Foot and leg conformation traits have a small effect 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, including dermatitis, heel horn erosion, and interdigital phlegmon; and laminitis-related claw disorder, including sole ulcer, white line disorder, and hemorrhage of sole and white line. The foot and leg conformation traits included were hoof quality, foot angle, rear leg rear view new, and rear leg rear view old. The data consisted of 183,728 daughters with claw health records and 421,319 daughters with foot and leg conformation scores. A 25K/54K single nucleotide polymorphism (SNP) data set 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, infectious claw disorder, and laminitis-related claw disorder 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 hoof quality and foot angle, 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 infectious claw disorder and laminitis-related claw disorder, 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 effect on the predictive correlation of GEBV. However, the small increase in predictive correlation of GEBV for CSC shows a possible gain when including moderate to high genetically correlated traits.

Key words: 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., van der Waaij et al., 2005; Uggla et al., 2008; 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 is 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**) is low compared with the accuracy of 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 with claw disorders may contribute additional information and thereby improve the predictive correlation of GEBV for claw disorders.

The study had 2 aims. (1) The first aim was to conduct genomic analyses of claw disorders in Norwegian Red, to evaluate predictive correlation of GEBV for CSC, infectious claw disorder (**INF**), and laminitis-related claw disorder (**LAM**). (2) The second aim was 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 was 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 one record from claw trimming. 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 the study by Ødegård et al. (2013).

Data were edited as described by Ødegård et al. (2013): only lactating cows with recorded claw health records, daughters of Norwegian Red AI sires, cows with at least one 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 was 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 first-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 (**FANG**), rear leg rear view (**RLRV**), and rear leg side view, 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 FANG, RLRV_O, and rear leg side view. Based on results from Ødegård et al. (2014a), the foot and leg conformation traits included in the analyses were HQ, FANG, RLRV_N, and RLRV_O (these traits had a genetic correlation significantly different from zero for at least one claw disorder). Foot and leg conformation score was available for HQ from 1996 to 2013, FANG from 1987 to 2013, RLRV_N from 2010 to 2013, and RLRV_O from 1987 to 2009.

Data were edited as described in Ødegård et al. (2014a): only daughters of Norwegian Red AI sires; cows with age at first calving between 18 and 33 mo; and cows that were 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 FANG; 52,330 daughters of 571 sires for RLRV_N; and 368,834 daughters of 2,710 sires for RLRV_O. Number