DOI: http://dx.doi.org/10.3168/jds.2014-9186

INTERPRETIVE SUMMARY

Foot and leg conformation traits have a small impact on genomic predictions of claw disorders in Norwegian Red cows. *Ødegård et al.* Predictive correlations of genomic breeding values (GEBV) for corkscrew claw, infectious claw disorder and laminitis related claw disorder were calculated using information on claw disorders only (recorded at claw trimming); and by analyzing claw disorders together with genetically correlated foot and leg conformation traits. Including the correlated traits gave a slight increase in the predictive correlation of GEBV for corkscrew claw, but had no effect on the other claw disorders.

Foot and leg conformation traits have a small impact on genomic predictions of claw disorders in Norwegian Red cows.

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ABSTRACT

The aim of this study was to evaluate whether the predictive correlation of genomic breeding values (**GEBV**) for claw disorders increased by including genetically correlated traits as additional information in the analyses. Predictive correlations of GEBV for claw disorders were calculated based on claw disorders only and by analyzing claw disorders together with genetically correlated foot and leg conformation traits. The claw disorders analyzed were: corkscrew claw (**CSC**); infectious claw disorder (**INF**), including dermatitis, heel horn erosion and interdigital phlegmon; and laminitis related claw disorder (**LAM**), including sole ulcer, white line disorder and hemorrhage of sole and white line. The foot and leg conformation traits included were: hoof quality (**HQ**), foot angle (**FA**), rear leg rear view new (**RLRV_N**) and rear leg rear view old (**RLRV_O**). The data consisted of 183,728 daughters with claw health records and 421,319 daughters with foot and leg conformation scores. A 25K/54K SNP dataset containing 48,249 SNP was available for the analyses. The number of genotyped sires with daughter information in the analyses was 1,093 including claw disorders, and 3,111 including claw disorders and foot and leg conformation traits. Predictive correlations of GEBV for CSC, INF and LAM were calculated from a 10-fold cross-validation and from an additional validation set including the youngest sires. Only sires having daughters with claw health records were in the validation sets, thus increasing the reference population when adding foot and leg conformation traits. The results showed marginal improvement in the predictive correlation of GEBV for CSC when including HQ and FA, both in 10-fold cross-validation (from 0.35 to 0.37) and in the validation including the youngest sires (from 0.38 to 0.49). For INF and LAM, including foot and leg conformation traits had no effect on the predictive correlation of GEBV. Claw disorders are novel traits with a limited amount of historical data and therefore a small reference population. Increasing the reference population by

including sires with daughter information on foot and leg conformation traits had small impact on the predictive correlation of GEBV. However, the small increase in predictive correlation of GEBV for CSC show a possible gain when including moderate to high genetically correlated traits.

Keywords: dairy cow, genomic breeding value, claw health, Norwegian Red

INTRODUCTION

Claw health is important for animal welfare (Bruijnis et al., 2012) and for dairy production economy (Bruijnis et al., 2010) by influencing milk production (Sogstad et al., 2007), fertility and production diseases (Sogstad et al., 2006). In Norway, claw health status at claw trimming has been reported to the Norwegian Dairy Herd Recording System since 2004. The frequencies of claw disorders in Norwegian Red are in general low, ranging from 0.2% (interdigital phlegmon) to 10% (corkscrew claw (**CSC**)) (Ødegård et al., 2013). Heritabilities (on the underlying scale) of claw disorders in different breeds ranged from 0.06 to 0.23 (e.g. Swalve et al., 2008; Buch et al., 2011; Ødegård et al., 2013). Estimated genetic correlations between claw disorders and foot and leg conformation traits are low to moderate, but with some variations between studies and breeds (e.g. Uggla et al., 2008; Van der Waaij et al., 2005; Ødegård et al., 2014a). Ødegård et al. (2014a) showed that 7 out of 15 genetic correlations between claw disorders and foot and leg conformation traits in Norwegian Red were significantly different from zero, ranging from -0.86 to 0.26. The strongest genetic correlation was found between CSC from claw trimming and hoof quality (**HQ**) from conformation score, which are supposed to measure the same trait. Hoof quality has the same definition as CSC, but are recorded by breeding advisors when the cow is standing.

Genomic selection has a huge potential to increase genetic gain (Meuwissen et al., 2001). In the selection program for Norwegian Red, the accuracy of genomic breeding values (**GEBV**) are low compared to the accuracy of estimated breeding values (**EBV**) from progeny testing, especially for health and fertility traits (e.g. Luan et al., 2009; Svendsen et al., 2013; Haugaard et al., 2014). The accuracy of GEBV, calculated as the correlation between EBV and GEBV, ranged from 0.16 (stillbirth, direct) to 0.77 (slaughter classification) in Norwegian Red (Svendsen et al., 2013). Similar results were found in other studies, where production traits showed higher accuracy or reliability of GEBV than functional traits (e.g. Solberg et al., 2011; Gao et al., 2013; Zhou et al., 2014). With novel traits such as claw disorders, the historical data and reference population is limited making genomic selection challenging. One way to improve the accuracy of GEBV is to increase the size of the reference population (e.g. Hayes et al., 2009) by including genetically correlated traits. Svendsen et al. (2013) calculated relatively high accuracy of GEBV for foot and leg conformation traits, ranging from 0.60 to 0.71. Foot and leg conformation traits that are genetically correlated to claw disorders may contribute additional information and thereby improve the predictive correlation of GEBV for claw disorders.

The aims were: 1) genomic analyses of claw disorders in Norwegian Red. First to evaluate predictive correlation of GEBV for CSC, infectious claw disorder (**INF**) and laminitis related claw disorder (**LAM**) and 2) to examine whether including genetically correlated foot and leg conformation traits in the analyses increased the genomic prediction of CSC, INF and LAM.

MATERIALS AND METHODS

Data and editing

Claw health. Claw health status at claw trimming reported to the Norwegian Dairy Herd Recording System from 2004 to 2013 were included in the analyses. Nine different claw disorders were recorded at claw trimming; CSC, dermatitis, heel horn erosion, interdigital phlegmon, sole ulcer, white line disorder, hemorrhage of sole and white line, lameness and acute trauma. Cows with no claw disorders present at claw trimming were recorded as having normal claws. Based on frequencies of and genetic correlations among claw disorders (Ødegård et al., 2013); 1 claw disorder and 2 groups of claw disorders were included in the analyses: CSC, INF (including dermatitis, heel horn erosion and interdigital phlegmon) and LAM (including sole ulcer, white line disorder and hemorrhage of sole and white line). A cow was defined as unaffected (0) or affected (1) for CSC, INF and LAM in each parity in which the cow had at least 1 record from claw trimming. The claw trimming practice varies among herds; in some herds all cows are routinely claw trimmed once a year, whereas in others, claw trimming is carried out occasionally on selected cows only. In Norway, claw trimming is performed by: professional claw trimmers (with certification), other claw trimmers (working as claw trimmers without certification), farmers or others (e.g. veterinarians). More details of claw health data in Norway can be found in Ødegård et al. (2013).

Data was edited as described by Ødegård et al. (2013): only lactating cows with recorded claw health records; daughters of Norwegian Red AI sires; at least 1 claw health record in a parity; and herds reporting at least 10% or 10 normal claw records from 2004 to 2013 (this to exclude herds reporting only affected cows) were included in the analyses. Sires were required to have at least 30 daughters with claw health records. Data included in the analyses consisted of 281,835 claw

health records from 183,728 daughters of 1,093 sires and the number of herds were 6,976. The mean frequencies of CSC, INF and LAM after editing were 11%, 7% and 8%, respectively.

Foot and leg conformation. Foot and leg conformation was scored on 1st parity cows and reported to the Norwegian Dairy Herd Recording System. Breeding advisors, at present about 50 people, score 4 defined foot and leg conformation traits: HQ, foot angle (**FA**), rear leg rear view (**RLRV**) and rear leg side view (**RLSV**) on a linear scale from 1 to 9. The definition and optimal value of RLRV changed in 2010, hence 2 traits were defined: RLRV new (**RLRV_N**) and RLRV old (**RLRV_O**). The optimum values were: 9 for HQ, 8 for RLRV_N, and 5 for FA, RLRV_O and RLSV. Based on results from Ødegård et al. (2014a), the foot and leg conformation traits included in the analyses were: HQ, FA, RLRV_N and RLRV_O (these traits had a genetic correlation significantly different from zero for at least one claw disorder). Available foot and leg conformation score were: HQ from 1996 to 2013, FA from 1987 to 2013, RLRV_N from 2010 to 2013, and RLRV_O from 1987 to 2009.

Data was edited as described in Ødegård et al. (2014a): only daughters of Norwegian Red AI sires; age at first calving between 18 and 33 months; and conformation scored within a defined time period (months after calving) were included. The data analyzed consisted of 305,195 daughters of 2,183 sires for HQ; 421,319 daughters of 3,111 sires for FA; 52,330 daughters of 571 sires for RLRV_N; and 368,834 daughters of 2,710 sires for RLRV_O. Number of records for each combination of claw disorders and foot and leg conformation traits are given in Table 1.

SNP dataset. An imputed 25K/54K SNP dataset was available for the analyses. Not all SNPs included in the 25K SNP-chip are in the 54K SNP-chip, so to exploit all available SNPs the dataset was imputed from 25K to 54K and vice versa. For details of the imputation refer to Solberg et al. (2011). After standard editing: removal of animals with an individual call rate < 97 %, deletion of Mendelian errors for animals with known parents, removal of SNP with Mendelian error rate > 2.5 %, deletion of SNP with a call rate < 25 %, and removal of SNP with MAF < 0.05, the dataset contained 48,249 SNP for a total of 3,768 Norwegian Red AI sires. Sires with genotype and informative daughters (with data on claw disorders, foot and leg conformation traits or both) were included in the analyses. Number of sires for each trait combination are given in Table 1.

Statistical analyses

Three sets of trait combinations were analyzed: (1) CSC, INF and LAM (**CH**); (2) CSC, INF, LAM, HQ and FA (**CF1**); and (3) CSC, INF, LAM, RLRV_N and RLRV_O (**CF2**). Because of convergence issues it was not possible to analyze all the claw disorders and foot and leg conformation traits together.

Estimated breeding values. Breeding values for CSC, INF and LAM were predicted using a linear sire model including effects as described in Ødegård et al. (2013). The model in matrix notation was:

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_\mathbf{h}\mathbf{h} + \mathbf{Z}_\mathbf{s}\mathbf{s} + \mathbf{e}$$

where $\mathbf{y}$ is a vector of observations on the trait, $\boldsymbol{\beta}$ is a vector of systematic effects, $\mathbf{h}$ is a vector of random herd effects, $\mathbf{s}$ is a vector of sire effects, $\mathbf{e}$ is a vector of residuals, and $\mathbf{X}$, $\mathbf{Z}_\mathbf{h}$ and $\mathbf{Z}_\mathbf{s}$ are the corresponding incidence matrices. The systematic effects were: parity with 4 classes, where the 4th

class included parity 4 to 13; year and month of calving with 119 classes; time of claw trimming (in months after calving) with 12 classes; and claw trimmer with 4 classes: (1) professional claw trimmer, (2) other claw trimmer, (3) farmer and (4) other person (e.g. veterinarian). The herd effects included 6,976 levels.

Breeding values for HQ, FA, RLRV_N and RLRV_O were predicted using a linear sire model including effects described in Ødegård et al. (2014a). The model in matrix notation was:

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_{\mathbf{hy}}\mathbf{hy} + \mathbf{Z}_{\mathbf{s}}\mathbf{s} + \mathbf{e}$$

where **y** is a vector of observations of the trait; **β** is a vector of systematic effects including year and month of calving, time from calving (months) and time from milking (hours) to scoring, and age at scoring (in months); **hy** is a vector of random herd-year effects; **s** is a vector of sire effects; **e** is a vector of residuals; and **X**, $\mathbf{Z}_{hy}$ and $\mathbf{Z}_{s}$ are the corresponding incidence matrices. Year and month of calving had 216 levels for HQ, 315 levels for FA, 51 levels for RLRV_N and 275 levels for RLRV_O; time from calving (months) and time from milking (hours) to scoring had 96 levels for HQ, FA, RLRV_N and RLRV_O; and age at scoring (in months) had 7 levels for HQ, FA, RLRV_N and RLRV_O. The herd-year effect included 98,820 levels for HQ; 149,249 levels for FA; 12,661 for RLRV_N; and 136,566 for RLRV_O.

The 3 datasets were analyzed using multivariate models with (co)variances: var(**h**) = **H** ⊗ **I**, var(**hy**) = **HY** ⊗ **I**, var(**s**) = $\mathbf{G}_0$ ⊗ **A**, and var(**e**) = **R** ⊗ **I**, where **H** is the 3×3 herd (co)variance matrix; **HY** is the 2×2 herd-year variance matrix (co-variances were assumed to be zero); **A** is the additive genetic relationship matrix; **I** are identity matrices; $\mathbf{G}_0$ and **R** are the 3×3, 5×5 and 5×5 corresponding genetic and residual (co)variance matrices for the datasets CH, CF1 and CF2,

respectively. The residual covariance between RLRV_N and RLRV_O was assumed zero, because no cows had observation on both traits. The pedigree of sires were traced as far as possible resulting in a pedigree file of 15,172 animals for CH and 26,120 animals for CF1 and CF2.

Deregressed proofs. To calculate deregressed proofs (**DRP**) (Lidauer and Strandén, 1999; Vuori et al., 2006), the EBV was used as the response variable and the residuals were weighted by effective daughter contribution (Fikse and Banos, 2001) calculated from reliabilities of EBV.

Genomic breeding values. Genomic breeding values were predicted using GBLUP (Meuwissen et al., 2001). Deregressed proofs were used as response variables for genomic predictions. The model in matrix notation was:

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

where **y** is a vector of DRP, **1** is a vector of ones, **μ** is the overall mean, **g** is a vector of genomic effects, **Z** is the incidence matrix of **g**, and **e** is a vector of residuals. It was assumed that var(**g**) = $\mathbf{G_0} \otimes \mathbf{G}$ and var(**e**) = $\mathbf{R} \otimes \mathbf{D}$; where **G** is the genomic relationship matrix; **D** is a diagonal matrix containing weighting factors for the residuals; $\mathbf{G_0}$ and **R** are the 3×3, 5×5 and 5×5 corresponding genetic and residual (co)variance matrix for CH, CF1 and CF2, respectively. The residual covariances between claw disorders and foot and leg conformation traits in CF1 and CF2 were set to zero. The residuals were weighted by reliabilities of EBV. The inverse G-matrix used in prediction of GEBV was obtained using the G-matrix package (Su and Madsen, 2012) and consisted of 1,093 sires in CH and 3,111 sire in CF1 and CF2.

Predictive correlation of GEBV. Predictive correlation of GEBV was calculated as the correlation between GEBV and DRP, where DRP was calculated from EBV predicted with all available information for each of the 3 datasets (CH, CF1 and CF2).

10-fold cross-validation. A 10-fold cross-validation (**CV**) was performed to assess predictive correlations of GEBV for CSC, INF and LAM from the datasets CH, CF1 and CF2. The 1,093 sires with daughter information on claw health were randomly assigned to 10 groups, including 109 or 110 sires. Therefore a sire was only represented in 1 group. In the CV, 1 group was used as validation set and the remaining 9 constituted the reference population. Sires having daughters with only foot and leg conformation scores were included in the reference population. The reference populations consisted of 983(984), 3,001(3,002) and 3,001(3,002) sires for the datasets CH, CF1 and CF2, respectively.

Validation by youngest sires. An additional validation set (**VAL**) consisting of the youngest sires having daughters with claw health information was analyzed. This validation set included 190 sires (born in 2007, 2008 and 2009), and the reference populations (sires born before 2007) consisted of 903, 2,797 and 2,797 sires for CH, CF1 and CF2, respectively.

The DMU software (Madsen and Jensen, 2010) was used to estimate (co)variances and predict EBV and GEBV. (Co)variances estimated from the full datasets were used in prediction of EBV for each of the reference populations in CV and VAL. Estimated heritabilities and genetic correlations are given in Table 2. The MiX99 software (Lidauer and Strandén, 1999; Vuori et al., 2006) was used to calculate DRP and reliabilities of EBV.

RESULTS AND DISCUSSION

Predictive correlation of GEBV

10-fold cross-validation. The mean predictive correlations of GEBV for CSC, INF and LAM were low, varying from 0.27 to 0.37 (Table 3). The mean predictive correlation of GEBV increased slightly, from 0.35 to 0.37, for CSC when including HQ and FA as correlated traits (CF1), whereas including RLRV_N and RLRV_O (CF2) slightly decreased the mean predictive correlation of GEBV. Including foot and leg conformation traits (CF1 and CF2) decreased the mean predictive correlations of GEBV for INF and LAM compared to using CH (Table 3). The results suggest that these genetically correlated traits may introduce more noise than additional information to the prediction of GEBV. This may be because few cows had records on both claw disorders and foot and leg conformation traits (Table 1), and that the genetic correlations among these traits were in general low (Table 2). The standard deviation (**SD**) of predictive correlations of GEBV ranged from 0.06 to 0.13 among the traits and datasets (Table 3), showing relatively large variation among the folds (Figure 1). The highest SD for CSC, INF and LAM occurred using CF2, which had the lowest mean predictive correlation of GEBV and lowest number of cows with records on both claw disorders and foot and leg conformation traits (Table 1). All mean predictive correlations of GEBV for CSC, INF and LAM using CF1 and CF2 were within the range of one SD of the mean predictive correlation of GEBV using the dataset CH. The overall best result for CSC was obtained using dataset CF1 (Figure 1), whereas for INF it was obtained using dataset CH (Figure 1). For LAM, datasets CH and CF1 gave very similar results over all folds (Figure 1). The large differences in predictive correlations of GEBVs among validation sets in CV could be due to unequal amount of information for sires in the validation set, or differences in the relationship of

a sire to the reference population. By using CV, and randomly assign sires in groups, some sires in a validation set may be older elite sires having sons with information in the reference population, and thereby gaining a lot of information in the CV compared to young sires with less data. This could lead to overestimation of predictive correlation of GEBV, therefore an additional validation set including the youngest sires were analyzed.

Validation by youngest sires. Including foot and leg conformation traits increased the predictive correlation of GEBV for CSC in VAL (Table 4), and the highest correlation was achieved using the dataset CF1 (0.49) which included HQ that had strong genetic correlation to CSC (Table 2). For INF the predictive correlation of GEBV was 0.33 to 0.34 in all 3 datasets, whereas for LAM the predictive correlation of GEBV decreased when including foot and leg conformation traits (Table 4). The predictive correlations of GEBV for INF and LAM from VAL (Table 4) were within the range of values found in CV (Table 3). For CSC the predictive correlations of GEBV from CF1 and CF2 were above the maximum value in CV. Infectious claw disorder had low genetic correlation with foot and leg conformation traits (Table 2), and was therefore expected to benefit less from including these as correlated traits in genomic prediction. This is reflected by the results, where INF had the lowest predictive correlation of GEBV among the claw disorders and no gain from correlated traits. The predictive correlations of GEBV for CSC, INF and LAM from validation based on the youngest sires were similar as those obtained in CV, indicating that overestimation was not a problem in this study. A benefit of using CV, compared to VAL, was the obtained variance of the predictive correlation of GEBV, which is a measure of precision.

It was beneficial to include the foot and leg conformation traits HQ and FA in genomic predictions for CSC, whereas for INF and LAM including foot and leg conformation traits introduced more noise than additional information. Ødegård et al. (2014b) calculated the predictive ability of GEBV (correlation between GEBV and daughter yield deviation) for CSC in a univariate (0.29) and bivariate model (0.32), including CSC and HQ, showing similar results as in the present study. The higher predictive correlation of GEBV for CSC found in the present study (Tables 3 and 4) compared to Ødegård et al. (2014b) could be due to different response variables and additional traits included in the analyses. Karoui et al. (2012) showed that accuracy of GEBV increased slightly in small breeds when highly genetic correlated traits from larger breeds were included in the analyses. The low genetic correlation among most of the claw disorders and foot and leg conformation traits (Table 2) could explain the small effect on predictive correlation of GEBV in the present study. Buitenhuis et al. (2007) detected 4 QTL associated with lameness (group of claw disorders), and these had small overlap with QTL found for foot and leg conformation traits. This indicate that different genes affect claw disorders and foot and leg conformation traits, which is also consistent with the low genetic correlations among these traits (e.g. van der Waaij et al., 2005; Ødegård et al., 2014a).

The accuracy of GEBV for other low heritability traits in Norwegian Red (e.g. Solberg et al., 2011; Svendsen et al., 2013; Haugaard et al., 2014) were in the same range as the predictive correlation of GEBV calculated in the present study. Haugaard et al. (2014) found accuracy of genomic predictions (correlation between EBV and GEBV) for 4 fertility related disorders in Norwegian Red ranging from 0.17 to 0.65. In Norwegian Red, correlations between GEBV and EBV were predicted for milk production traits to be around 0.6, whereas for health and fertility traits the

301 correlations ranged from 0.2 to 0.4 (Svendsen et al., 2013). Similar results were found in other
302 breeds (e.g. Karoui et al., 2012; Pintus et al., 2012; Zhou et al. 2014), where the accuracy of GEBV
303 were lowest for low heritable traits. Despite the limited historical data and the small reference
304 population available for claw disorders, the predictive correlations of GEBV for CSC, INF and
305 LAM were in the same range as accuracies of GEBV obtained for other low heritable traits in
306 Norwegian Red.
307
308 **Increasing the predictive correlation of GEBV**
309 Claw disorders are novel traits with limited historical data and therefore fewer animals in the
310 reference population. Including foot and leg conformation traits had little or no effect on the
311 predictive correlations of GEBV for CSC, INF and LAM, despite the increased number of sires in
312 the reference population. This could partly be because most sires had few daughters with claw
313 health information (average 168, minimum 30) and few cows had information on both claw health
314 and foot and leg conformation score. The high effective population size in Norwegian Red (Geno,
315 2013) and the low genetic correlations among the traits also affected the results. Better predictive
316 correlations of GEBV could possibly be obtained by increasing the number of animals in the
317 reference population, increasing the number of phenotypic records (claw health records) and by
318 genotyping of cows.
319
320 Genomic predictions across breeds and populations is one approach to obtain larger reference
321 populations (e.g. Brøndum et al., 2011; Heringstad et al., 2011; Lund et al., 2011) and thereby
322 increase predictive correlation of GEBV. Reliabilities of GEBV for Norwegian Red calculated in
323 a joint Nordic reference population (including Norwegian Red, Swedish Red, Finnish Ayrshire

and Danish Red) increased slightly for production traits compared to a reference population consisting of only Norwegian Red. However, for health traits there was no gain in reliability and for fertility traits the reliability of GEBV decreased (Heringstad et al., 2011). Lund et al. (2011) showed increased reliability of genomic prediction using a common reference population within breed, and Hozé et al. (2014) found increased gain in accuracy of genomic evaluation methods using a multi-breed reference population in a small breed where bulls had missing sires in the reference population. The results in these studies varied among breeds and populations, which partly could be explained by variation in relationship among animals, as confirmed by Brøndum et al. (2011) who concluded that reliabilities of direct breeding values increased when strong genetic links between animals in a multi-breed reference population were present.

The number of yearly claw health records has increased since national recording started in 2004, to approximately 70,000 records per year. There is however a huge potential to further increase the recording of claw health in Norway, as only 33% of the herds recorded claw health at claw trimming in 2013. Number of daughters with claw health records for the 1,093 Norwegian Red sires in the present study varied from 30 to 6,524, and reliabilities of their EBV for CSC, INF and LAM varied from 0.20 to 0.99. Mean reliability of EBV for CSC increased from 0.67 (using CH and CF1) to 0.72 using CH1, whereas for INF and LAM it did not change between the 3 datasets. The increased reliability of EBV for CSC using CF1 can be explained by more informative daughters available for analyses, because of the strong genetic correlation between CSC and HQ. In the present analyses only sires having at least 30 daughters with information were included, whereas in routine genetic evaluations most sires have less than 30 daughters with claw health records at the time of their first official proof. However, claw health information from more herds

can contribute with more information per sire and increased reliability of EBV, and thereby improved phenotypes for genomic prediction.

Genotyping of females to be included in the reference population is another possibility to increase the predictive correlation of GEBV. Several studies have shown that genotyping of females are beneficial in genomic predictions (e.g. Mc Hugh et al., 2011; Pryce et al., 2012; Egger-Danner et al., 2014), especially in breeds with small reference populations or for novel traits. In a study where the reference population consisted of genotyped cows with phenotypic records on new traits, including genotyped bulls in the reference population with records on a positive genetic correlated index increased the accuracy of selection (Calus et al., 2013). Egger-Danner et al. (2014) stated that for novel traits, the reliability of GEBV would increase if genotyped cows with reliable phenotypes were added to a small reference population, because bulls in the reference population would have few daughters with records on the novel traits, and thereby less reliable GEBV. For claw disorders in Norwegian Red, it might be beneficial to genotype cows with claw health records to increase the reference population and thereby improve genomic predictions.

This was the first genomic analyses of claw disorders in Norwegian Red. Although claw disorders are novel traits with limited historical data and small reference population, the predictive correlations of GEBV for CSC, INF and LAM were in the same range as for other health traits in Norwegian Red. Further increase in predictive correlation of GEBV may be achieved by getting more herds to record claw health, and by genotyping cows to be included in the reference population.

CONCLUSION

The predictive correlations of GEBV for CSC, INF and LAM were in general low, and including genetically correlated foot and leg conformation traits had little or no effect, despite the increased reference population. The predictive correlation of GEBV for CSC increased slightly when including HQ and FA, whereas for other traits a small decrease were observed when including the correlated traits. The results illustrate the challenges related to genomic selection of novel traits with limited historical data and a small reference population. Including traits with strong genetic correlation may have some slight, positive influence on the predictive correlation of GEBV.

ACKNOWLEDGEMENTS

The authors would like to thank the Norwegian Dairy Herd Recording System and the Norwegian Cattle Health Service (Ås, Norway) for access to data, Geno SA for access to SNP data, Harald Grove, Cigene, NMBU, for imputation of SNP data, and the Norwegian Research Council and Geno SA for funding (project 212864).

REFERENCES

Bruijnis, M. R. N., B. Beerda, H. Hogeveen, and E. N. Stassen. 2012. Assessing the welfare impact of foot disorders in dairy cattle by modeling approach. Animal 6:962-970.

Bruijnis, M. R. N., H. Hogeveen, and E. N. Stassen. 2010. Assessing economic consequences of foot disorders in dairy cattle using a dynamic stochastic simulation model. J. Dairy Sci. 93:2419-2432.

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

Buitenhuis, A. J., M. S. Lund, J. R. Thomasen, B. Thomsen, V. Hunnicke Nielsen, C. Bendixen, and B. Guldbrandtsen. 2007. Detection of quantitative trait loci affecting lameness and leg conformation traits in Danish Holstein cattle. J. Dairy Sci. 90:472-481.

Brøndum, R. F., E. Rius-Vilarrasa, I. Strandén, G. Su, B. Guldbrandtsen, W. F. Fikse, and M. S. Lund. 2011. Reliabilities of genomic prediction using combined reference data of the Nordic Red dairy cattle populations. J. Dairy Sci. 94:4700-4707.

Calus, M. P. L., Y. de Haas, M. Pszczola, and R. F. Veerkamp. 2013. Predicted accuracy of and response to genomic selection for new traits in dairy cattle. Animal 7:183-191.

Egger-Danner, C., H. Schwarzenbacher, and A. Willam. 2014. Short communication: Genotyping of cows to speed up availability of genomic estimated breeding values for direct health traits in Austrian Fleckvieh (Simmental) cattle – Genetic and economic aspects. J. Dairy Sci. 97:4552-4556.

Fikse, W. F. and G. Banos. 2001. Weighting factors of sire daughter information in international genetic evaluations. J. Dairy Sci. 84:1759-1767.

Gao, H., M. S. Lund, Y. Zhang, and G. Su. 2013. Accuracy of genomic prediction using different models and response variables in the Nordic Red cattle population. J. Anim. Breed. Genet. 130:333-340.

Geno, 2013. Årsberetning og regnskap 2013. Page 13. Accessed Feb. 10, 2015. http://viewer.zmags.com/publication/d5a081bc#/d5a081bc/1. (In Norwegian).

Haugaard, K., M. Svendsen, and B. Heringstad. 2014. Genomic predictions of fertility related disorders in Norwegian Red using 30 years of data. Proc. 10th World Congress on Genetics Applied to Livestock Production (WCGALP), Vancouver, Canada.

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

Heringstad, B., G. Su, T. R. Solberg, B. Guldbrantsen, M. Svendsen, and M. S. Lund. 2011. Genomic predictions based on a joint reference population for Scandinavian red breeds. Proc. 62th European Federation for Animal Science (EAAP) Annual Meeting, Stavanger, Norway.

Hozé, C., S. Fritz, F. Phocas, D. Boichard, V. Ducrocq, and P. Croiseau. 2014. Efficiency of multi-breed genomic selection for dairy cattle breeds with different sizes of reference population. J. Dairy Sci. 97:3918-3929.

Karoui, S., M. J. Carabaño, C. Díaz, and A. Legarra. 2012. Joint genomic evaluation of French dairy cattle breeds using multiple-trait models. Genet. Sel. Evol. 44:39

Lidauer, M., and I. Strandén, 1999. Fast and flexible program for genetic evaluation in dairy cattle. International workshop in high performance computing and new statistical methods in dairy cattle breeding, Tuusula, Finland. Interbull bull. 20:20-25.

Luan, T., J. A. Woolliams, S. Lien, M. Kent, M. Svendsen, and T. H. E. Meuwissen. 2009. The accuracy of genomic selection in Norwegian Red cattle assessed by cross-validation. Genetics 183:1119-1126.

Lund, M. S., A. P. W. de Roos, A. G. de Vries, T. Druet, V. Ducrocq, S. Fritz, F. Guillaume, B. Guldbrandtsen, Z. Liu, R. Reents, C. Schrooten, F. Seefried, and G. Su. 2011. A common reference population from four European Holstein populations increases reliability of genomic predictions. Genet. Sel. Evol. 43:43.

Madsen, P., and J. Jensen. 2010. An 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.

Mc Hugh, N., T. H. E. Meuwissen, A. R. Cromie, and A. K. Sonesson. 2011. Use of female information in dairy cattle genomic breeding programs. J. Dairy Sci. 94:4109-4118.

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

Pintus, M. A., E. L. Nicolazzi, J. B. C. H. M. Van Kaam, S. Biffani, A. Stella, G. Gaspa, C. Dimauro, and N. P. P. Macciotta. 2012. Use of different statistical models to predict direct genomic values for productive and functional traits in Italian Holsteins. J. Anim. Breed. Genet. 130:32-40.

Pryce, J. E., B. J. Hayes, and M. E. Goddard. 2012. Genotyping dairy females can improve the reliability of genomic selection for young bulls and heifers and provide farmers with new management tools. Proc. International Committee for Animal Recording (ICAR), Cork, Irland.

Sogstad, Å. M., O. Østerås, and T. Fjeldaas. 2006. Bovine claw and limb disorders related to reproductive performance and production diseases. J. Dairy Sci. 89:2519-2528.

Sogstad, Å. M., O. Østerås, T. Fjeldaas, and A. O. Refsdal. 2007. Bovine claw and limb disorders at claw trimming related to milk yield. J. Dairy Sci. 90:749-759.

Solberg, T. R., B. Heringstad, M. Svendsen, H. Grove, and T. H. E. Meuwissen. 2011. Genomic predictions for production- and functional traits in Norwegian Red from BLUP analyses of imputed 54K and 777K SNP data. Interbull Bull. 44:240-243.

Su, G., and P. Madsen. 2012. User's guide for Gmatrix. A program for computing genomic relationship matrix. Departments of Genetics and Biotechnology, Aarhus University.

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

Swalve, H. H., H. Alkhoder, and R. Pijl. 2008. Estimates of breeding values for sires based on diagnoses recorded at hoof trimming: Relationships with EBV for conformation traits. Interbull Bull. 38:87-90.

Uggla, E., J. H. Jakobsen, C. Bergsten, J.-Å. Eriksson, and E. Strandberg. 2008. Genetic correlations between claw health and feet and leg conformation traits in Swedish dairy cows. Interbull Bull. 38:91-95.

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

Vuori, K., I. Strandén, M. Lidauer, and E. A. Mäntysaari. 2006. MiX99 – Effective solver for large and complex linear models. Proc. 8th World Congress on Genetics Applied to Livestock Production (WCGALP), Belo Horizonte, MG, Brazil.

474 Zhou, L., B. Heringstad, G. Su, B. Guldbrandtsen, T. H. E. Meuwissen, M. Svendsen, H. Grove,
475 U. S. Nielsen, and M. S. Lund. 2014. Genomic predictions based on a joint reference
476 population for the Nordic Red cattle breeds. J. Dairy Sci. 97:4485-4496.
477 Ødegård, C., M. Svendsen, and B. Heringstad. 2013. Genetic analyses of claw health in Norwegian
478 Red cows. J. Dairy Sci. 96:7274-7283.
479 Ødegård, C., M. Svendsen, and B. Heringstad. 2014a. Genetic correlations between claw health
480 and feet and leg conformation in Norwegian Red cows. J. Dairy Sci. 97:4522-4529.
481 Ødegård, C., M. Svendsen, and B. Heringstad. 2014b. Predictive ability of genomic breeding
482 values for corkscrew claw in Norwegian Red. Proc. 10th World Congress on Genetics Applied
483 to Livestock Production (WCGALP), Vancouver, Canada.
484

Table 1. Number of claw health records above diagonal and number of Norwegian Red sires with genotype and informative daughters (claw health records, foot and leg conformation scores or both) below diagonal for each combination of corkscrew claw (CSC), infectious claw disorder (INF), laminitis related claw disorder (LAM), hoof quality (HQ), foot angle (FA), rear leg rear view new (RLRV_N) and rear leg rear view old (RLRV_O).

	CSC	INF	LAM	HQ	FA	RLRV_N	RLRV_O
CSC	1,093	281,835	281,835	281,835	25,598	25,598	11,803	13,795
INF	1,093	1,093	281,835	281,835	25,598	25,598	11,803	13,795
LAM	1,093	1,093	1,093	281,835	25,598	25,598	11,803	13,795
HQ	1,093	1,093	1,093	2,183	305,195	305,195	52,330	252,865
FA	1,093	1,093	1,093	2,183	3,111	421,319	52,330	368,834
RLRV_N	447	447	447	571	571	571	52,330	0
RLRV_O	816	816	816	1,782	2,710	170	2,710	368,834

493 **Table 2**. Estimated heritability of corkscrew claw (CSC), infectious claw disorder (INF), laminitis
494 related claw disorder (LAM), hoof quality (HQ), foot angle (FA), rear leg rear view new
495 (RLRV_N) and rear leg rear view old (RLRV_O) and their genetic correlation (standard errors) to
496 claw disorders.

		Genetic correlation		
Trait	Heritability	CSC	INF	LAM
CSC	0.06			
INF	0.03	0.09 (0.07)		
LAM	0.03	0.26 (0.06)	0.25 (0.08)	
HQ	0.03	-0.79 (0.04)	-0.09 (0.07)	-0.27 (0.07)
FA	0.09	0.08 (0.05)	0.10 (0.06)	0.11 (0.06)
RLRV_N	0.08	0.03 (0.08)	-0.09 (0.09)	0.15 (0.09)
RLRV_O	0.07	0.14 (0.06)	-0.02 (0.07)	0.14 (0.07)

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Table 3. Mean, standard deviation (SD), minimum value (Min) and maximum value (Max) of predictive correlation of genomic breeding values (GEBV) for corkscrew claw (CSC), infectious claw disorder (INF) and laminitis related claw disorder (LAM) from a 10-fold cross-validation. Correlation between GEBV and deregressed proofs from multivariate models using 3 datasets: CH[1], CF1[2] and CF2[3].

	CSC				INF				LAM			
Dataset	Mean	SD	Min	Max	Mean	SD	Min	Max	Mean	SD	Min	Max
CH[1]	0.35	0.07	0.25	0.45	0.32	0.10	0.13	0.52	0.33	0.06	0.24	0.42
CF1[2]	0.37	0.07	0.28	0.47	0.29	0.08	0.17	0.49	0.32	0.06	0.22	0.41
CF2[3]	0.31	0.10	0.15	0.42	0.27	0.13	0.00	0.53	0.29	0.07	0.16	0.36

[1]CH – dataset including CSC, INF and LAM.

[2]CF1 – dataset including CSC, INF, LAM, hoof quality and foot angle.

[3]CF2 – dataset including CSC, INF, LAM, rear leg rear view new and rear leg rear view old.

Table 4. Predictive correlation of genomic breeding values (GEBV) for corkscrew claw, infectious claw disorder and laminitis related claw disorder from validation by the 190 youngest sires. Correlation between GEBV and deregressed proofs from multivariate models using 3 datasets: CH[1], CF1[2] and CF2[3].

	CH[1]	CF1[2]	CF2[3]
Corkscrew claw	0.38	0.49	0.43
Infectious claw disorder	0.33	0.34	0.33
Laminitis related claw disorder	0.41	0.36	0.36

[1]CH – dataset including corkscrew claw, infectious claw disorder and laminitis related claw disorder.

[2]CF1 – dataset including corkscrew claw, infectious claw disorder, laminitis related claw disorder, hoof quality and foot angle.

[3]CF2 – dataset including corkscrew claw, infectious claw disorder, laminitis related claw disorder, rear leg rear view new and rear leg rear view old.

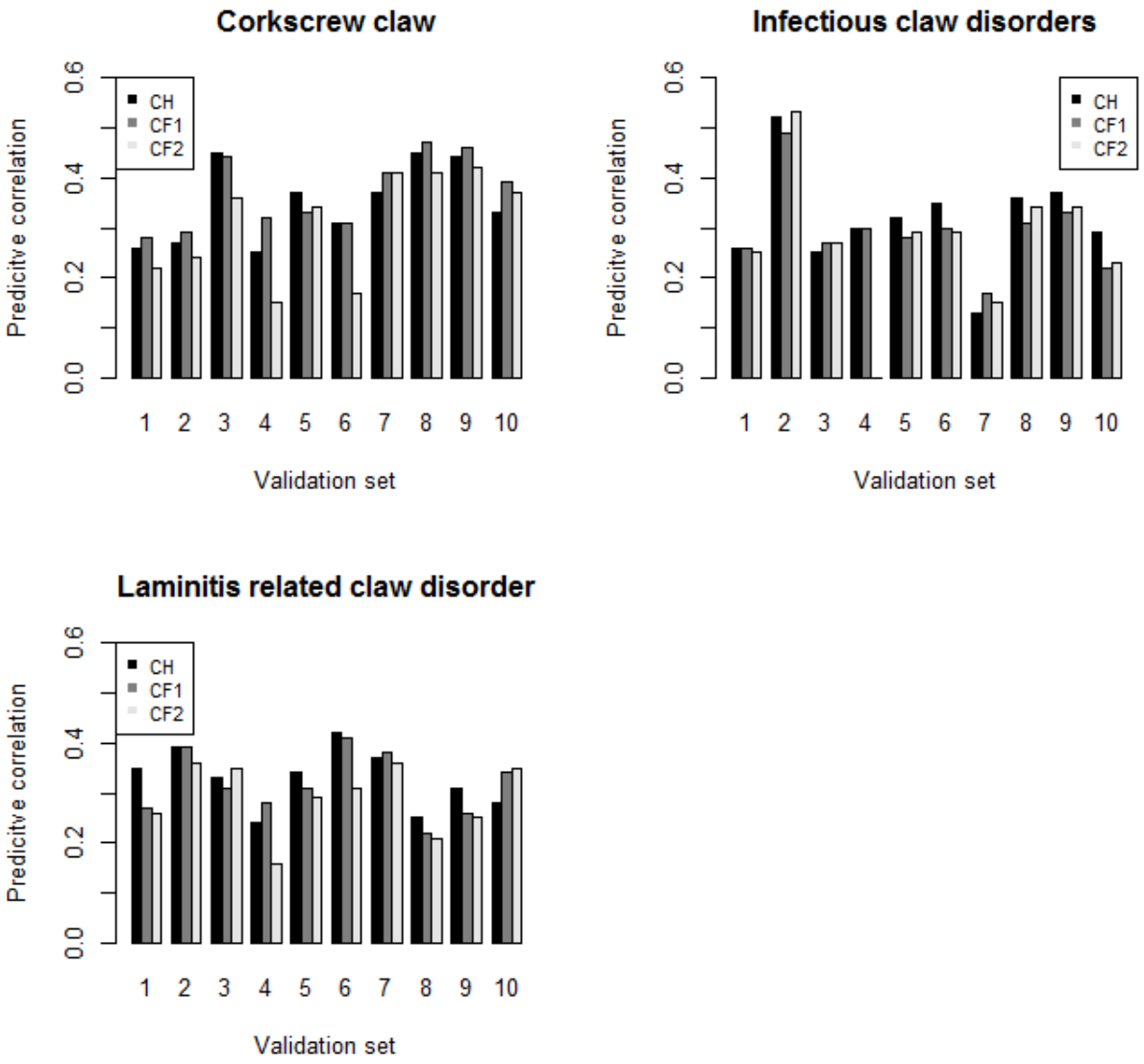

Figure 1. Predictive correlations of GEBV for corkscrew claw (CSC), infectious claw disorder (INF) and laminitis related claw disorder (LAM) from 10-fold cross-validation using 3 datasets: CH (CSC, INF and LAM); CF1 (CSC, INF, LAM, hoof quality and foot angle); and CF2 (CSC, INF, LAM, rear leg rear view new and rear leg rear view old).