi ved innkjøp av seminokseemner i NRF avlen. *Husdyrforsøksmøte*. (In Norwegian).

Ødegård, C., Svendsen, M. & Heringstad, B. 2013. Genetic analyses of claw health in Norwegian Red cows. *J. Dairy Sci.* (In press).