Genetic analyses of claw health in Norwegian Red

Genetiske analyser av klauvhelse hos norsk rødt fe (NRF)

Philosophiae Doctor (PhD) Thesis

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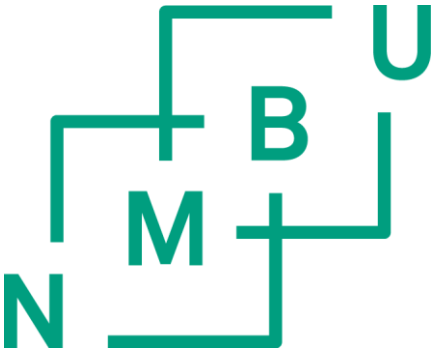

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Breeding for better lives

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Summary

The main objective of this PhD-study was genetic analyses of claw disorders recorded at claw trimming, to exploit the most efficient way of including claw health in the breeding scheme of Norwegian Red. Claw health data recorded to the Norwegian Dairy Herd Recording System since 2004 was included in the analyses. Normal claws and nine claw disorders were recorded at claw trimming: corkscrew claw, dermatitis, heel horn erosion, interdigital phlegmon, sole ulcer, white line disorder, hemorrhage of sole and white line, lameness and acute trauma. In 2014, approximately 85,000 claw health records from 65,000 cows were recorded. Number of daughters with claw health records per sire are in general low, where sires at their first official proof had less than 10 daughters.

The aim of paper I was a first genetic analysis of claw health in Norwegian Red cows, to estimate genetic parameters for the nine claw disorders and three groups of claw disorders. The groups were overall claw disorder (a cow was defined as affected if she had at least one claw disorder present in a parity); infectious claw disorder (dermatitis, heel horn erosion and interdigital phlegmon); and laminitis-related claw disorder (sole ulcer, white line disorder and hemorrhage of sole and white line). The data was analyzed using single and multivariate threshold sire models. Posterior mean of heritability of liability ranged from 0.04 (lameness and acute trauma) to 0.23 (corkscrew claw). The highest posterior mean of genetic correlations were between dermatitis and heel horn erosion (0.65) and between sole ulcer and white line disorder (0.79). Claw disorders had sufficient heritabilities to be genetically improved, but the data was scarce with few records per sire. Grouping of claw disorders as infectious claw disorder and laminitis-related claw disorder were a good strategy for breeding of improved claw health.

Genetic correlations between claw disorders and foot and leg conformation traits were estimated in paper II. Three claw disorders: corkscrew claw, infectious claw disorder and laminitis-related claw disorder, and five foot and leg conformation traits (hoof quality, foot angle, rear leg side view, and rear leg rear view, new and old) were analyzed using multivariate sire models. Seven of the 15 genetic correlations between claw disorders and foot and leg conformation traits were significantly different from zero, but were in general low. One exception was between corkscrew claw and hoof quality, which had the same definition and therefore were supposed to measure the same trait. The results indicated that direct selection

against claw disorders was the most efficient way for improving claw health in Norwegian Red cows.

Paper III aimed to examine predictive correlation of genomic breeding values (GEBV) for corkscrew claw, infectious claw disorder and laminitis-related claw disorder. Predictive correlation was defined as the correlation between GEBV and deregressed proofs. Because claw disorders are novel traits with limited historical data, inclusion of four genetic correlated foot and leg conformation traits to increase the reference population were evaluated. Results showed a slight increase in predictive correlation of GEBV for corkscrew claw when including the genetic correlated traits hoof quality and foot angle. For the other claw disorders, including genetic correlated traits had no effect. To benefit from including genetic correlated traits, the traits should be moderate to highly genetic correlated. The aim of paper IV was to evaluate the performance of genomic predictions of corkscrew claw, infectious claw disorder and laminitis-related claw disorders when including genotypes of sires and cows (having claw health records) in a single-step GBLUP. The predictions improved when the relationship matrix included genotyped sires compare to pedigree information only. Including genotyped cows, in addition to genotyped sires, gave no further improvement. The lack of improvement was probably because few cows were genotyped. Further analyses should be carried out when more genotypes of cows with claw health records become available. Paper III and Paper IV showed possibilities of improving genomic predictions for novel traits with limited historical data, but further studies of utilizing genomic information are necessary.

Sammendrag

Hovedmålet for doktorgradsarbeidet var genetiske analyser av klauvlidelser registrert ved klauvskjæring, for å undersøke hvordan klauvhelse kan implementeres i avlsarbeidet for Norsk Rødt Fe (**NRF**). Siden 2004 har det vært mulig å registrere klauvhelse fra klauvskjæring til Kukontrollen, hvor normale klauver og ni klauvlidelser har blitt registrert: korketrekkerklauv, hudbetennelse, hornforråtnelse, klauvspalteflegmone, såleknusning, løsning i den hvite linje, blødning i såle og hvite linje, halthet og akutt traume. I 2014 ble det registrert omtrent 85 000 klauvhelseregistreringer fra 65 000 kyr, og siden 2010 har i underkant av 3 000 besetninger registrert klauvhelse hvert år. Okser har få døtre med klauvhelseregistreringer, hvor okser som blir avkomsgransket første gang har færre enn 10 døtre med klauvhelseinformasjon.

I artikkel I var målet en første genetisk analyse av klauvhelsedata. Genetiske parametere ble estimert for de ni klauvlidelsene nevnt ovenfor, samt for tre grupper av klauvlidelser: infeksiøse klauvlidelser (hudbetennelse, hornforråtnelse og klauvspalteflegmone), forfangenhetsrelaterte klauvlidelser (såleknusning, løsning i den hvite linje og blødning i såle og hvite linje) og samlet klauvlidelse (ei ku ble definert som syk hvis hun hadde minst en klauvlidelse registrert i løpet av laktasjonen). Arvegrader, beregnet på underliggende skala, varierte fra 0.04 (halthet og akutt traume) til 0.20 (korketrekkerklauv). De høyeste genetiske korrelasjonene ble funnet mellom hudbetennelse og hornforråtnelse (0.65) og mellom såleknusning og løsning i den hvite linje (0.79). Resultatene viste at klauvlidelser er arvelige, og at gruppering av klauvlidelser som infeksiøse klauvlidelser og forfangenhetsrelaterte klauvlidelser er mulig. Klauvlidelser kan inkluderes i avlsarbeidet, selv om det foreløpig er forholdsvis lite data tilgjengelig.

Estimering av genetiske korrelasjoner mellom klauvlidelser og beineksteriør var målet for artikkel II. Tre klauvlidelser: korketrekkerklauv, infeksiøse klauvlidelser og forfangenhetsrelaterte klauvlidelser, og fem beineksteriøregenskaper (kodeledd, vridde klauver, hasevinkel og beinstilling bak, gammel og ny) ble analysert med multivariate farmodeller. Sju av 15 genetiske korrelasjoner var signifikant forskjellig fra null, men generelt var korrelasjonene lave. Unntaket var korrelasjonen mellom korketrekkerklauv og vridde klauver, som hadde samme definisjon og derfor var forventet å måle samme egenskap. Resultatene indikerte at direkte seleksjon mot klauvlidelser var den mest effektive måten å forbedre klauvhelse på i NRF.

I artikkel III og artikkel IV ble det beregnet genomiske avlsverdier for korketrekkerklauv, infeksiøse klauvlidelser og forfangenhetsrelaterte klauvlidelser. Klauvlidelsene er nye egenskaper med begrenset historisk data. For artikkel III var målet å undersøke om sikkerheten på genomiske avlsverdier økte ved å inkludere informasjon fra genetisk korrelerte beineksteriøregenskaper. Dette ga en fordobling av dyr i referansepopulasjonen, men kun en liten økning i sikkerheten på genomiske avlsverdier for korketrekkerklauv. For de to andre klauvlidelsene var det ingen endring i sikkerhet. Konklusjonen var at egenskaper med høy genetisk korrelasjon kan bidra med noe tilleggsinformasjon, og dermed øke sikkerhetene på de genomiske avlsverdiene noe. I artikkel IV var målet å undersøke om genomiske avlsverdier kunne forbedres ved å inkludere genotyper av okser og kyr (med klauvhelsedata) i en ett-stegs metode (ssGBLUP). Resultatene viste at prediksjonene ble forbedret ved å inkludere genotypede okser i slektskapsmatrisen kontra å bare inkludere stambokinformasjon. Inkludering av genotypede kyr, i tillegg til genotypede okser, ga ingen ekstra effekt, mest sannsynlig på grunn av få tilgjengelige genotypede kyr. Artikkel III og artikkel IV viste at det var mulig å forbedre de genomiske prediksjonene for nye egenskaper, selv med begrenset tilgjengelig informasjon. Det er imidlertid nødvendig med flere undersøkelser for å optimalisere utnyttelsen av genomisk informasjon.

List of abbreviations

CSC	- corkscrew claw
DE	- dermatitis
DRP	- deregressed proofs
EBV	- estimated breeding value
GEBV	- genomic breeding value
HH	- heel horn erosion
HSW	- hemorrhage of sole and white line
IDP	- interdigital phlegmon
INF	- infectious claw disorder
LAM	- laminitis-related claw disorder
LD	- linkage disequilibrium
QTL	- quantitative trait loci
SU	- sole ulcer
TMI	- total merit index
WLD	- white line disorder

List of papers

I. Ødegård, C., M. Svendsen, and B. Heringstad. 2013. Genetic analyses of claw health in Norwegian Red cows. Journal of Dairy Science 96:7274-7283.

II. Ødegård, C., M. Svendsen, and B. Heringstad. 2014. Genetic correlations between claw health and feet and leg conformation in Norwegian Red cows. Journal of Dairy Science 97:4522-4529.

III. Ødegård, C., M. Svendsen, and B. Heringstad. 2015. Foot and leg conformation traits have a small effect on genomic predictions of claw disorders in Norwegian Red cows. Journal of Dairy Science. 98:4139-4147.

IV. Ødegård, C., M. Svendsen, and B. Heringstad. 2015. Use of single-step GBLUP improved the genetic predictions of claw disorders in Norwegian Red. Manuscript.

General introduction

Claw health has become more important in Norway due to an increased number of free stalls (Simensen et al., 2010), where lameness is more crucial. However, claw disorders are present in both tie stall and free stall (Fjeldaas et al., 2006), indicating that focus on claw health is important regardless of housing system. Lameness and claw disorders result in economic loss for the farmer (Bruijnis et al., 2010) by reduced milk yield and increased treatment cost. Moreover, claw disorders are associated with production diseases and fertility (e.g. Sogstad et al., 2006), supporting the importance of good claw health. Another issue is animal welfare; as severe cases of claw disorders are painful and give the affected cow reduced welfare (Bruijnis et al., 2012).

The incidence of claw disorders is affected by several environmental effects (e.g. Bielfeldt et al., 2005; Koenig et al., 2005; Fjeldaas et al., 2011), for example interval between claw trimmings, flooring, feeding, milk yield and parity. To prevent claw disorders, improvement of both genetic and environmental effects are essential. In a short-term perspective, optimizing the environment is of importance, whereas in a long-term perspective it is efficient to include claw disorders in the breeding scheme. This PhD-thesis carried out genetic analyses of claw health, including traditional and genomic analyses, and evaluated feasible ways of implementing claw health in the total merit index (**TMI**).

Recording of claw health

Recording of claw health status at claw trimming to the Norwegian Dairy Herd Recording System started in 2004. In this PhD-thesis, data recorded from 2004 until September 2014 was included in the analyses. Nine claw disorders (Table 1): corkscrew claw (**CSC**), heel horn erosion (**HH**), dermatitis (**DE**), interdigital phlegmon (**IDP**), sole ulcer (**SU**), white line disorder (**WLD**), hemorrhage of sole and white line (**HSW**), lameness and acute trauma, and normal claws were recorded at claw trimming. In addition, date of claw trimming and identification of herd, cow and claw trimmer were specified. In Norway, claw trimmers and farmers mostly perform claw trimming and report to the Norwegian Dairy Herd Recording System. In this thesis, four groups of claw trimmers were defined: professional claw trimmers, other claw trimmers, farmers, and other persons (e.g. veterinarians). Certification as professional claw trimmer requires education entailing diagnosing and treatment of claw disorders and procedure of claw trimming. At present about 40 professional claw trimmers are

working in Norway. It is not mandatory to have any education to perform claw trimming, therefore claw trimmers lacking this certification were defined as other claw trimmers. All professional claw trimmers had a personal id when recording claw health, providing the opportunity to separate recordings on individual levels. Other claw trimmers were using a universal id, meaning identification at an individual level was not possible. The latter was also the case for farmers; they used a universal id when recording claw health.

The recording of claw health in Norway is not mandatory, but farmers are encouraged to report all claw health records to the Norwegian Dairy Herd Recording System. The Norwegian Cattle Health Service recommend claw trimming twice a year on all cows from 18 month of age (The Norwegian Cattle Health Service, 2008). The practice, however, is variable among farmers. Some farmers routinely claw trim all cows in their herd twice a year, whereas others are claw trimming only selected cows when needed. The recording of claw health have increased since 2004 to approximately 85,000 records in 2014 (Figure 1). Number of cows having claw health records have increased to approximately 65,000 (in 2014), showing that few cows had more than one claw health record (Figure 1). In total 6,861 herds had claw health recorded at least once in the period from 2004 to 2014, and in 2013 almost 3,000 herds had claw health recorded. This was about 33% (in 2013) of all dairy herds in Norway, and on average, claw health was recorded on 30% of the cows in these herds. A total of 3,478 sires had daughters with claw health records, and the number of daughters per sire ranged from 1 to 4,903, with an average of 75. However, at the time of the sires' first official genetic evaluation, the number of daughters with claw health records were below 10. An increased recording of claw health is therefore necessary in Norway, in order to obtain reliable estimated breeding values (**EBV**) for the young sires.

Electronic recording

In October 2014, some of the professional claw trimmers got access to an electronic recording system that report directly to the Norwegian Dairy Herd Recording System (this will be available for all professional claw trimmers). The system from Denmark, Finland and Sweden was adapted to Norwegian conditions and the definition of claw disorders in the Nordic countries were harmonized (Nordic claw atlas, 2013). Due to the harmonization, an extended list of claw disorders were included in the claw health recording in Norway in October 2014. These new claw disorders were not included and discussed in this thesis.

Table 1. Definition of claw disorders[1] (Refsum, 2012).

Claw disorder	Definition
Corkscrew claw	Small to large twist in the abaxial wall on the lateral hind claws
Heel horn erosion	Moderate to severe degree of erosion in the heel bulb with distinct V-shape
Dermatitis	Dermatitis (bleeding, exuding, or wart-like) in front or rear in the interdigital claw
Interdigital phlegmon	Severe infection in the interdigital claw, with swelling of the leg
Sole ulcer	Defect in the horn near the corium between the sole and heel bulb
White line disorder	Defect in the white line, in severe cases it can reach the corium
Hemorrhage of sole and white line	Hemorrhage of more than 20% of the sole or white line or both
Lameness	Locomotion score ≥ 3
Acute trauma	Acute, trauma for example, fractures and dislocation of joint

[1] Details and pictures of claw disorders can be found in the Nordic Claw Atlas (2013) and Egger-Danner et al. (2015b)

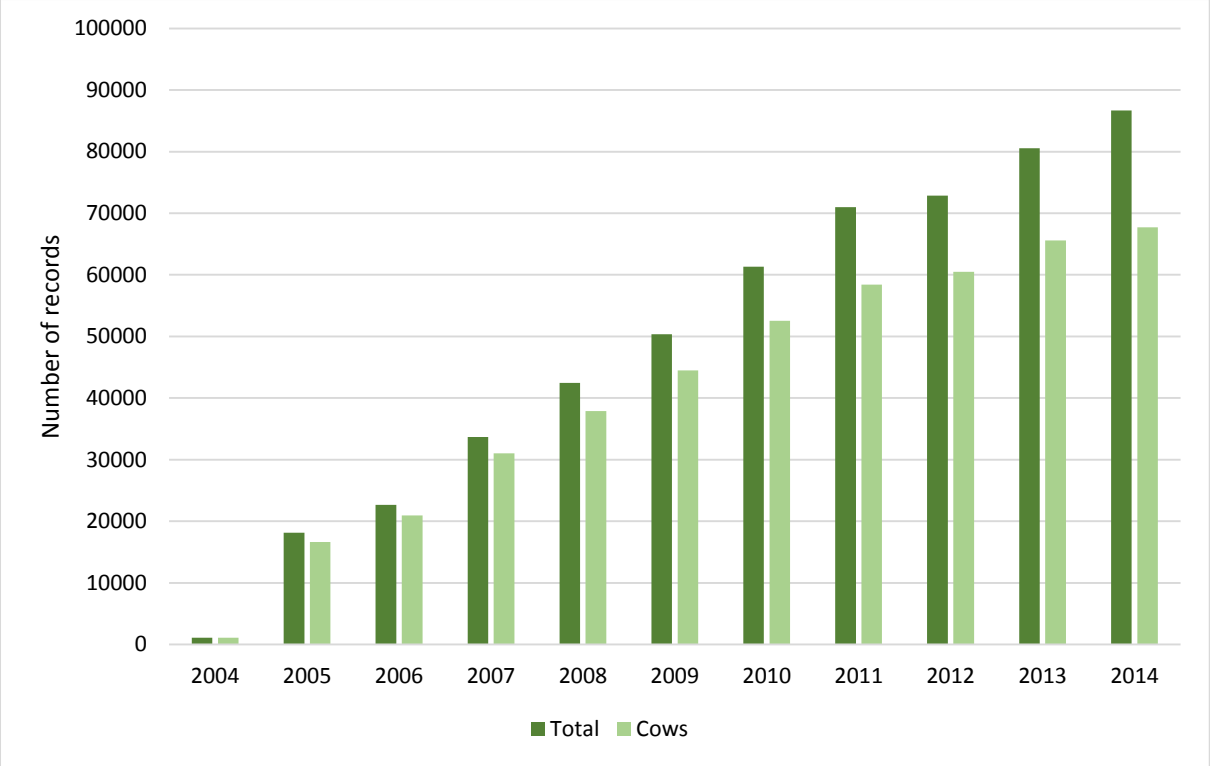

Figure 1. Total number of records and number of cows having at least one claw health record per year.

Frequency of claw disorders

The frequencies of claw disorders in Norway were low, ranging from 0.02% (IDP and acute trauma) to 10% (CSC) (Figure 2). About 75% of the total recordings were normal claws. Interdigital phlegmon could be underestimated because it is an acute disorder often treated by veterinarians and hence not always recorded in relation to claw health recording. From 2004 to 2014, the frequency of all claw disorders (except IDP, lameness and acute trauma) increased, mainly because of increased recording of claw health to the Norwegian Dairy Herd Recording System. Acute trauma was defined as an acute injury (Table 1) and thus is not a claw disorder. The recording of lameness was not consistent on all trimmed cows. Therefore, acute trauma and lameness were not emphasized in this PhD-thesis.

Because of low frequencies, some of the claw disorders having similar causative factors were grouped: HH, DE and IDP are caused by bacteria and were defined as infectious claw disorder (**INF**), and SU, WLD and HSW are often seen in conjunction with laminitis due to horn disruption and were defined as laminitis-related claw disorder (**LAM**). Grouping the claw disorders into INF and LAM both gave frequencies of approximately 7%. Grouping claw

disorders into an overall claw disorder, where a cow was defined as affected if she had at least one claw disorder present at the claw trimming, gave a frequency of 21%. The frequencies of claw disorders in Norway were in general low compared to other countries (e.g. van der Linde et al., 2010; Buch et al., 2011; Johansson et al., 2011), except for CSC. A study from Northern Ireland showed lower incidence of some claw disorders in Norwegian Red compared to Holstein (Baird et al., 2009).

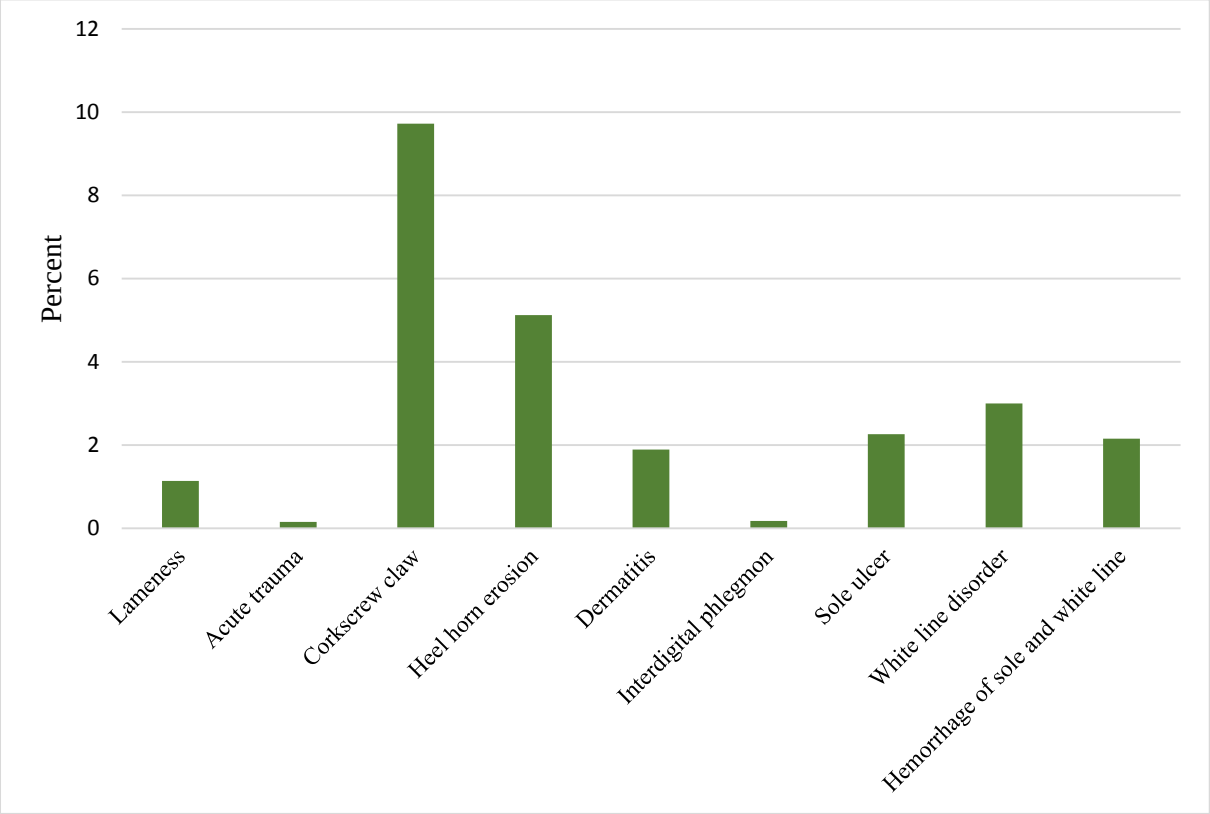

Figure 2. Frequencies of claw disorders in percentage of all claw health records from 2004 to 2014.

Breeding for improved claw health

A cow can be genetically predisposed for certain claw disorders, and detection of genetic components give the opportunity to breed for improved claw health in Norwegian Red. Claw disorders were defined as binary traits and a cow was defined as affected or unaffected for each claw disorder in each parity she had at least one claw health record. To take into account that claw disorders are categorical traits, analyses were performed using threshold models (Paper I and Paper II). The threshold model assume an underlying normal distributed variable, liability, such that the observed binary response takes the value 1 (affected) if the liability is larger than

a fixed threshold, and 0 (unaffected) otherwise. Other studies have estimated heritability for different claw disorders, both on the observed and underlying scale (e.g. Swalve et al., 2008; Buch et al., 2011; Johansson et al., 2011), showing the possibility of improving claw health by breeding. With low heritability traits, it is important to have data from large progeny groups to obtain precise EBV. In Norwegian Red, it has been demonstrated that genetic improvement of low heritable traits is possible if traits are given enough weight in the TMI (Heringstad et al., 2003; Andersen-Ranberg et al., 2005; Heringstad et al., 2007). For claw disorders, a major challenge is the limited amount of data available and small daughter groups, especially for young sires. Therefore, obtaining additional information would be valuable. Several studies have estimated genetic correlations between claw disorders and foot and leg conformation traits, lameness and locomotion ranging from -0.51 to 0.64 (e.g. van der Waaij et al., 2005; Uggla et al., 2008; Häggman and Juga, 2013). For Dutch dairy cattle, van der Linde et al. (2010) showed that the reliability of the claw health index increased when including the correlated traits feet and leg, rear leg rear view, foot angle and locomotion.

Bruijnis et al. (2010) estimated economic consequences of claw disorders. They showed that in addition to treatment cost, loss in income due to reduced milk yield was substantial. Therefore, focus on claw health in the herd is of importance, including emphasis on breeding. The International Committee for Animal Recording (ICAR) has recently published an international claw health atlas including the most common claw disorders, where the aim was to harmonize terminology and definitions of claw disorders, and thereby improve the quality of claw health records and facilitate breeding of claw disorders (Egger-Danner et al., 2015a). So far, few countries have included claw health in the genetic evaluations. However, Denmark, Finland and Sweden have since 2011 published a claw index consisting of seven claw disorders recorded at claw trimming (Johansson et al., 2011) for Holstein, Viking Red and Jersey; and. The Netherlands has a claw health index consisting of six claw disorders (van der Linde et al., 2010). In Norway, claw disorders were included in the TMI for Norwegian Red in September 2014.

Genomic selection

Using genomic information in selection of candidates for breeding gives a large potential for increasing the genetic gain per year by reducing the generation interval in dairy cattle. Meuwissen et al. (2001) suggested genomic selection; using genome-wide dense markers to capture all genetic variation, because all quantitative trait loci (**QTL**) are in linkage

disequilibrium (**LD**) with at least one marker. The reliability of genomic predictions depends on several factors, among others: number of animals in the reference population, heritability of the trait, LD, number and distribution of QTL, proportion of genetic variance explained by the markers, and effective population size (Hayes et al., 2009; Meuwissen et al., 2013). The main challenge of genomic selection, especially for low heritability traits, in Norwegian Red is obtaining reliable predictions of genomic breeding values (**GEBV**), partly because of the high effective population size (Geno, 2015). For claw disorders, which are novel, low heritable traits, a limited amount of historical data and a small reference population were available, contributing to the challenges of genomic selection. Several studies attempted to improve genomic predictions by using a joint reference population, including different breeds or populations, with divergent results (e.g. Brøndum et al., 2011; Heringstad et al., 2011; Lund et al., 2011). Heringstad et al. (2011) and Zhou et al. (2014) found little or no improvement in genomic predictions of low heritability traits in Norwegian Red using a joint reference population consisting of Norwegian Red, Danish Red, Finnish Ayrshire and Swedish Red. This was partly explained by the weak genetic link between Norwegian Red and the other breeds (Zhou et al., 2014). Other options to increase the reference population for claw health were therefore investigated in this PhD-thesis. First, the reference population was increased by including genotyped sires having daughters with information on genetic correlated foot and leg conformation traits (Paper III). Second, increased reference population was obtained by including genotypes of sires and cows in a one-step approach (Paper IV). The expectation was that the genomic predictions of claw disorders would improve.

Aims

The main objective of the PhD-thesis was genetic analyses of claw disorders recorded at claw trimming, to decide the most efficient way of including claw disorders in the TMI of Norwegian Red. Evaluation of both traditional and genomic selection methods of exploiting the claw health data were conducted.

The thesis consist of four sub-projects:

1. For a first genetic analysis of claw health for Norwegian Red using information from claw trimming, the aim was to estimate genetic parameters for nine claw disorders and three groups of claw disorders. In addition, evaluate possibilities of improving claw health through breeding.

2. The second aim was to evaluate if foot and leg conformation traits included as correlated traits in genetic analyses of claw disorders added information. Genetic correlations between claw disorders, recorded at claw trimming, and foot and leg conformation traits, recorded on first parity cows by breeding advisors, were estimated.

3. The third aim was to predict GEBV for claw disorders in Norwegian Red, and to evaluate whether the predictive correlation of GEBV increased when including genetic correlated foot and leg conformation traits in the analyses.

4. The last aim was to evaluate whether use of one-step approach and inclusion of sire and cow genotypes improved genomic predictions of claw disorders. In addition, estimation of genetic parameters using animal model were carried out.

General discussion

Genetic improvement

Genetic improvement of claw health using direct selection against claw disorders is possible, although the frequencies of claw disorders are low and sires have small daughter groups. The posterior mean of heritability of liability ranged from 0.04 (lameness and acute trauma) to 0.23 (CSC) in Paper I, confirming the possibility of including claw disorders in the breeding scheme. Other studies showed similar heritabilities on the underlying scale for claw disorders in different breeds (e.g. van der Waaij et al., 2005; Swalve et al., 2008; Buch et al., 2011). The heritabilities for CSC, INF and LAM presented in Paper I and Paper II were in accordance with each other, showing consistency in the data. Posterior mean of genetic correlations among claw disorders ranged from 0.02 to 0.79 (Paper I), where the strongest genetic correlations were between DE and HH (0.65) and between SU and WLD (0.79). The genetic correlations (Paper I) showed that grouping of claw disorders, as INF and LAM, were reasonable and may be preferred for genetic evaluation due to low frequencies and heritabilities for the single traits. Based on results from Paper I, claw disorders included in the further studies were CSC, INF and LAM (Paper II, Paper III and Paper IV).

To investigate the possibility of gaining additional information in the genetic evaluation of claw disorders, it was of interest to estimated genetic correlations to foot and leg conformation traits. The foot and leg conformation traits, scored on first parity cows by breeding advisors in Norway, were foot angle, rear leg rear view, rear leg side view and hoof quality. Rear leg rear view changed optimum value in 2010 and were defined as two traits: old and new. Hoof quality had the same definition as CSC recorded at claw trimming, and was therefore expected to measure the same trait. Low to moderate genetic correlations (from -0.33 to 0.26) were estimated between claw disorders and foot and leg conformation traits (Paper II), except between CSC and hoof quality (-0.86). This latter strong favorable genetic correlation showed that almost the same trait was measured at claw trimming and conformation score. Corkscrew claw from claw trimming should be favored because of a more thoroughly examination of the claw, including the sole. However, including hoof quality as a correlated trait in genetic evaluation of CSC would be beneficial, because hoof quality would add information and thereby improve the predictions. In general, foot and leg conformation traits, lameness or locomotion could be used as indicator traits for claw disorders (e.g. van der Waaij et al., 2005; Buch et al., 2011; Weber et al., 2013). However, Sogstad et al. (2012) recommended that a

thorough evaluation of locomotion and claw health status in a herd should include claw trimming. Therefore, if the intention is to improve claw health in the population, direct selection against claw disorders in the breeding scheme is the most efficient.

Claw health index

Grouping claw disorders as INF and LAM (Paper I) would be beneficial in genetic evaluation, because most sires have few daughters with claw health records available. By grouping the claw disorders, the frequency of the trait increases, giving slightly more information per trait. Based on results from Paper I and Paper II, claw health was included in the routine genetic evaluation of Norwegian Red in September 2014. The new claw health index, which has a relative weight of 4% in the TMI of Norwegian Red, consist of three claw disorders: CSC, INF and LAM (Table 2). However, for young sires the amount of information at their first official proof were limited (<10 daughters with claw health records). An increase in the recording of claw health is therefore necessary to obtain further improvement in the genetic evaluation.

Table 2. Relative weight on claw disorders included in the claw health index for Norwegian Red.

Trait	Relative weight (%)
Corkscrew claw	50
Infectious claw disorder	30
Laminitis-related claw disorder	20

Data quality

Normal claw

Claw disorders were binary traits, and the cow was defined as either affected or unaffected. Two possibilities of defining unaffected cows were considered. One was to include only cows having at least one claw health record in the parity, and if not affected for the specific claw disorder the cow was defined as unaffected for this disorder. The other possibility was to, in addition to the latter, include cows without claw health records in the herd at the time of claw trimming, and assume these cows as unaffected for all claw disorders. Cows not selected for claw trimming by the farmer may seem healthy, but mild cases of claw disorders could be present. Therefore, defining cows without claw health records as unaffected may lead to an underestimation of the frequency of claw disorders. A study by van der Spek et al. (2013) found

no differences in heritabilities on the underlying scale when untrimmed cows in herds with claw trimming records were included as unaffected, compared to including only trimmed cows. In this thesis, only cows having at least one claw health record were included in the analyses.

Claw trimmer

The ability of diagnosing claw disorders correctly may vary among claw trimmers, due to differences in experience. To account for this, effect of claw trimmer were included in the models used for genetic analyses and shown to have significant effect. The frequencies of HH, DE, SU, WLD and HSW were lower when farmers did the claw trimming, whereas for CSC no clear differences were seen among the groups of claw trimmers (Paper I). Because of the coding system currently used, it was not possible to identify other claw trimmers and farmers on individual level. Therefore, grouping of claw trimmers were chosen as an option to include the effect of claw trimmers. Holzhauer et al. (2006) found variation in diagnosing of claw disorders among trained claw trimmers and suggested that effect of claw trimmer should be accounted for. Using only claw health data recorded by professional claw trimmers could improve the data quality. However, this would reduce the number of records available for genetic analyses considerably, and was therefore not an option at the time. Norwegian farmers should be encouraged to use professional claw trimmers, as this probably will give more consistent recording of claw health. Over the latest years, the data recorded by professional claw trimmers have been increasing, and the expectation is that it will continue increasing when the electronic recording system is thoroughly implemented in Norway.

Genomic prediction

Genomic selection is an important tool for animal breeding, and genomic information should be utilized in the genetic evaluation. However, in Norwegian Red, several studies have shown that for low heritability traits, like fertility and health traits, there are some challenges in obtaining reliable genomic predictions (e.g. Paper III; Paper IV; Svendsen et al., 2013; Haugaard et al., 2015). Fertility and health are important traits in the breeding profile of Norwegian Red, and therefore it is important to solve these challenges before fully implementing genomic selection in the breeding scheme.

One issue is how the results are interpreted. Different methods for calculating accuracy or reliability of GEBV exist, and it is important to be careful in the comparison of results from

different studies. For claw disorders, deregressed proofs (**DRP**) calculated from EBVs were used as response variable in Paper III and the predicted GEBV were correlated to DRP calculated using all known information. However, the reliability of the EBV for these traits were low, making the response variable (DRP) used in the genomic prediction less certain, which also affect the predicted GEBV. Another issue is proper validation of the results from genomic predictions. Claw disorders are novel traits with limited historical data (recorded since 2004), and the youngest sires having daughters with claw health records are born in 2008 and 2009. Using the youngest sires in the validation set and excluding all claw health records from 2008 and onwards in the analyses would result in exclusion of about ⅔ of the available records, as nearly all claw health data are recorded later than 2008 (Table 1). To overcome the problem of excluding too much data, 10-fold cross-validations were performed (Paper III and Paper IV). A cross-validation will provide standard deviations, making it possible to interpret the consistency and precision of the results. However, cross-validation may overestimate the predictive ability, because sires in the validation sets may have several sons in the reference population and thereby obtain a lot of information from their close relatives. This situation will not occur in the evaluation of young sires.

To improve genomic predictions, the reference population should be increased with genotyped animals having reliable phenotypes. Increasing the reference population by including sires having daughters with information on genetic correlated traits, showed no improvement of genomic predictions unless the traits were strong genetic correlated (Paper III). Single-step GBLUP (**ssGBLUP**) (Legarra et al., 2009; Christensen and Lund, 2010) combines additive and genomic relationship matrices, making it possible to utilize all available information despite not having genotyped all animals having phenotypic records. The relationship matrix based on genotype information is supposed to give a more accurate relationship among the genotyped animals compared to pedigree information, thereby improve the predictions. The expectation was that inclusion of genotyped cows having claw health records, in addition to genotyped sires, in a ssGBLUP-analysis would improve the genomic predictions. However, this was not achieved, mainly caused by too few available cow genotypes. To investigate the benefit of including genotyped cows in the genomic predictions, as presented by other authors (Pryce et al., 2012; Egger-Danner et al., 2014; Luan et al., 2014), more cows with claw health records need to be genotyped. Based on the findings in Paper III and Paper IV, the most promising method for improving genomic prediction is use of ssGBLUP, where a large number of genotypes from animals having phenotypic records are included. Before implementing

genomic prediction on claw disorders in the genetic evaluation, further investigations are essential.

Further research

When more claw health records become available, further improvement of the genetic evaluation of claw health will be possible. As stated in the introduction, 33% (in 2013) of Norwegian herds and on average 30% of cows in a herd had at least one claw health record. This show the potential to increase the number of records per year, by increasing the number of herds where claw health is routinely recorded on all heifers and cows. With the new electronic recording system for claw health, the expectation is that number of records will increase. In addition, as more of the claw health records come from professional claw trimmers, the data quality is expected to improve. With more data available, it will be beneficial to include single claw disorders in the claw health index instead of grouped claw disorders. In addition, include new claw disorders implemented in relation to the harmonization of claw health across the Nordic countries. A harmonization against the ICAR Claw Health Atlas should also be carried out for Norwegian Red (Egger-Danner et al., 2015b).

There are several possibilities to optimize the genetic evaluation of claw disorders, to be able to utilize the information most efficiently. At this point, claw disorders are defined as the same disorder across lactations. With more information available, it could be possible to examine whether claw disorders are genetically different traits across lactations. As shown in paper IV, housing system had a significant effect on the model. The frequency of claw disorders in tie stall and free stall were 13% and 38%, respectively (these frequencies are based on claw health records recorded in herds having known housing systems, which were approximately 70% of the records). This indicate a possible difference in the incidence of claw disorders among housing systems, which should be considered in the prediction of breeding values for claw disorders. Genetic correlation to other important traits in the breeding scheme is also of interest, like milk yield, mastitis and fertility traits. At present, no published work on Norwegian Red is available.

Exploiting the use of genomic information in breeding for claw health is of importance, for example by genome-wide association study (GWAS). So far, Paper III and Paper IV represent the only genomic studies of claw health in Norwegian Red. However, with available genotypes on cows with claw health records, a GWAS to identify genetic markers associated with claw

disorders would be of interest. Other studies have found associations between genetic markers and claw disorders: Swalve et al. (2014) found a strong association between sole hemorrhage and the gene IQGAP1 in Holstein cattle, and van der Spek et al. (2015) detected 10 significant SNP associated with SU and 45 suggestive SNP associated with double sole, interdigital hyperplasia, SU and laminitis-related claw disorders. These studies demonstrated the possibility to detect genes affecting claw disorders, which could be valuable in the breeding for improved claw health. A GWAS should therefore be conducted on Norwegian claw health data to detect possible genes and thereby improving the breeding for claw health. However, more genotypes should be available, preferable from a high density SNP-chip, as this will increase the possibility to detect genes associated with claw disorders.

General conclusions

Claw disorders are traits with low frequency and low heritability, but this PhD-thesis showed that breeding for improved claw health using data recorded at claw trimming was possible. Grouping of claw disorders into INF and LAM were feasible due to strong genetic correlations among the claw disorders within the groups. The claw disorders and foot and leg conformation traits had in general low to moderate genetic correlations, implying that direct selection against claw disorders is the most efficient for improved claw health in the Norwegian Red population. Predictive ability of GEBV for claw disorders were low. Including strong genetic correlated traits (e.g. hoof quality) in the reference population gave a slightly better predictive correlation of GEBV for CSC. Use of ssGBLUP including genotypes of sires improved the genomic predictions of claw disorders, whereas adding genotypes of cows with claw health records gave no further improvement. However, the results showed possibilities for improving genomic predictions of novel, low heritable traits with limited amount of historical data.

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Genetic analyses of claw health in Norwegian Red cows

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Genetic analyses of claw health in Norwegian Red cows

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ABSTRACT

The aim of this study was genetic analyses of claw health in Norwegian Red. Claw health status at claw trimming has, since 2004, been recorded in the Norwegian Dairy Herd Recording System. The claw trimmer records whether the cow has normal (healthy) claws or if one or more claw disorders are present. Nine defined claw disorders were recorded: corkscrew claw (CSC), heel horn erosion (HH), dermatitis (DE), sole ulcer (SU), white line disorder (WLD), hemorrhage of sole and white line (HSW), interdigital phlegmon (IDP), lameness (LAME), and acute trauma (AT). Data from 2004 to 2011, with a total of 204,892 claw health records, were analyzed. The disorders were defined as binary traits with 1 record per cow per lactation. Further, 3 groups of claw disorders were analyzed: infectious claw disorders (INFEC, containing HH, DE, and IDP); laminitis-related claw disorders (LAMIN, containing SU, WLD, and HSW); and overall claw disorder. The 9 single traits and the 3 groups were analyzed using univariate threshold sire models. Multivariate threshold models were performed for the 5 most frequent single traits (CSC, HH, DE, SU, and WLD) and for CSC together with the grouped traits INFEC and LAMIN. Posterior mean of heritability of liability ranged from 0.04 to 0.23, where CSC had the highest heritability. The posterior standard deviations of heritability were low, between 0.01 and 0.03, except for IDP (0.06). Heritability of liability to INFEC and LAMIN were both 0.11 and for overall claw disorders, the heritability was 0.13. Posterior means of the genetic correlation among the 5 claw disorders varied between 0.02 and 0.79, and the genetic correlations between DE and HH (0.65) and between WLD and SU (0.79) were highest. Genetic correlation between INFEC and CSC was close to zero (0.06), between LAMIN and CSC it was 0.31, and between LAMIN and INFEC it was 0.24. The results show that claw disorders are sufficiently heritable for genetic evaluation and inclusion in the breeding scheme. At present, data are scarce with few recorded daughters per sire. Claw trimming records from more herds would therefore be beneficial for routine genetic evaluation of claw health.

Key words: claw disorder, dairy cow, genetic parameter, threshold model

INTRODUCTION

Claw health has become important in Norway due to the increased use of freestalls (Simensen et al., 2010). The incidence of claw disorders in Norwegian Red treated by veterinarians has increased from 1990 to 2005 (Østerås et al., 2007). Sogstad et al. (2005) found, in a cross-sectional study, that 71.8 and 47.8% of the cows in freestalls and tiestalls, respectively, had claw lesions. Lameness causes economic losses to the farmer (Enting et al., 1997) because it influences production diseases (Sogstad et al., 2006), fertility (Sogstad et al., 2006; Walker et al., 2008), early culling (Sogstad et al., 2007a), and milk production (Sogstad et al., 2007b). Not all cases of claw disorders show clinical signs, so the number of cows with claw disorders may be higher than the number of lame cows. Environmental factors, such as herd, flooring, and feeding, affect claw disorders (e.g., Bielfeldt et al., 2005; Fjeldaas et al., 2011; Buttchereit et al., 2012). Experience in detecting claw disorders may vary between claw trimmers. Holzhauer et al. (2006) found differences between trained claw trimmers in their ability to diagnose chronic laminitis, interdigital dermatitis or heel horn erosion, sole hemorrhage, and white line disease. Claw disorders can be grouped into infectious (hygiene) or laminitis (feed)-related claw disorders depending on the cause of disease. For example, dermatitis and heel horn erosion are infectious disorders, whereas sole ulcer and white line disorder are laminitis-related claw disorders (Fjeldaas et al., 2007; Buch et al., 2011).

The heritabilities of claw disorders are generally low and genetic correlations among them vary between −0.19 and 0.95 (e.g., van der Waaij et al., 2005; Buch et al., 2011; Johansson et al., 2011). Genetic correlations among claw disorders and feet and leg conformation traits have been estimated by several researchers (e.g., van der Waaij et al., 2005; Laursen et al., 2009; Häggman et al., 2013). Laursen et al. (2009) found the

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highest genetic correlation for overall claw health with locomotion (0.46) and with rear leg rear view (0.21). Among single claw disorders and leg and conformation traits, van der Waaij et al. (2005) estimated that the highest genetic correlations were for foot angle with white line disease (0.64) and for locomotion with interdigital hyperplasia (0.82). Uggla et al. (2008) concluded that genetic correlations among claw health traits and feet and leg conformation traits in Swedish Red and Swedish Holstein were insufficient to select indirectly for claw health.

Currently, corkscrew claw is the only claw disorder included in routine genetic evaluation of Norwegian Red. This trait is recorded together with other conformation traits on first-lactation cows (Geno Breeding and AI Association, 2011). Recording corkscrew claw at claw trimming would probably be a more accurate measure, because the cow is fixed and each claw examined more thoroughly. Claw health recorded at claw trimming has, since 2004, been an integrated part of the Norwegian Dairy Herd Recording System, but has so far not been used for genetic evaluation.

The objective of this study was the first genetic analysis of Norwegian claw health records. The aims were to estimate heritabilities of and genetic correlations among claw disorders, for single disorder, grouped disorder, and overall claw disorder.

MATERIALS AND METHODS

Data

Data from the Norwegian Dairy Herd Recording System from 2004 to 2011 were used in the analyses. The data included 309,885 claw health records from 178,452 cows recorded at claw trimming. The claw trimmers recorded whether the cow had normal (healthy) claws or if one or more of 9 claw disorders were present (Table 1). Claw disorders included were corkscrew claw (**CSC**), heel horn erosion (**HH**), dermatitis (**DE**), sole ulcer (**SU**), white line disorder (**WLD**), hemorrhage of sole and white line (**HSW**), interdigital phlegmon (**IDP**), lameness (**LAME**), and acute trauma (**AT**). Identification of claw trimmer, date of claw trimming, and other disorders or remarks were also recorded. Claw trimmers were categorized into professional claw trimmers, other claw trimmers, farmers, and others such as veterinarians or veterinary students. Professional claw trimmers are certified by the Norwegian Cattle Health Services (Sogstad and Fjeldaas, 2008), whereas other claw trimmers and farmers lack certification. Professional claw trimmers have a unique code so that they can be identified when recording claw health, whereas other claw trimmers and farmers use a universal group code. A cow could have several claw disorders reported on the same day; however, the leg involved (front or rear) was not reported. Because reporting is voluntary, not all claw health records are reported to the central database and some herds fail to report healthy cows. In Norway, most herds do claw trimming once or occasionally twice per year, but not all cows are necessarily trimmed at each claw trimming.

The number of claw health records per year has increased gradually to about 70,000 in 2011 (Figure 1), and the number of herds reporting claw health records (Figure 2) has increased to approximately 3,000. On average, about 30% of the cows in a herd had at least one claw health record, and 23% of the claw health records noted a claw disorder. Frequencies of each of the single claw disorders have increased from 2004 to 2011, except for IDP, LAME, and AT (Table 2). In 2011, the frequency of single claw disorders (% of all claw health records) varied from 0.2% (IDP) to 10% (CSC). Veterinarian-treated cases of IDP were not reported in the claw health recording, and therefore not included in these data. The frequency of IDP may therefore be higher than shown here. A total of 2,651 sires and 6,773 herds were represented in the data.

The average herd size for herds contributing with claw health data was 26 cows, with standard deviation (**SD**) of 17. On average, there were 110, 46, and 1.7 claw health records per sire (includes all available

Table 1. Definitions of normal claws and claw disorders included in the Norwegian claw health recording system (Refsum, 2012)

Claw health	Abbreviation	Definition
Normal		No claw disorders when examined under claw trimming
Corkscrew claw	CSC	Small to large twist in the abaxial wall on the lateral hind claws
Heel horn erosion	HH	Moderate to severe degree of erosion in the heel bulb with distinct V-shape
Dermatitis	DE	Dermatitis (bleeding, exuding, or wart-like) in front or rear in the interdigital claw
Sole ulcer	SU	Defect in the horn near the corium between the sole and heel bulb
White line disorder	WLD	Defect in the white line, in severe cases it can reach the corium
Hemorrhage of sole and white line	HSW	Hemorrhage of more than 20% of the sole or white line or both
Interdigital phlegmon	IDP	Severe infection in the interdigital claw, with swelling of the leg
Lameness	LAME	Locomotion score $\geq$3
Acute trauma	AT	For example, fractures and dislocation of joint

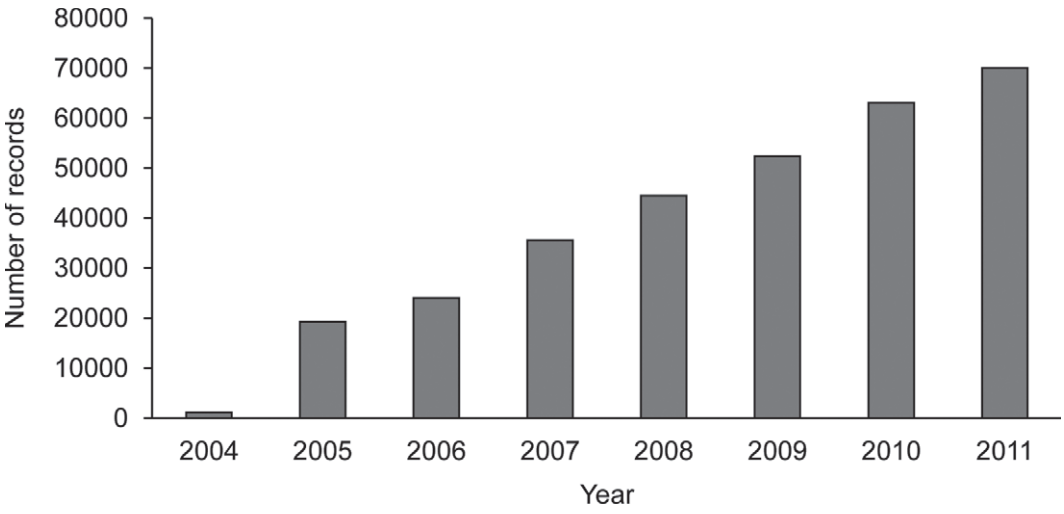

Figure 1. Number of claw health records per year.

records for both elite and young sires), herd, and cow, respectively, with corresponding SD of 406, 67, and 1. The maximum number of records per sire, herd, and cow was 6,013, 1,227, and 18, respectively. The average daughter group with claw health records for sires that got their first official proofs in 2010 and 2011 was 34 and 37, respectively. Approximately 18% of the cows had 2 or more claw health records during one lactation.

Data Editing

Editing of the data was performed in SAS (SAS Institute, 2002). Only cows with claw health data were included in the analyses. Herds reporting less than 10% or fewer than 10 normal claw records from 2004 to 2011 were excluded; cows must have had Norwegian Red AI sire; and age at calving was within defined intervals. The intervals for calving age in months were as follows: first calving between 16 and 48 mo; second calving between 26 and 61 mo; third calving between 36 and 74 mo; and fourth calving between 45 and 87 mo. After editing, the data set contained 204,892 claw health records from 141,659 cows, 1,904 sires, and 6,156 herds. The data set included no records of HSW before 2007, so it was smaller for this trait and contained 174,877 claw health records from 123,511 cows, 1,679 sires, and 5,637 herds.

Trait Definitions

Each single claw disorder was defined as a binary trait, 0 (normal) or 1 (disorder), for each cow and lactation. A lactation was defined from calving to 365 d after calving or, until next calving or culling if either occurred before 365 d. Because some claw disorders had a low frequency (Table 3), grouping them is an option. Overall claw disorder (**OCD**) was defined based on whether or not the cow had at least one claw disorder

Table 2. Development of normal (healthy) claws and claw disorders (percentage of all claw trimming records) in Norway from 2004 to 2011

	Year							
Claw health	2004	2005	2006	2007	2008	2009	2010	2011
Normal	91.1	83.2	85.2	85.9	77.2	77.2	73.8	69.8
Corkscrew claw	4.0	7.6	6.8	6.8	9.2	9.5	10.2	11.0
Heel horn erosion	1.0	1.7	1.9	2.2	4.0	4.0	4.8	6.6
Dermatitis	0.1	0.7	0.6	0.7	1.7	1.4	1.8	2.6
Sole ulcer	0.9	2.4	2.0	1.8	2.2	2.2	2.5	2.5
White line disorder	0.3	1.9	1.7	1.4	2.3	2.3	3.1	3.9
Hemorrhage of sole and white line	0	0	0	0.2	1.9	1.7	2.2	2.3
Interdigital phlegmon	0.1	0.2	0.3	0.1	0.1	0.2	0.3	0.2
Lameness	2.7	2.2	1.4	1.1	1.3	1.1	1.1	1.0
Acute trauma	0.1	0.1	0.2	0.2	0.2	0.3	0.2	0.1

(any of the 9) recorded during a lactation. Two groups of claw disorders were also defined by the cause of the disorder: infectious claw disorders (**INFEC**, containing DE, HH, and IDP), and laminitis-related claw disorders (**LAMIN**, containing SU, WLD, and HSW). The mean frequency of the claw disorders and groups of claw disorders (Table 3) ranged from 0.1 to 21.3%. For each single trait or group of claw disorders, only the first occurrence per lactation was used. The time of the corresponding claw trimming was included in the analyses. For healthy cows, the time of first trimming was used.

Table 3. Mean frequency of single and grouped claw disorders analyzed, where cows have 1 record per trait per lactation

Trait	Frequency, %
Corkscrew claw	10.2
Heel horn erosion	4.4
Dermatitis	1.7
Sole ulcer	2.7
White line disorders	2.9
Hemorrhage of sole and white line	2.2
Interdigital phlegmon	0.2
Lameness	1.3
Acute trauma	0.1
Infectious claw disorders	5.7
Laminitis-related claw disorders	6.8
Overall claw disorder	21.3

Statistical Analyses

Heritabilities and genetic correlations were inferred by a Bayesian approach using Gibbs sampling. Threshold sire models (e.g., Gianola and Foulley, 1983) were used for analyses. Univariate analyses of all 9 single traits and the 3 groups were performed. Multivariate models were used to estimate genetic correlations among the 5 single claw disorders with highest frequency: CSC, DE, HH, SU, and WLD, and among the 2 groups of claw disorders (INFEC and LAMIN) and CSC. In matrix notation, the threshold sire model used was

$$\boldsymbol{\lambda} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z_h}\mathbf{h} + \mathbf{Z_s}\mathbf{s} + \mathbf{e},$$

where $\boldsymbol{\lambda}$ is a vector of unobserved liabilities for the trait; $\boldsymbol{\beta}$ is a vector of systematic effects, including lactation number, calving year and month, time for claw trimming (months after calving), and claw trimmer; $\mathbf{h}$ is a vector of random herd effects with 6,156 levels, except for HSW, which had 5,637 levels; $\mathbf{s}$ is a vector of sire effects with 20,886 levels, $\mathbf{e}$ is a vector of residuals, and $\mathbf{X}$, $\mathbf{Z_h}$, and $\mathbf{Z_s}$ are the corresponding incidence matrices. Lactation number had 4 classes, where the fourth class included lactations 4 to 13. Calving year and month had 93 classes from April 2004 to December 2011, where the first class included all records before April 2004 because of few records in these months. Time for claw trimming, in months after calving, had 12 classes. Claw trimmers were divided into 4 classes: (1) professional claw trimmers with 58,633 claw health records; (2) other claw trimmers with 142,687 records; (3) farmers with 35,793 records; and (4) other persons with 6,045 records. The HSW had 72 classes for calving year and month (January 2007 to December 2011), where months before January 2007 were merged. Because of the low frequency of IDP and AT (Table 3), a reduced model without effect of calving year and month were used for these traits, to avoid extreme category problems.

For the univariate threshold models it was assumed that $\mathbf{s} \sim N\left(0, \mathbf{A}\sigma_s^2\right)$, $\mathbf{h} \sim N\left(0, \sigma_h^2\right)$, and $\mathbf{e} \sim N\left(0,1\right)$, where σ_s^2 is sire variance, σ_h^2 is herd variance, and the residual

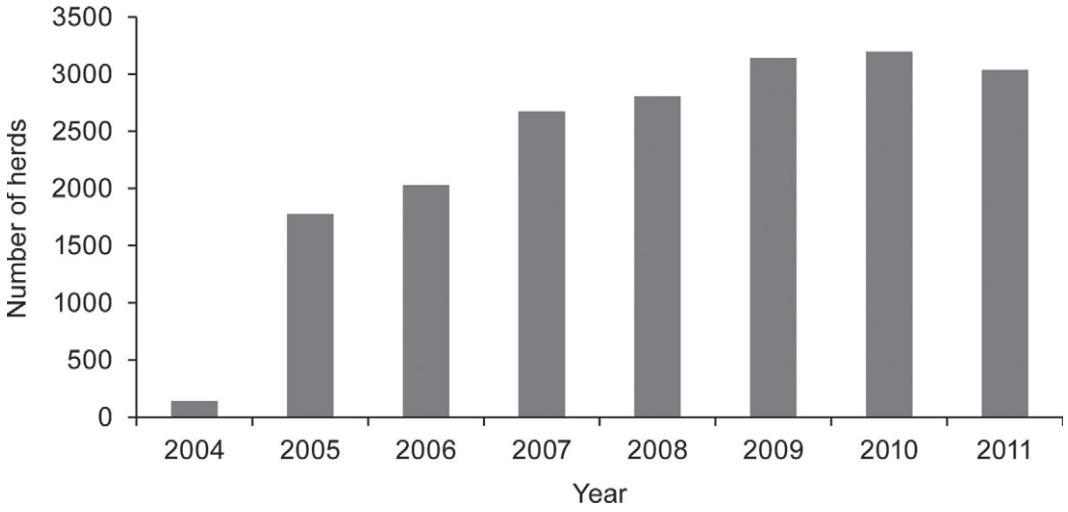

Figure 2. Number of herds with claw health records per year.

variance $\left(\sigma_e^2\right)$ was set equal to 1; **A** is the additive genetic relationship matrix. The pedigree file contained 20,886 animals, including sires of cows with claw health records, and their pedigree traced back as far as possible. In the multivariate analyses, it was assumed that $\text{var}(\mathbf{s}) = \mathbf{G} \otimes \mathbf{A}$, $\text{var}(\mathbf{h}) = \mathbf{H} \otimes \mathbf{I}$, and $\text{var}(\mathbf{r}) = \mathbf{R} \otimes \mathbf{I}$, where **I** is an identity matrix and **G**, **H**, and **R** are the 5 × 5 matrices containing genetic, herd, and residual variances, respectively, and covariance among the 5 traits. Heritability (h^2) was calculated using

$$h^2 = \frac{4 \times \sigma_s^2}{\sigma_s^2 + \sigma_e^2}.$$

Sampling and Convergence Diagnostics

The RJMC procedure of the DMU software (Madsen and Jensen, 2008) was used for analyses. Test for convergence were done using the Raftery and Lewis method in BOA (Bayesian Output Analyses; Smith, 2005). For the univariate analyses, burn-in was set to 10,000 iterations for all traits, and the total number of iterations varied between 130,000 and 575,000. For the multivariate analyses, the first 40,000 samples were discarded as burn-in and the total numbers of iterations for the 5 single disorders and the 3 groups were 900,000 and 750,000, respectively.

RESULTS AND DISCUSSION

Fixed Effects

Effects of claw trimmer were similar for HH, DE, INFEC, WLD, HSW, SU, and LAMIN, with lower frequencies when farmers performed claw trimming; for CSC, almost no differences were detected between the 4 categorizes of claw trimmers. Calving year and month had an effect but showed no clear trend for any of the claw disorders. Stage of lactation showed a peak 3 to 5 mo after calving for SU and HSW. Most of the other traits showed a slight increase in number of claw disorders in later stage of lactation. The effect of lactation number for OCD indicated more cases of claw disorders in later lactations.

Single Claw Disorders

Heritabilities. The posterior mean of heritability of liability from univariate analyses of single claw disorders ranged from 0.04 (LAME and AT) to 0.23 (CSC; Table 4). The SD of the heritabilities was low, ranging from 0.01 to 0.03, except for IDP, where SD was 0.06. The 95% highest probability density interval (**95% HPD**) presented in Table 4 did not include zero for any of the disorders. The widest 95% HPD were found for DE and IDP and the narrowest for HSW and LAME (Table 4). Results from the multivariate model (Table 5) were in accordance with the univariate analyses (Table 4). The posterior distribution of heritability of liability for the 5 claw disorders was symmetric, as shown in Figure 3, with SD ranging from 0.01 (HH) to 0.03 (DE; Table 5). Results from this study were in accordance with results found by Swalve et al. (2008) and Buch et al. (2011), where heritability at the underlying scale ranged from 0.07 to 0.17 for similar claw disorders. In contrast, Huang and Shanks (1995) found lower heritability for CSC (0.036) and SU (0.024) and higher heritabilities for HH (0.144) and WLD (0.150). This could be due to different scoring and definitions of the claw disorders and because their data came from a research herd. van der Waaij et al. (2005) found similar heritabilities using linear and threshold models, ranging from 0.01 to 0.10. Other studies have investigated different claw disorders and presented heritabilities from 0.01 to 0.12 on the observed scale (Koenig et al., 2005; van der Linde et al., 2010; Johansson et al., 2011).

Genetic Correlations. Posterior mean of genetic correlations among the 5 claw disorders ranged between 0.02 and 0.79, with posterior SD between 0.01 and 0.14 (Table 5). The highest genetic correlations were found between WLD and SU (0.79) and between DE and HH (0.65). Genetic correlations among CSC, DE, and WLD were all close to zero (≤0.04). Figure 4 shows the posterior distributions of genetic correlations within and between some of the single claw disorders that were grouped. The distributions were slightly skewed to the left, except for the genetic correlation between WLD and DE (Figure 4). The 95% HPD for the genetic correlations between WLD and SU, and between DE and HH ranged from 0.63 to 0.92, and 0.46 to 0.81, respectively (Table 5). The 95% HPD for 6 of the genetic correlations (Table 5) included zero, of which 5 involved WLD or CSC. Figure 4 shows 2 of these distributions: WLD and DE, and HH and CSC. High correlations may be expected between DE and HH, because both are infectious disorders, caused by bacteria and related to poor hygiene and wet flooring. The claws lose hardness (Webster, 1993) and become more available for infectious bacteria in such an environment. A high-concentrate feeding regimen increases the risk of capsule disruption of the claw that in turn increases the risk for SU and WLD (Webster, 1993). van der Linde et al. (2010) estimated genetic correlations among sole hemorrhage, digital dermatitis, interdigital dermatitis, and SU, and these varied between −0.33 and 0.93. Buch et al. (2011) estimated a genetic correlation of 0.87 ($P < 0.05$) between DE and HH, whereas genetic correla-

Table 4. Posterior mean, standard deviation (SD), and 95% highest probability density interval (95% HPD) of heritability of liability and posterior mean and SD of sire variance $\left(\sigma_s^2\right)$ and herd variance $\left(\sigma_h^2\right)$ from a univariate threshold model analyses of claw disorders

	Heritability			σ_s^2		σ_h^2	
Trait	Mean	SD	95% HPD	Mean	SD	Mean	SD
Corkscrew claw	0.23	0.02	[0.19; 0.26]	0.06	0.01	0.58	0.02
Heel horn erosion	0.09	0.02	[0.06; 0.13]	0.02	<0.01	1.43	0.07
Dermatitis	0.20	0.03	[0.14; 0.26]	0.05	0.01	1.05	0.07
Sole ulcer	0.18	0.02	[0.13; 0.22]	0.05	0.01	0.26	0.01
White line disorder	0.06	0.02	[0.03; 0.10]	0.02	<0.01	0.51	0.02
Hemorrhage of sole and white line	0.07	0.01	[0.04; 0.09]	0.02	<0.01	0.54	0.03
Interdigital phlegmon	0.14	0.06	[0.03; 0.24]	0.04	0.02	0.79	0.09
Lameness	0.04	0.01	[0.01; 0.06]	0.01	<0.01	0.64	0.04
Acute trauma	0.04	0.02	[0.01; 0.08]	0.01	0.01	0.56	0.06
Infectious claw disorders	0.11	0.02	[0.08; 0.14]	0.03	<0.01	1.23	0.05
Laminitis-related claw disorders	0.11	0.02	[0.08; 0.14]	0.03	<0.01	0.38	0.01
Overall claw disorder	0.13	0.01	[0.10; 0.15]	0.03	<0.01	0.64	0.02

tions between SU and DE (−0.19) and HH (0.13) were not different from zero. Genetic correlation between SU and HH were in contrast to the estimate of 0.42 in this study (Table 5). Koenig et al. (2005) found a moderate to high genetic correlation between digital dermatitis and SU (0.56).

Grouped Claw Disorders

Heritability. The posterior mean of heritability of liability from the univariate model was 0.11 for both INFEC and LAMIN (Table 4), and the results from multivariate analyses were almost the same (Table 6). The heritability of CSC was 0.23 in both models (Tables 4 and 6). For OCD, the posterior mean of heritability of liability was 0.13 (SD 0.01) and the 95% HPD ranged from 0.10 to 0.15. The heritability of OCD was higher than that for INFEC and LAMIN, most likely because CSC was included, which has the highest frequency and heritability of all claw disorders. The estimated heritability of OCD was in accordance with Buttchereit et al. (2012) but higher than the heritability on the underlying scale found by Häggman et al. (2013).

Genetic Correlations. The posterior mean of the genetic correlations between INFEC and CSC, LAMIN and CSC, and LAMIN and INFEC were 0.06, 0.31,

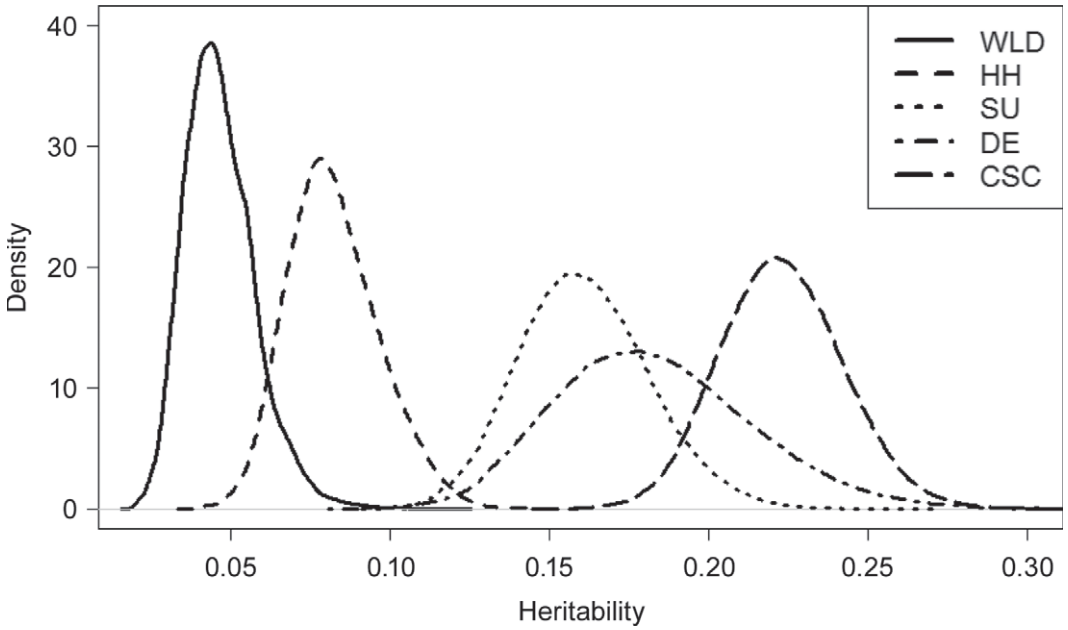

Figure 3. Posterior distribution of heritability of liability for (from left) white line disorder (WLD), heel horn erosion (HH), sole ulcer (SU), dermatitis (DE), and corkscrew claw (CSC), from multivariate analyses.

Table 5. Posterior mean (SD in parentheses, 95% highest probability density intervals in brackets) of heritability of liability (on diagonal) and genetic correlation (below diagonal) among corkscrew claw (CSC), heel horn erosion (HH), dermatitis (DE), sole ulcer (SU), and white line disorder (WLD)

	CSC	HH	DE	SU	WLD
CSC	0.22 (0.02) [0.19; 0.26]				
HH	0.13 (0.10) [−0.06; 0.32]	0.08 (0.01) [0.06; 0.11]			
DE	0.02 (0.10) [−0.18; 0.20]	0.65 (0.09) [0.46; 0.81]	0.18 (0.03) [0.13; 0.25]		
SU	0.42 (0.08) [0.27; 0.56]	0.42 (0.10) [0.23; 0.60]	0.19 (0.11) [−0.02; 0.39]	0.16 (0.02) [0.12; 0.20]	
WLD	0.04 (0.11) [−0.18; 0.26]	0.22 (0.14) [−0.06; 0.49]	0.04 (0.14) [−0.22; 0.32]	0.79 (0.08) [0.63; 0.92]	0.05 (0.01) [0.03; 0.07]

and 0.24, respectively (Table 6). The 95% HPD for the genetic correlation between INFEC and CSC included zero (−0.12 to 0.23), whereas between LAMIN and CSC and LAMIN and INFEC, the 95% HPD ranged from 0.15 to 0.46 and from 0.04 to 0.44, respectively (Table 6). The genetic correlations among the single claw disorders in the 2 groups INFEC and LAMIN were high within groups and lower between groups (Table 5). Other authors found moderate to high genetic correlations among single claw disorders grouped in a similar manner as in this study (van der Linde et al., 2010; Buch et al., 2011; Johansson et al., 2011). van der Linde et al. (2010) estimated genetic correlations between hygiene-related claw disorders (digital dermatitis, interdigital dermatitis, and interdigital hyperplasia) and laminitis-related claw disorders (sole hemorrhage, SU, and WLD), which ranged from −0.35 to 0.18. Buch et al. (2011) defined hygiene-related (DE and HH) and laminitis-related (sole hemorrhage and SU) hoof diseases based on high genetic correlations between the claw disorders within each group, and low genetic correlations between the single disorders in the 2 groups. The highest correlations were found between sole hemorrhage and SU (van der Linde et al., 2010; Buch et al., 2011), dermatitis and heel horn erosion (Buch et al., 2011), and digital dermatitis and interdigital dermatitis (van der Linde et al., 2010). Genetic correlations among CSC, infectious-related, and feed-related traits found by Johansson et al. (2011) varied between −0.13 and 0.40. Because the single claw dis-

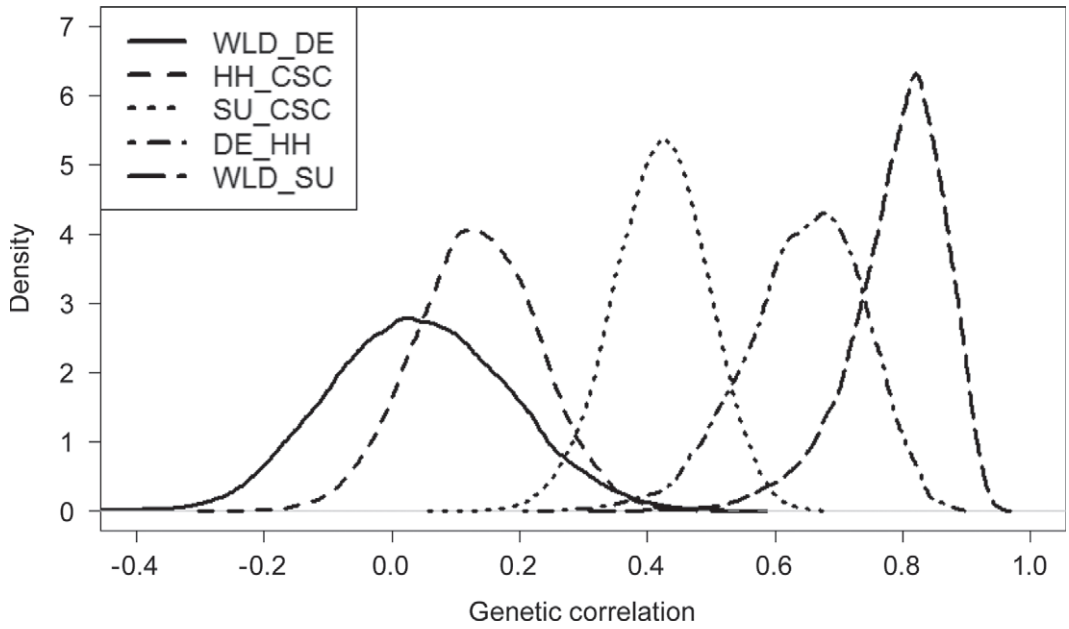

Figure 4. Posterior distribution of genetic correlation between (from left) white line disorder and dermatitis (WLD_DE), heel horn erosion and corkscrew claw (HH_CSC), sole ulcer and corkscrew claw (SU_CSC), dermatitis and heel horn erosion (DE_HH), and white line disorder and sole ulcer (WLD_SU).

Table 6. Posterior mean (SD in parentheses, 95% highest probability density intervals in brackets) of heritability of liability (on diagonal) and genetic correlation (below diagonal) among corkscrew claw (CSC), infectious claw disorders (INFEC), and laminitis-related claw disorders (LAMIN)

	CSC	INFEC	LAMIN
CSC	0.23 (0.02) [0.19; 0.26]		
INFEC	0.06 (0.09) [−0.12; 0.23]	0.10 (0.02) [0.07; 0.13]	
LAMIN	0.31 (0.08) [0.15; 0.46]	0.24 (0.10) [0.04; 0.44]	0.10 (0.01) [0.08; 0.13]

orders showed low frequency, a grouping of these could be advantageous for genetic evaluation to get higher prevalence for the defined claw trait. This is only valid if the genetic correlations among claw disorders within each group are high, so it becomes reasonable to assume they are almost the same trait or are affected by some common genes.

Herd and Residual Correlations

The posterior mean of residual correlations were all close to zero (−0.14 to 0.14; Tables 7 and 8), except for the correlation between DE and HH (0.34). Posterior mean of herd correlations ranged from 0.26 (DE and CSC) to 0.65 (DE and HH) for the 5 claw disorders analyzed in the multivariate model (Table 7), and from 0.37 to 0.55 for CSC, INFEC, and LAMIN (Table 8). Dermatitis and HH had the highest mean herd variance together with INFEC (Table 4), whereas SU and LAMIN had the lowest herd variance. The results indicate that different claw disorders are affected by similar environmental effects, as shown by other authors (e.g., Nielsen et al., 1997; Bielfeldt et al., 2005). Herd factors such as types of flooring, cubicle, nutrition, and feeding system can affect claw disorders. For example, small or poorly formed cubicles can reduce the lying time and thereby increase the risk of claw disorders (Leonard et al., 1996) such as SU and WLD.

The model used in the present study did not include the permanent environmental effect of cow, because few cows had more than one record and most of the cows were healthy. The herd effect would therefore include a possible permanent effect of cow.

Claw Health Data

Not every cow in a herd had a claw health record because claw trimming may not have been needed at a visit. Such cows may be healthy, but not necessarily, because some claw disorders can only be observed at claw trimming. To define healthy cows, one alternative is to include only cows with claw health records in the analyses, another is to include all cows in a herd and assume that cows without claw health records are healthy. The latter would underestimate the frequency of claw disorders, whereas excluding them would lead to an overestimation. The frequencies of single claw disorders in Norwegian Red were generally lower than those in other Nordic countries (Johansson et al., 2011), except CSC, which had considerably higher frequency. In Norway, DE includes both digital and interdigital dermatitis, because few cases of digital dermatitis were found (Sogstad et al., 2005). Our results for DE are therefore difficult to compare with results from other studies (e.g., Koenig et al., 2005; Swalve et al., 2008; Häggman et al., 2013) in which the 2 traits (digital dermatitis and interdigital dermatitis) are defined as separate traits.

The accuracy of diagnosis of claw disorders may vary between categories of claw trimmers. Farmers who only perform claw trimming in their own herd may have less experience in diagnosis of claw disorders. The group of "other" claw trimmers had the greatest number of claw health records, but individual claw trimmers cannot be distinguished within the group. Experience in diagnosing claw disorders and the number of claw trimmings per person per year will vary within this group.

More daughters with claw health information per sire would be beneficial for genetic evaluation. At present, the number of daughters with claw health records available at the time when the sires get their first official proof is low compared with other health traits in Norwegian Red. Denmark, Finland, and Sweden implemented a claw health index in 2011, and the average daughter groups per sire varied from 11 to 59 between

Table 7. Posterior mean (SD) of herd correlation (above diagonal) and residual correlation (below diagonal) among corkscrew claw (CSC), heel horn erosion (HH), dermatitis (DE), sole ulcer (SU), and white line disorder (WLD)

	CSC	HH	DE	SU	WLD
CSC		0.40 (0.02)	0.26 (0.03)	0.37 (0.02)	0.46 (0.02)
HH	−0.06 (0.01)		0.65 (0.02)	0.44 (0.02)	0.54 (0.02)
DE	−0.14 (0.02)	0.34 (0.02)		0.47 (0.03)	0.52 (0.03)
SU	0.06 (0.01)	0.11 (0.02)	0.07 (0.02)		0.51 (0.02)
WLD	0.01 (0.01)	0.08 (0.02)	0.00 (0.02)	0.14 (0.02)	

Table 8. Posterior mean (SD) of herd correlation (above diagonal) and residual correlation (below diagonal) among corkscrew claw (CSC), infectious claw disorders (INFEC), and laminitis-related claw disorders (LAMIN)

	CSC	INFEC	LAMIN
CSC		0.37 (0.02)	0.45 (0.02)
INFEC	−0.10 (0.01)		0.55 (0.02)
LAMIN	0.02 (0.01)	0.02 (0.01)	

breeds (Holstein and Red Dairy Cattle) and countries (Johansson et al., 2011). Claw health status recorded at claw trimming provides useful information that can be used for genetic evaluation and gives opportunities for more efficient selection for improved claw health in Norwegian Red.

CONCLUSIONS

Claw disorders are heritable, and CSC, DE, and SU have the highest heritabilities (≥0.18). The genetic correlations among the 5 most frequent claw disorders support the grouping of claw disorders into CSC, INFEC, and LAMIN, which could be a way to include claw health in the breeding scheme. Including claw health in the total merit index will have positive effects on the prevalence of claw disorders in the long term.

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Genetic correlations between claw health and feet and leg conformation in Norwegian Red cows

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ABSTRACT

The aim of this study was to estimate genetic correlations between claw disorders and feet and leg conformation traits in Norwegian Red cows. A total of 188,928 cows with claw health status recorded at claw trimming from 2004 to September 2013 and 210,789 first-lactation cows with feet and leg conformation scores from 2001 to September 2013 were included in the analyses. Traits describing claw health were corkscrew claw, infectious claw disorders (dermatitis, heel horn erosion, and interdigital phlegmon), and laminitis-related claw disorders (sole ulcer, white line disorder, and hemorrhage of sole and white line). The feet and leg conformation traits were rear leg rear view (new and old definition), rear leg side view, foot angle, and hoof quality. Feet and leg conformation traits were scored linearly from 1 to 9, with optimum scores depending on the trait. Claw disorders were defined as binary (0/1) traits for each lactation. Threshold sire models were used to model claw disorders, whereas the feet and leg conformation traits were described by linear sire models. Three multivariate analyses were performed, each including the 5 feet and leg conformation traits and 1 of the 3 claw disorders at a time. Posterior means of heritability of liability of claw disorders ranged from 0.10 to 0.20 and heritabilities of feet and leg conformation traits ranged from 0.04 to 0.11. Posterior standard deviation of heritability was ≤0.01 for all traits. Genetic correlations between claw disorders and feet and leg conformation traits were all low or moderate, except between corkscrew claw and hoof quality (−0.86), which are supposed to measure the same trait. The genetic correlations between rear leg rear view (new) and infectious claw disorders (−0.20) and laminitis-related claw disorders (0.26), and between hoof quality and laminitis-related claw disorders (−0.33) were moderate. Eight of the 15 genetic correlations between claw disorders and feet and leg conformation traits had 0 included in the 95% highest posterior density interval. These results imply that selection for feet and leg conformation is not an efficient approach to genetically improve claw health in Norwegian Red cattle.
Key words: claw disorder, feet and leg conformation, genetic correlation, dairy cow

INTRODUCTION

More freestalls (Simensen et al., 2010) and a focus on claw health have increased the interest in breeding for better claw health in Norwegian Red cattle. Since 2004, claw health status at claw trimming has been reported to the Norwegian Dairy Herd Recording System, and Ødegård et al. (2013) showed that these data are suitable for genetic evaluation of Norwegian Red cattle. The current feet and leg index included in the total merit index (**TMI**) for Norwegian Red cattle contains 3 feet and leg conformation traits: rear leg rear view (**RLRV**), foot angle (**FANG**), and hoof quality (**HQ**), with weights of 35, 25, and 40%, respectively. The feet and leg index receives a relative weight of 6% in the TMI (Geno, 2013). All conformation traits are scored on first-lactation cows by breeding advisors.

The number of claw health records from claw trimming has gradually increased over time, but the data are still limited (Ødegård et al., 2013). In 2012, about 60,000 Norwegian Red cows had at least 1 claw health record and about 30% of Norwegian dairy herds reported claw health. Daughter groups for claw health at first official proof of the sires are small compared with other health traits in the Norwegian Red breeding scheme, where at least 140 daughters are required. In 2012, 123 sires got their first official breeding values. These sires had, on average, 39 daughters with claw health records at the time of their first official proof. To use the new claw health information from claw trimming, claw disorders will be included in the feet and leg index. Information from genetically correlated traits could be used to increase reliability of breeding values for claw disorders.

Several authors have estimated genetic correlations between claw disorders and feet and leg conformation

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traits (e.g., Uggla et al., 2008; Häggman and Juga, 2013; van der Linde et al., 2010) and the results vary between breeds and populations. Uggla et al. (2008) estimated low to moderate genetic correlations in Swedish Red cattle, ranging from −0.31 (hock quality and heel horn erosion) to 0.17 [rear leg side view (**RLSV**) and heel horn erosion], whereas van der Waaij et al. (2005) estimated higher genetic correlations, ranging from −0.35 (RLRV and interdigital hyperplasia) to 0.64 (FANG and white line disorder) in Dutch dairy cattle. In Finnish Ayrshire cows, the genetic correlations between overall claw disorder and feet and leg conformation traits ranged from −0.40 (bone structure) to 0.42 (RLSV; Häggman et al., 2013), whereas Finnish Holstein cows had genetic correlations ranging from −0.51 (FANG and sole ulcer) to 0.45 (FANG and heel horn erosion; Häggman and Juga, 2013). With such a large range of estimates of genetic correlations in other breeds and populations, it is of interest to study these associations in Norwegian Red cattle. The aim of this study was to estimate genetic correlations between claw disorders and feet and leg conformation traits in Norwegian Red cattle.

MATERIALS AND METHODS

Claw Health

Claw health status, recorded at claw trimming, from 2004 to September 2013 was used in the analyses. Nine different claw disorders were recorded as healthy or diseased: corkscrew claw (**CSC**), dermatitis, heel horn erosion, interdigital phlegmon, sole ulcer, white line disorder, hemorrhage of sole and white line, lameness, and acute trauma. All trimmed cows were recorded, including healthy cows. A cow could have more than 1 claw disorder recorded on the same day. Also, the identification of claw trimmer and date of claw trimming were recorded at each claw trimming. The recording is voluntary and therefore not reported by all herds. Approximately 30% of the cows in a herd had claw health recorded and about 18% of the cows had more than 1 claw health record during a lactation (Ødegård et al., 2013). More details of claw health data in Norway can be found in Ødegård et al. (2013).

Based on results from Ødegård et al. (2013), 1 single claw disorder (CSC) and 2 groups of claw disorders [infectious (**INF**) and laminitis-related (**LAM**) claw disorders] were included in the analyses (Table 1). The INF claw disorders included dermatitis, heel horn erosion, and interdigital phlegmon; and LAM claw disorders included sole ulcer, white line disorder, and hemorrhage of sole and white line. Claw health data was edited as described in Ødegård et al. (2013); only cows and lactations with claw health records, daughters of Norwegian Red AI sires, and herds recording more than 10% or at least 10 cows with normal claws were included. In addition, age at calving should be between 16 and 48 mo for first lactation, 26 and 61 mo for second lactation, 36 and 74 mo for third lactation, and 45 and 87 mo for fourth lactation. After editing, the total number of claw health records was 285,581 from 188,928 cows in 6,891 herds and 2,101 sires had daughters with claw health data in the final data set. A cow was defined as either healthy (0) or diseased (1) for each of the 3 traits (CSC and INF and LAM claw disorders) in each lactation where at least 1 claw-trimming record was present. If a cow had more than 1 case of a claw disorder during a lactation, only the first observation was included in the analyses. Few cows had claw health records for more than 1 lactation and, therefore, a possible permanent environment effect was ignored in the analyses. The mean frequency of CSC and INF and LAM claw disorders was 0.11, 0.06 and 0.07, respectively (Table 1).

Feet and Leg Conformation

Feet and leg conformation scores from 1987 to 2013 were available, but only data from 2001 to September 2013 were used in the analyses, due to changes in the scoring system in 2001. Breeding advisors score feet and leg conformation together with other conformation traits on first-lactation cows. Four feet and leg conformation traits are recorded: RLRV, RLSV, FANG, and HQ (Table 1). The definition of RLRV changed in 2010 and was, therefore, treated as 2 correlated traits: new (**RLRV_N**) and old (**RLRV_O**). Hoof quality from conformation scoring and CSC from claw trimming measures the same trait, but are recorded differently (Table 1). Hoof quality is scored when the cow is standing, whereas CSC is measured when the cow is fixed and the sole is inspected. The feet and leg conformation traits are scored on a scale from 1 to 9, with the optimum value depending on the trait (Table 1). Data editing for feet and leg conformation traits was performed as in routine genetic evaluation (Interbull, 2011): only daughters of Norwegian Red AI sires with age at first calving between 18 and 33 mo, and time for conformation scoring within defined intervals (months after calving) were included. The final data set had feet and leg conformation scores for 210,789 first-lactation cows in 13,659 herds and by 1,655 sires. The number of records for all trait combinations of claw health and feet and leg conformation are presented in Table 2.

The total number of sires with daughter information on claw health, feet and leg conformation, or both was

Table 1. Definitions and optimum values of claw disorders and feet and leg conformation traits,[1] frequency of the claw disorders, and average scoring of feet and leg conformation traits with SD in the analyzed data

Trait	Abbreviation	Definition	Scoring	Optimum value	Average score	SD
Corkscrew claw	CSC	Small to large twist in the abaxial wall on the lateral hind claw	0 = healthy; 1 = disorder	0	0.11	0.3
Infectious claw disorders	INF	Heel horn erosion, dermatitis and interdigital phlegmon	0 = healthy; 1 = disorder	0	0.06	0.2
Laminitis-related claw disorders	LAM	Sole ulcer, white line disorder and hemorrhage of sole and white line	0 = healthy; 1 = disorder	0	0.07	0.3
Rear leg rear view (new)	RLRV_N	Rear legs should be parallel (from 2010)	1 = toes out; 9 = bow-legged	8	6.27	1.5
Rear leg rear view (old)	RLRV_O	Rear legs should be parallel (before 2010)	1 = toes out; 9 = bow-legged	5	4.60	0.9
Rear leg side view	RLSV	Optimum angle is 150–155 degrees	1 = straight; 9 = sickled	5	4.80	1.1
Foot angle	FANG	Optimum angle is 45 degrees	1 = low; 9 = steep	5	4.80	1.0
Hoof quality	HQ	Small to large twist in the abaxial wall on the lateral hind claw	1 = severe twisted; 9 = no twist	9	8.00	1.7

[1]Geno (2011) and Refsum (2012).

2,145. Of these sires, 1,611 had daughter information on both trait groups. The pedigree of sires with daughters was traced back as far as possible and the final pedigree file contained 18,895 animals.

Statistical Model

A Bayesian approach using Gibbs sampling was applied. The 3 claw disorders (CSC and INF and LAM claw disorders) were defined as binary traits and analyzed with threshold models, whereas the 5 feet and leg conformation traits (RLRV_N, RLRV_O, RLSV, FANG, and HQ) were assumed to be normally distributed and analyzed with linear models.

The threshold sire model used for claw disorders was as described in Ødegård et al. (2013):

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

where $\boldsymbol{\lambda}$ is a vector of unobserved liabilities of the trait; $\boldsymbol{\beta}$ is a vector of systematic effects, including lactation number, calving year and month, time for claw trimming (months after calving), and claw trimmer; $\mathbf{h}$ is a vector of herd effects, with 6,891 levels; $\mathbf{s}$ is a vector of sire effects; $\mathbf{X}$, $\mathbf{Z}_{\mathbf{h}}$, and $\mathbf{Z}_{\mathbf{s}}$ are the corresponding incidence matrices; and $\mathbf{e}$ is a vector of residuals. Lactation number had 4 levels, where the fourth class included lactation 4 to 13; calving year and month had 114 levels; time for claw trimming (months after calving) had 12 levels; and claw trimmer was divided into 4 groups: certified claw trimmers, other claw trimmers, farmers, and others (e.g., veterinarian).

The linear sire model for feet and leg conformation traits included the same effects as the linear animal model used in routine genetic evaluation for Norwegian Red cattle (Interbull, 2011):

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

where $\mathbf{y}$ is a vector of observations of the trait; $\boldsymbol{\beta}$ 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); $\mathbf{hy}$ is a vector of herd-year effects; $\mathbf{s}$ is a vector of sire effects; $\mathbf{X}$, $\mathbf{Z}_{\mathbf{hy}}$, and $\mathbf{Z}_{\mathbf{s}}$ are the corresponding incidence matrices; and $\mathbf{e}$ is a vector of residuals. Year and month of calving had 46 levels for RLRV_N, 116 for RLRV_O, and 151 levels for RLSV, FANG, and HQ; time from calving (months) and time from milking (hours) to scoring had 96 levels for all traits; age (in months) at scoring had 7 levels for all traits; and number of herd-year classes were 10,395 for RLVR_N, 50,199 for RVLR_O, and 60,594 for RLSV, FANG, and HQ. Classifier (breeding advisor) was not included in

Table 2. Number of records for trait combinations of corkscrew claw (CSC); infectious claw disorders (INF); laminitis-related claw disorders (LAM); rear leg rear view, new (RLRV_N); rear leg rear view, old (RLRV_O); rear leg side view (RLSV); foot angle (FANG); and hoof quality (HQ)

Trait	CSC	INF	LAM	RLRV_N	RLRV_O	RLSV	FANG	HQ
CSC	285,581							
INF	285,581	285,581						
LAM	285,581	285,581	285,581					
RLRV_N	11,850	11,850	11,850	47,474				
RLRV_O	14,888	14,888	14,888	0	163,315			
RLSV	26,738	26,738	26,738	47,474	163,315	210,789		
FANG	26,738	26,738	26,738	47,474	163,315	210,789	210,789	
HQ	26,738	26,738	26,738	47,474	163,315	210,789	210,789	210,789

the model because this effect is confounded with the herd-year effect.

Because of computational time, the 5 feet and leg conformation traits were analyzed together with 1 of the 3 claw disorders at a time. It was assumed that $var(\mathbf{h}) \sim N\left(0, \sigma_h^2\right)$, $var(\mathbf{hy}) = \mathbf{HY} \otimes \mathbf{I}$, $var(\mathbf{s}) = \mathbf{G} \otimes \mathbf{A}$, and $var(\mathbf{e}) = \mathbf{R} \otimes \mathbf{I}$, where σ_h^2 is the herd variance for claw disorders, $\mathbf{HY}$ is the 5 × 5 matrix containing herd-year variances among the 5 feet and leg conformation traits, herd-year covariances were assumed to be 0 among these traits (same as in the routine evaluation), $\mathbf{I}$ is the identity matrix, $\mathbf{A}$ is the additive genetic relationship matrix, and $\mathbf{G}$ and $\mathbf{R}$ are the 6 × 6 genetic and residual (co)variance matrices, respectively, for the 5 feet and leg conformation traits and 1 of the 3 claw disorders. For the binary claw disorders, the residual variance was assumed to be 1. Residual covariance was assumed to be 0 between RLRV_N and RLRV_O, because no cows had observation for both new and old RLRV, and between claw disorders and the 5 feet and leg conformation traits. These assumptions reduced computational time without affecting the results.

To analyze the data, the RJMC procedure in DMU software (Madsen and Jensen, 2010) was used. The Raftery and Lewis method in BOA software (Smith, 2005) was used for convergence diagnostics. The length of burn-in was set to 10,000 iterations for all 3 models. The total number of iterations, after burn-in, was 200,000 for the models including CSC and INF claw disorders and 350,000 for the model including LAM claw disorders.

Heritability (h^2) was calculated using

$$h^2 = \frac{4 \times \sigma_s^2}{\sigma_s^2 + \sigma_e^2},$$

where σ_s^2 is the sire variance and σ_e^2 is the residual variance.

RESULTS AND DISCUSSION

Heritabilities

Posterior means of heritability of liability of CSC and INF and LAM claw disorders was 0.20, 0.12, and 0.10, respectively (Table 3), which corresponds well with those of Ødegård et al. (2013). Estimated heritabilities were also in accordance with other studies (e.g., van der Waaij et al., 2005; Swalve et al., 2008; Buch et al., 2011). van der Spek et al. (2013) found that the underlying heritability of some claw disorders changed when including herds where at least 70% of the cows were trimmed compared with herds were less than 35% of the cows were trimmed. At present, our editing criteria were less strict due to limited data. The heritability estimates may, therefore, be affected and higher heritabilities may be obtained with more complete data in the future. The heritabilities for the 5 feet and leg conformation traits ranged from 0.04 (HQ) to 0.11 (RLSV), with small standard deviations (≤0.01; Table 3), and were in accordance with heritabilities used in routine genetic evaluations for these traits in Norwegian Red cattle (Geno, 2013). Heritabilities of RLRV_N, RLSV, and FANG were lower (0.09–0.11) in this study than estimates by Laursen et al. (2009), Uggla et al. (2008), and van der Waaij et al. (2005). However, heritabilities of RLRV_N and FANG were in accordance with those of Häggman et al. (2013).

Herd Variance

The herd variance for CSC and INF and LAM claw disorders was 0.55, 1.15, and 0.36, respectively (Table 3). For the feet and leg conformation traits, the herd-year variance varied between 0.08 (RLRV_O) and 0.89 (HQ; Table 3). The models did not include a permanent environment effect for claw disorders, meaning that the herd effect could possibly include a permanent effect of the cow.

Table 3. Posterior mean and SD of heritability, sire variance $\left(\sigma_s^2\right)$, and herd variance $\left(\sigma_h^2\right)$ of claw disorders and feet and leg conformation traits

	Heritability[1]		σ_e^2		σ_h^2	
Trait	Mean	SD	Mean	SD	Mean	SD
Corkscrew claw	0.20	0.01	0.05	<0.01	0.55	0.02
Infectious claw disorders	0.12	0.01	0.03	<0.01	1.15	0.04
Laminitis related claw disorders	0.10	0.01	0.02	<0.01	0.36	0.01
Rear leg rear view (new)	0.09	0.01	0.03	<0.01	0.54	0.01
Rear leg rear view (old)	0.07	<0.01	0.01	<0.01	0.08	<0.01
Rear leg side view	0.11	0.01	0.03	<0.01	0.13	<0.01
Foot angle	0.10	0.01	0.02	<0.01	0.15	<0.01
Hoof quality	0.04	<0.01	0.02	<0.01	0.89	0.01

[1] $h^2 = \frac{4 \times \sigma_s^2}{\sigma_s^2 + \sigma_e^2}$, where σ_e^2 is the residual variance.

Genetic Correlations

The posterior distributions of the genetic correlations between claw disorders and feet and leg conformation traits were, in general, symmetric (Figure 1), with standard deviations varying between 0.03 and 0.08 (Table 4). Figure 1 show that many of the distributions overlap and have means close to 0. The strongest genetic correlation (−0.86) was found between CSC and HQ (Table 4), with the 95% highest posterior density interval ranging from −0.92 to −0.79. The high genetic correlation was expected because CSC and HQ are supposed to measure the same trait. The genetic correlation has a negative sign because of opposite scaling (Table 1) and indicates a favorable genetic correlation. The result shows that CSC can replace HQ in the feet and leg index, which is preferable because CSC is expected to be a more accurate measure of the trait. However, the high genetic correlation indicates that HQ can be used as an indicator trait for CSC. The genetic correlation between RLRV_N and INF (−0.20) and LAM (0.26) claw disorders, respectively, were moderate and in opposite directions, meaning that bowed legs are associated with more INF claw disorders and toes out are associated with more LAM claw disorders. The genetic correlation of −0.33 between HQ and LAM claw disorders is favorable in the sense that selection for better HQ will reduce LAM claw disorders. Between RLRV_O and INF and LAM claw disorders, respectively, the genetic correlations were not significantly different from 0. Foot angle had genetic correlations that were low but significantly different from 0 to LAM (0.17) and INF (0.16) claw disorders. The genetic correlations between claw disorders and feet and leg conformation traits were, in general, low and the 95% highest posterior density included 0 for 8 out of 15 correlations (Table 4). Despite relatively few cows with information on both claw health and feet and leg conformation (Table 2), the estimated genetic correlations were relatively precise (Table 4 and Figure 1).

Uggla et al. (2008) showed that dermatitis and heel horn erosion, which are INF claw disorders, and sole hemorrhage and sole ulcer, which are LAM claw disorders, had genetic correlation to RLSV that differed significantly from 0 in Swedish Red cattle. However, they found no significant genetic correlation between the mentioned claw disorders and RLRV. Also, van der Linde et al. (2010) found significant genetic correlation between RLSV and sole ulcer (0.41) for first-lactation cows. These results differ from the present study, where no significant genetic correlations between RLSV and INF or LAM claw disorders were found, whereas moderate genetic correlations were found between RLRV_N and both INF and LAM claw disorders. Häggman and Juga (2013) estimated negative correlation between RLRV and heel horn erosion (−0.29) and a significant positive genetic correlation between FANG and heel horn erosion (0.45), whereas most other genetic correlations were not significantly different from 0. van der Waaij et al. (2005) found high genetic correlation between FANG and white line disorder (0.64), whereas in the present study, FANG and LAM claw disorders (which include white line disorder) had low genetic correlation (0.17). The different result could be due to a low genetic correlation between FANG and the other traits included in LAM claw disorders. Moderate genetic correlation between RLRV and digital dermatitis (−0.32) and interdigital dermatitis (−0.23) for first-lactation cows was found by van der Linde et al. (2010), which was in agreement with the genetic correlation found between RLRV_N and INF claw disorders in the current study (−0.20).

Rear leg side view is not included in the current TMI in Norway, and results from the present study show that claw disorders will not gain additional information from RLSV (Table 4). This was in contrast to a study by Häggman et al. (2013), who estimated moderate genetic correlation between RLSV and overall claw health (0.42) in Finnish Ayrshire cattle and suggested to use

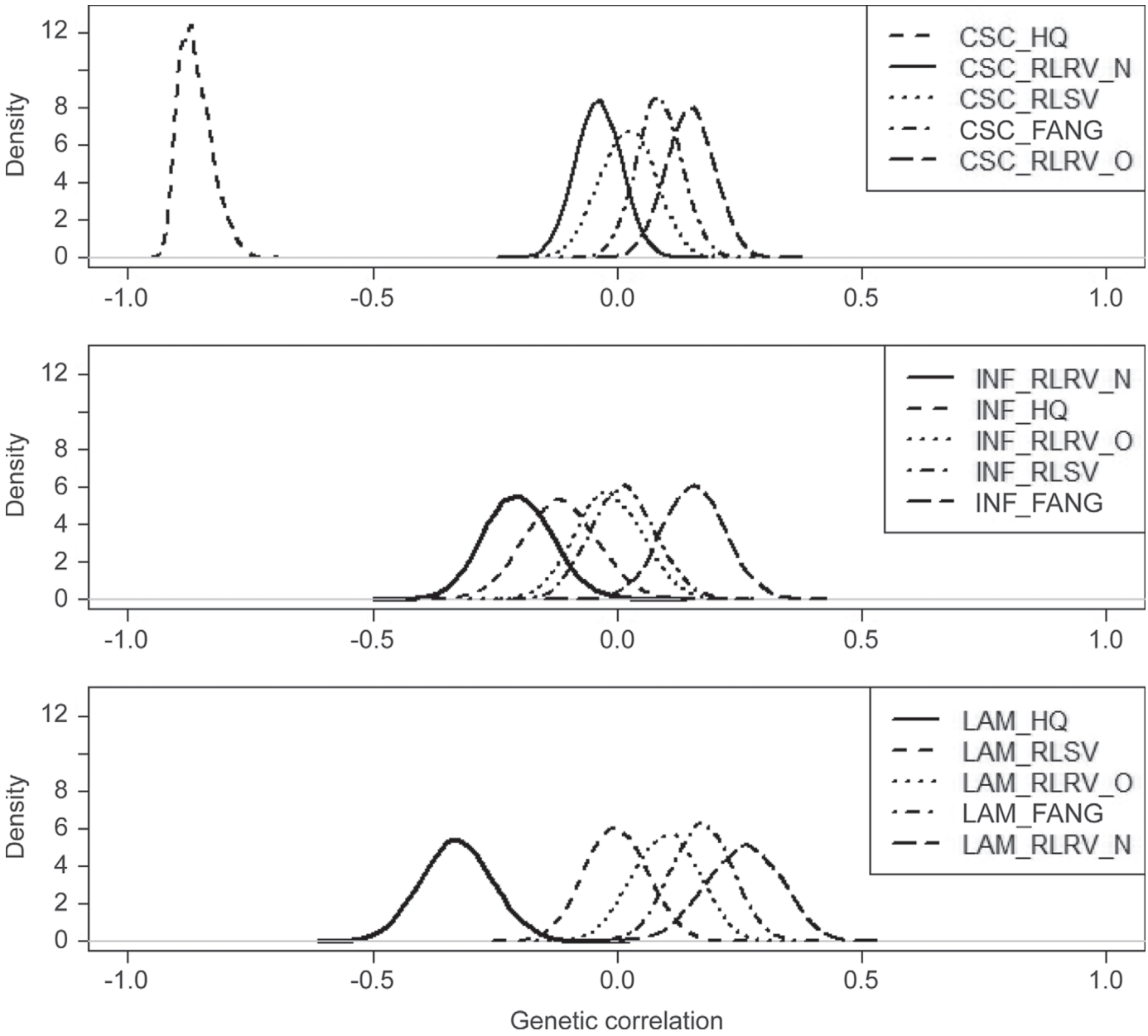

Figure 1. Posterior distribution of genetic correlations between claw disorders [corkscrew claw (CSC), infectious (INF) claw disorders, and laminitis-related (LAM) claw disorders] and feet and leg conformation traits [rear leg rear view, new (RLRV_N); rear leg rear view, old (RLRV_O); rear leg side view (RLSV); foot angle (FANG); and hoof quality (HQ)].

it as indicator trait for claw disorders. Gernand et al. (2013) estimated favorable genetic correlations between claw disorder and RLSV and FANG. The contradicting results found between different studies could be due to differences in trait definitions and frequency of claw disorders between breeds and populations. Battagin et al. (2012) investigated the genetic correlation of the trait overall feet and leg conformation among different countries and found a correlation of 0.68 across countries. Another study by Battagin et al. (2013) estimated changes in genetic correlation of overall feet and leg conformation over time and concluded that further harmonization of the traits is needed to obtain better genetic correlations across countries. In the Nordic countries, harmonization of conformation traits and claw disorders will be implemented, and this will provide a better comparison of these traits between the Nordic breeds.

Although the results indicate that selection for feet and leg conformation traits is not an efficient approach

Table 4. Genetic correlations between claw disorders and feet and leg conformation traits (posterior means, with SD in parentheses and 95% highest posterior density intervals in brackets)

	Conformation trait				
Claw disorder	Rear leg rear view new	Rear leg rear view old	Rear leg side view	Foot angle	Hoof quality
Corkscrew claw	0.02 (0.06) [−0.09; 0.13]	0.15 (0.05) [0.05; 0.25]	−0.04 (0.05) [−0.13; 0.05]	0.09 (0.05) [−0.01; 0.18]	−0.86 (0.03) [−0.92; −0.79]
Infectious claw disorders	−0.20 (0.07) [−0.33; −0.05]	−0.02 (0.07) [−0.15; 0.12]	0.01 (0.07) [−0.11; 0.14]	0.16 (0.07) [0.03; 0.29]	−0.12 (0.08) [−0.26; 0.04]
Laminitis-related claw disorders	0.26 (0.08) [0.11; 0.41]	0.10 (0.07) [−0.03; 0.23]	0.00 (0.07) [−0.13; 0.13]	0.17 (0.06) [0.05; 0.30]	−0.33 (0.07) [−0.47; −0.18]

to genetically improve claw health, feet and leg conformation traits may be of value to other health and welfare aspects of the cow.

Other possible indicator traits for claw health are locomotion and lameness (e.g., van der Waaij et al., 2005; Laursen et al., 2009; Weber et al., 2013). van der Waaij et al. (2005) concluded that locomotion was useful for predicting claw disorders later in life, but more investigation was needed. Several authors concluded that direct selection against claw disorders is the most efficient way to improve claw health (e.g., Laursen et al., 2009; Häggman et al., 2013; Weber et al., 2013). Gernand et al. (2013) discussed selection strategies for claw health, comparing direct and indirect selection, and concluded that including direct claw health in the ultimate breeding goal was the most promising alternative. In Norwegian Red cattle, locomotion and lameness are not recorded routinely, and direct selection against claw disorders would be the best choice for genetic improvement of claw health.

CONCLUSIONS

Genetic correlations between claw disorders and feet and leg conformation traits were, in general, low and selection for feet and leg conformation is, therefore, not an efficient approach for genetic improvement of claw health in Norwegian Red cattle. The exception was HQ, which, with a genetic correlation of −0.86 to CSC, is a useful indicator trait that can provide additional information to CSC.

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

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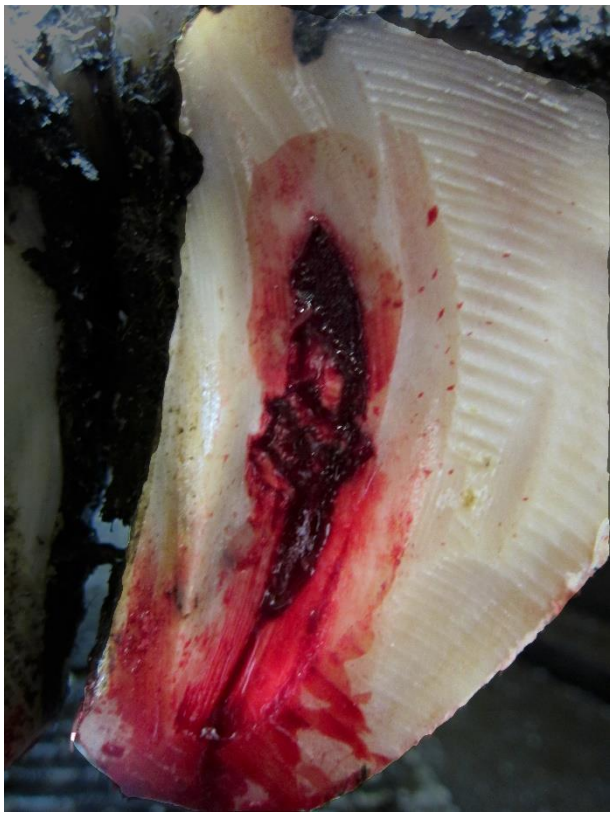

Paper III

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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.

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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

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

Item	CSC	INF	LAM	HQ	FANG	RLRV_N	RLRV_O
Claw health records (no.)							
CSC	281,835	281,835	281,835	25,598	25,598	11,803	13,795
INF		281,835	281,835	25,598	25,598	11,803	13,795
LAM			281,835	25,598	25,598	11,803	13,795
HQ				305,195	305,195	52,330	252,865
FANG					421,319	52,330	368,834
RLRV_N						52,330	0
RLRV_O							368,834
Norwegian Red sires with genotype and informative daughters (no.)							
CSC	1,093						
INF	1,093	1,093					
LAM	1,093	1,093	1,093				
HQ	1,093	1,093	1,093	2,183			
FANG	1,093	1,093	1,093	2,183	3,111		
RLRV_N	447	447	447	571	571	571	
RLRV_O	816	816	816	1,782	2,710	170	2,710

of records for each combination of claw disorders and foot and leg conformation traits is given in Table 1.

SNP Data Set. An imputed 25K/54K SNP data set was available for the analyses. Not all SNP included in the 25K SNP chip are in the 54K SNP chip, so to exploit all available SNP, the data set 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 minor allele frequency <0.05), the data set 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. Numbers 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 FANG (**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.

EBV. 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 fourth 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, FANG, RLRV_N, and RLRV_O were predicted using a linear sire model including effects described in the study by 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 $\mathbf{y}$ is a vector of observations of the trait; $\boldsymbol{\beta}$ 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); $\mathbf{hy}$ is a vector of random herd-year effects; $\mathbf{s}$ is a vector of sire effects; $\mathbf{e}$ is a vector of residuals; and $\mathbf{X}$, $\mathbf{Z}_{\mathbf{hy}}$, and $\mathbf{Z}_{\mathbf{s}}$ are the corresponding incidence matrices. Year and month of calving had 216 levels for HQ, 315 levels for FANG, 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, FANG, RLRV_N, and RLRV_O; and age at scoring (in months) had 7 levels for HQ, FANG, RLRV_N, and RLRV_O. The herd-year effect included 98,820 levels for HQ; 149,249 levels for FANG; 12,661 for RLRV_N; and 136,566 for RLRV_O.

The 3 data sets were analyzed using multivariate models with (co)variances: var($\mathbf{h}$) = $\mathbf{H} \otimes \mathbf{I}$, var($\mathbf{hy}$) = $\mathbf{HY} \otimes \mathbf{I}$, var($\mathbf{s}$) = $\mathbf{G_0} \otimes \mathbf{A}$, and var($\mathbf{e}$) = $\mathbf{R} \otimes \mathbf{I}$, where $\mathbf{H}$ is the 3 × 3 herd (co)variance matrix; $\mathbf{HY}$ is the 2 × 2 herd-year variance matrix (co-variances were assumed to be zero); $\mathbf{A}$ is the additive genetic relationship matrix; $\mathbf{I}$ are identity matrices; and $\mathbf{G_0}$ and $\mathbf{R}$ are the 3 × 3, 5 × 5, and 5 × 5 corresponding genetic and residual (co)variance matrices for the data sets 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 pedigrees 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

$$\mathbf{y} = \mathbf{1}\boldsymbol{\mu} + \mathbf{Zg} + \mathbf{e},$$

where $\mathbf{y}$ is a vector of DRP, $\mathbf{1}$ is a vector of ones, $\boldsymbol{\mu}$ is the overall mean, $\mathbf{g}$ is a vector of genomic effects, $\mathbf{Z}$ is the incidence matrix of $\mathbf{g}$, and $\mathbf{e}$ is a vector of residuals. It was assumed that var($\mathbf{g}$) = $\mathbf{G_0} \otimes \mathbf{G}$ and var($\mathbf{e}$) = $\mathbf{R} \otimes \mathbf{D}$, where $\mathbf{G}$ is the genomic relationship matrix; $\mathbf{D}$ is a diagonal matrix containing weighting factors for the residuals; and $\mathbf{G_0}$ and $\mathbf{R}$ are the 3 × 3, 5 × 5, and 5 × 5 corresponding genetic and residual (co)variance matrices 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 sires in CF1 and CF2.

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

10-Fold Cross-Validation. A 10-fold cross-validation (**CVal**) was performed to assess predictive correlations of GEBV for CSC, INF, and LAM from the data sets 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 one group. In the CVal, one group was used as the 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 data sets 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 data sets were used in prediction of EBV for each of the reference populations in CVal 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 FANG 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 with 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 the genetic correlations among these traits were in general low (Table 2). The standard deviation of predictive correlations of GEBV ranged from 0.06 to 0.13 among the traits and data sets (Table 3), showing relatively large variation among the folds (Figure 1). The highest standard deviation

Table 2. Estimated heritability of corkscrew claw (CSC), infectious claw disorder (INF), laminitis-related claw disorder (LAM), hoof quality (HQ), foot angle (FANG), rear leg rear view new (RLRV_N), and rear leg rear view old (RLRV_O) and their genetic correlation (SE) to 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)
FANG	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)

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 standard deviation of the mean predictive correlation of GEBV using the data set CH. The overall best result for CSC was obtained using data set CF1 (Figure 1), whereas for INF it was obtained using data set CH (Figure 1). For LAM, data sets CH and CF1 gave very similar results over all folds (Figure 1). The large differences in predictive correlations of GEBV among validation sets in CVal 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 CVal, 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 CVal compared with young sires with less data. This could lead to overestimation of predictive correlation of GEBV; therefore, an additional validation set including the youngest sires was 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 data set 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 data sets, 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 CVal (Table 3). For CSC the predictive correlations of GEBV from CF1 and CF2 were above the maximum value in CVal. 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 CVal, indicating that overestimation was not a problem in this study. A benefit of using CVal, compared with 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 FANG 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

Table 3. Mean, 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[1]

	CSC				INF				LAM			
Data set	Mean	SD	Min	Max	Mean	SD	Min	Max	Mean	SD	Min	Max
CH	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	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	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]Correlation between GEBV and deregressed proofs from multivariate models using 3 data sets: CH1, CF1, and CF2. CH = data set including CSC, INF, and LAM; CF1 = data set including CSC, INF, LAM, hoof quality, and foot angle; CF2 = data set 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[1]

Item	CH	CF1	CF2
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]Correlation between GEBV and deregressed proofs from multivariate models using 3 data sets: CH, CF1, and CF2. CH = data set including corkscrew claw, infectious claw disorder, and laminitis-related claw disorder; CF1 = data set including corkscrew claw, infectious claw disorder, laminitis-related claw disorder, hoof quality, and foot angle; CF2 = data set including corkscrew claw, infectious claw disorder, laminitis-related claw disorder, rear leg rear view new and rear leg rear view old.

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 with the findings of 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

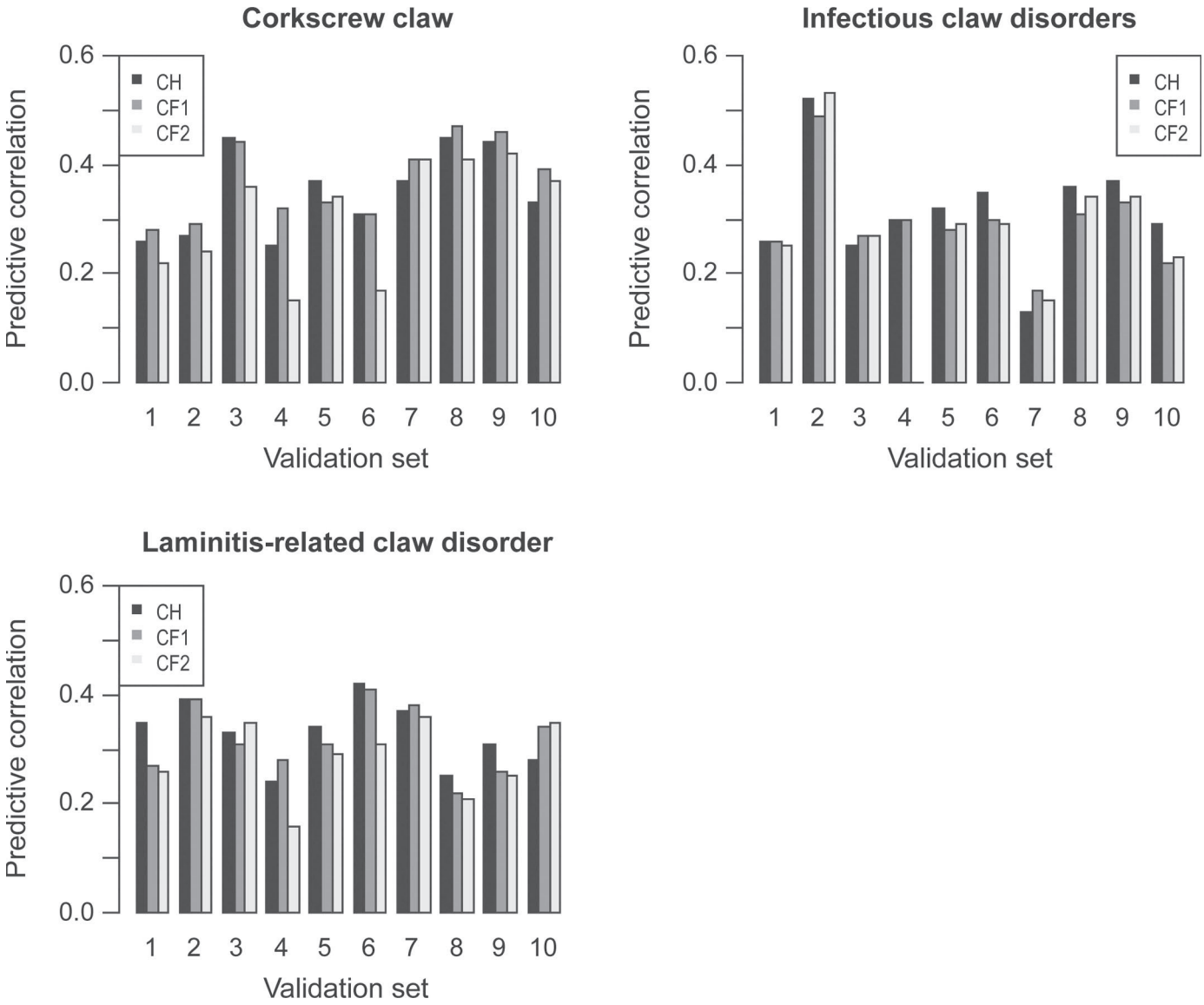

Figure 1. Predictive correlations of genomic breeding values (GEBV) for corkscrew claw (CSC), infectious claw disorder (INF), and laminitis-related claw disorder (LAM) from 10-fold cross-validation using 3 data sets: CH (CSC, INF, and LAM); CF1 (CSC, INF, LAM, hoof quality, and foot angle); and CF2 (CSC,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

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 indicates 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 correlations ranged from 0.2 to 0.4 (Svendsen et al., 2013). Similar results were found in other breeds (e.g., Karoui et al., 2012; Pintus et al., 2013; Zhou et al. 2014), where the accuracy of GEBV was lowest for low-heritable traits. Despite the limited historical data and the small reference population available for claw disorders, the predictive correlations of GEBV for CSC, INF, and LAM were in the same range as accuracies of GEBV obtained for other low-heritable traits in Norwegian Red.

Increasing the Predictive Correlation of GEBV

Claw disorders are novel traits with limited historical data and therefore fewer animals in the reference population. Including foot and leg conformation traits had little or no effect on the predictive correlations of GEBV for CSC, INF, and LAM, despite the increased number of sires in the reference population. This could partly be because most sires had few daughters with claw health information (average 168, minimum 30) and few cows had information on both claw health and foot and leg conformation score. The high effective population size in Norwegian Red (Geno, 2013) and the low genetic correlations among the traits also affected the results. Better predictive correlations of GEBV could possibly be obtained by increasing the number of animals in the reference population, increasing the number of phenotypic records (claw health records), and by genotyping of cows.

Genomic predictions across breeds and populations is one approach to obtain larger reference populations (e.g., Brøndum et al., 2011; Heringstad et al., 2011; Lund et al., 2011) and thereby increase predictive correlation of GEBV. Reliabilities of GEBV for Norwegian Red calculated in a joint Nordic reference population (including Norwegian Red, Swedish Red, Finnish Ayrshire, and Danish Red) increased slightly for production traits compared with a reference population consisting of only Norwegian Red. However, for health traits reliability did not increase, 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 multibreed 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 multibreed 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; 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 data sets. 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 is 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 a 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.

CONCLUSIONS

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 FANG, 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.

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Use of single-step GBLUP improved the genetic predictions of claw disorders in Norwegian Red

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Manuscript

Paper IV

Use of single-step GBLUP improved the genetic predictions of claw disorders in Norwegian Red

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ABSTRACT

The aim was to evaluate whether genetic predictions of claw disorders improved when increasing the number of genotypes included in the relationship matrix in a single-step GBLUP (ssGBLUP). Among the Norwegian Red cows genotyped with a customized 54K Affymetrix SNP-chip, 1,613 had at least one claw health record and were defined as randomly selected cows for claw health. In addition, 113 Norwegian Red cows from herds with thoroughly recording of claw health were selected for genotyping. Among the genotyped sires, 2,037 had daughters with claw health records. A total of 3,763 genotyped animals and a dataset containing 318,349 claw health records, from 206,533 cows of 2,221 sires and 6,303 herds were included in the analyses. Three claw disorders: corkscrew claw, infectious claw disorder and laminitis-related claw disorder, were analyzed using a multivariate animal repeatability model. Additive relationship matrix (**A**) and adjusted genomic relationship matrix (**G**) were combined to an **H** matrix in ssGBLUP. A 10-fold cross-validation was performed with 4 different relationship matrices: 1) **A** matrix (REL_{ped}); 2) **H** matrix, with **G** including genotyped sires (REL_{sire}); 3) **H** matrix, with **G** including genotyped sires and randomly selected cows (REL_{rand}); and 4) **H** matrix, with **G** including genotyped sires, randomly selected cows and selected cows (REL_{all}). The 10 validation sets constituted in total 1,202 genotyped sires having at least 30 daughters with claw health records. Estimated breeding values from the validation sets were correlated to EBV predicted from the full dataset and REL_{all}. The mean correlations increased for all 3 traits when including REL_{sire} in ssGBLUP compare to using REL_{ped} in BLUP. Whereas including REL_{rand} and REL_{all} gave no further increase in the mean correlations, due to few genotyped cows being available. Further analyses should be conducted to conclude on the benefit of including genotyped cows in genomic predictions of claw disorders.

Keywords: claw health, cow genotype, single-step GBLUP, Norwegian Red

INTRODUCTION

Genomic selection aim to select the best animals for breeding using genotype information (Meuwissen et al., 2001). For novel traits with limited historical data available and sires having few daughters with records, genomic selection would be beneficial if reliable results could be obtained. The reliability of genomic predictions depends on heritability of the trait, effective population size, number and distribution of quantitative trait locus, linkage disequilibrium, number of animals in the reference population, and the relationship between selection candidates and reference animals (Hayes et al., 2009; Meuwissen et al., 2013). These aspects illustrate some of the main challenges related to genomic predictions of claw disorders in Norwegian Red. Claw disorders are low heritable traits with limited historical data, and thereby having a small reference population. A large effective population size in Norwegian Red (Geno, 2015) add challenge to the predictions. Ødegård et al. (2015) found low predictive correlation of genomic breeding values (**GEBV**) for claw disorders in Norway, also when genetic correlated foot and leg conformation traits were included in the analyses to increase the reference population. Using a joint Nordic reference population gave little or no improvement in the genomic predictions of other low heritability traits (health and fertility traits) in Norwegian Red (Heringstad et al., 2011; Zhou et al., 2014). Therefore, it was of interest to explore other options for improving the genomic predictions, such as increasing number of genotyped animals and using improved statistical methods.

Improvement of genomic prediction have in other studies been obtained by increasing the reference population with genotypes from cows having phenotypic records (e.g. Buch et al., 2011; Mc Hugh et al. 2011; Luan et al., 2014) and by use of single-step GBLUP (**ssGBLUP**) (Legarra et al., 2009; Christensen and Lund, 2010). Single-step GBLUP exploits all available data and make use of animal model feasible, despite lack of genotypes on cows having phenotypic records. By including genotypes of both sires and cows, the hypothesis was that genetic evaluation of claw disorders would improve. It was of interest to examine this regarding claw health in Norwegian Red, because claw disorders are included in the total merit index but sires have small daughter groups (below 10) at their first official proof.

The aims were to predict estimated breeding values (**EBV**), from BLUP and ssGBLUP, for corkscrew claw (**CSC**), infectious claw disorder (**INF**) and laminitis-related claw disorder (**LAM**); and evaluate the performance of genetic predictions when increasing the number of genotyped animals in the relationship matrix. In addition, estimation of genetic parameters for CSC, INF and LAM using an animal model were carried out.

MATERIALS AND METHODS

Claw health data

Since 2004, claw health recorded at claw trimming have been reported to the Norwegian Dairy Herd Recording System. Based on previous estimated genetic parameters (Ødegård et al., 2013), 1 claw disorder: CSC, and 2 groups of claw disorders: INF (dermatitis, heel horn erosion and interdigital phlegmon) and LAM (sole ulcer, white line disorder and hemorrhage of sole and white line) were included in the analyses. The claw disorders were defined as binary traits within each

parity. Data was edited as described in Ødegård et al. (2013): only lactating cows of Norwegian Red AI sires that had at least one claw health record in a parity were included, and herds should have recorded at least 10% or 10 normal claws from 2004 to September 2014. If a cow had repeated records of a claw disorder in the same parity, the first record was included in the analyses. The final dataset consisted of claw health records from 2004 to September 2014, in total 318,349 records from 206,533 cows of 2,221 sires and from 6,303 herds. The overall mean frequencies of CSC, INF and LAM were 11%, 7% and 8%, respectively.

SNP data

SNP data from sires genotyped with a 25K Affymetrix or 54K Illumnia SNP-chip were imputed to a customized 54K Affymetrix SNP-chip, whereas all cow genotypes were from the customized 54K Affymetrix SNP-chip. After standard editing, 54,574 markers were utilized and a total of 10,314 animals were genotyped. Of the genotyped sires, 2,037 had daughters with claw health records. Number of genotyped cows having at least 1 claw health record were 1,613. These cows were genotyped for other reasons and defined, in the present study, as randomly selected genotyped cows for claw health. In addition, 347 Norwegian Red cows from 11 herds routinely recording claw health were selected for genotyping in the spring 2014 and genotyped during spring 2015. Because of the time lag between the selection of cows to be genotyped and to the DNA-sampling was carried out, some cows had been slaughtered, were still at pasture, or were unavailable for other reasons. In addition, some of the received DNA-samples did not meet the required quality. Therefore, the total number of selected genotyped cows were reduced to 113 from 11 herds. The selection of cows and herds were based on the following criteria: herds should have routinely recorded claw health from 2010 to 2013; claw trimming performed by professional claw

trimmers; and at least 95% of the cows in the herd should have a claw health record. Corkscrew claw, dermatitis, heel horn erosion, interdigital phlegmon, sole ulcer, white line disorder and hemorrhage of sole and white line had to be present in each herd. Only lactating daughters of Norwegian Red AI sires were selected for genotyping. The distribution of sires were approximately equal among herds. The average frequencies of normal claw, CSC, INF and LAM in the selected herds were 50%, 14%, 16% and 19%, respectively. The total number of genotyped animals included in the analyses were 3,763.

Statistical analyses

Breeding values were predicted using BLUP and ssGBLUP. All analyses of CSC, INF and LAM were performed with a multivariate linear animal repeatability model, in matrix notation:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Z}_{pe}\mathbf{pe} + \mathbf{Z}_{h}\mathbf{h} + \mathbf{Z}_{a}\mathbf{a} + \mathbf{e},$$

where **y** was a vector of response variables. The systematic effects (**b)** included parity, housing system, calving year and month, time of claw trimming and claw trimmer. Random effects were permanent environment (**pe**), herd (**h**), animal (**a**) and residual (**e**). **X**, $\mathbf{Z}_{pe}$, $\mathbf{Z}_{h}$ and $\mathbf{Z}_{a}$ were the corresponding incidence matrices. Parity had 4 classes, where the 4^{th} included parity 4 to 13; housing system had 4 classes: tie stall, free stall, milking robot and unknown; calving year and month had 126 classes; time of claw trimming had 12 classes (months after calving); and claw trimmer had 4 classes: professional claw trimmer, other claw trimmer, farmer and other person (e.g. veterinarian). It was assumed that var(**pe**) = $\mathbf{W} \otimes \mathbf{I}$, var(**h**) = $\mathbf{S} \otimes \mathbf{I}$, and var(**e**) = $\mathbf{R} \otimes \mathbf{I}$, where **I** was the identity matrix; and **W**, **S** and **R** were the corresponding 3×3 permanent environment-, herd- and residual (co)variance matrices, respectively. In the BLUP-analyses it were assumed that var(**a**) = $\mathbf{G_0} \otimes \mathbf{A}$, where **A** was the additive genetic relationship matrix, and $\mathbf{G_0}$ was the

corresponding 3×3 genetic (co)variance matrix. The pedigree was traced back as far as possible and consisted of 643,903 animals. **G** was the genomic relationship matrix, obtained using the Gmatrix package (Su and Madsen, 2012). Using ssGBLUP, the **A** and an adjusted **G** were combined to the relationship matrix **H**, assuming var(**a**) = $\mathbf{G_0} \otimes \mathbf{H}$. The weight between **G** and **A** when making **H** was set to zero, i.e. pedigree information was not included in the estimation of relationship among the genotyped animals. Four relationship matrices were included in the analyses. 1) Additive relationship matrix **A** for all animals (REL_{ped}). 2) Relationship matrix **H**, where **G** included the 2,037 genotyped sires with daughter information on claw health (REL_{sire}). 3) Relationship matrix **H**, where **G** included the 2,037 genotyped sires and the 1,613 randomly genotyped cows (REL_{rand}). 4) Relationship matrix **H**, where **G** included the 2,037 genotyped sires, the 1,613 randomly genotyped cows and the 113 selected genotyped cows (REL_{all}).

To assess predictive ability of the genetic predictions based on each of the 4 relationship matrices, 10-fold cross-validations were carried out. The 1,202 sires having at least 30 daughters with claw health records were randomly assign to 10 validation sets and each validation set constituted 120 or 121 sires. The sires' daughter information were deleted in the datasets used for validation. The predictive ability was calculated as the correlation between EBV from 10-fold cross-validation and the EBV from the full dataset and REL_{all}, for each of the validation sets.

Genetic parameters were estimated and EBV predicted, utilizing the DMUAI and DMU4 procedures of the DMU software (Madsen and Jensen, 2013). The full dataset combined with REL_{ped} or REL_{all} were used to estimate (co)variances for the 10-fold cross-validation. Heritabilities

(h^2) from animal model were calculated as $h^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_e^2}$, where σ_g^2 was genetic variance and σ_e^2 was the residual variance.

RESULTS AND DISCUSSION

Genetic parameters

(Co)variance components for CSC, INF and LAM estimated from the full dataset using either REL_{ped} or REL_{all} were similar. The heritabilities for CSC, INF and LAM were 0.09, 0.04 and 0.03, respectively, from $REL_{ped,}$ and 0.10, 0.04 and 0.04, respectively, from REL_{all} (Table 1). Slightly higher heritability of CSC were found in the present study compared to previous result using sire model, whereas heritabilities of INF and LAM were similar (Ødegård et al., 2015). Genetic correlations among the claw disorders obtained using REL_{ped} were 0.12 (CSC and INF), 0.38 (CSC and LAM) and 0.29 (INF and LAM), respectively, and approximately the same in ssGBLUP (Table 1). These correlations were slightly higher than the genetic correlations estimated by Ødegård et al. (2015). Dhakal et al. (2015) showed a small increase in heritabilities of hoof lesions using single-step genomic analysis, but explained the increase by differences in base population and scaling of relationship matrices. Based on results from the present study, it could be argued that the same variance components could be used in BLUP- and ssGBLUP-analyses of claw disorders in Norwegian Red.

Housing system

Reporting of the herds housing system is, after a revision of the Norwegian Dairy Herd Recording System, possible and was included as a new systematic effect in the analyses. Of the analyzed claw health records, 35% were from tie stall, 15% from free stall, 19% from herds having milking robot,

and 31% from herds with unknown housing system. Housing system had significant effect (p-value<0.05) on all the 3 traits. Figure 1 indicates that the risk of having a claw disorder were higher in free stall and milking robot herds compared to tie stall. This is supported by the findings of Fjeldaas et al. (2006), who reported different frequencies of claw disorders in tie stall and free stall. The majority of herds in the unknown group are most likely tie stalls, which also could be assumed by the solutions presented in Figure 1. In Norway, herds having milking robot tend to be above average herd size, and their management may differ. This could affect the herd incidence of claw disorders, and was a reason for separating milking robot from other free stall systems in these analyses. However, almost no differences could be seen between these 2 groups (Figure 1). Results showed that animal model including effect of housing system would be beneficial to use in the genetic evaluation of claw health.

Including genotypes

The 10-fold cross-validation showed increased mean correlations to the full dataset for CSC, INF and LAM when including genotypes of sires in addition to pedigree (Table 2). For CSC the mean correlation increased from 0.67 using REL_{ped} to 0.77 using REL_{sire}. The same trend was found for INF and LAM, where the mean correlations increased from 0.67 to 0.79 for INF and from 0.68 to 0.80 for LAM, respectively. Similar findings were presented by Dhakal et al. (2015), who compared reliability of PTA (using pedigree analysis) and genomic PTA (using single-step genomic analysis) for hoof lesions in US Holsteins, showing increased reliability when including genotyped sires. Including randomly genotyped cows (REL_{rand}) gave almost no change in the correlations compared to using REL_{sire} (Table 2; Figure 2). Including genotypes of selected cows (REL_{all}) had no effect on the correlations (Figure 2), most likely because of the small number of

selected genotyped cows. The standard deviation of the mean correlations varied from 0.03 to 0.05, indicating consistency among the validation sets. Genotyped daughters of the 1,202 sires included in the 10-fold cross-validation were evenly distributed among the 10 validation sets. Number of progeny per sire becomes a limiting factor for the accuracy of GEBV in low heritability traits (Lillehammer et al., 2011), which could be illustrated by results of Haugaard et al. (2015) and Ødegård et al. (2015). Both studies evaluated genomic predictions of novel, low heritability traits in Norwegian Red, but the amount of historical data differed. In Haugaard et al. (2015), data from 1979 onwards was available and sires had a minimum 150 daughters with information, concluding that genomic predictions performed better than previous results reported on low heritability traits in Norwegian Red. Whereas, in Ødegård et al. (2015), the data was from 2004 onwards and sires had a minimum 30 daughters with information, concluding that more information was needed to improve genomic predictions. Several studies have found improved genomic predictions by including genotyped cows (e.g. Buch et al., 2011; Egger-Danner et al., 2014; Koivula et al., 2014), and results from Buch et al. (2011) indicated a positive effect for novel traits where phenotypic records were limited. Therefore, it was expected that including genotypes of cows should improve the predictions. However, the lack of improvement in the present study could be due to too few cows with phenotypic records being genotyped.

To maximize the gain from including cow genotypes, the strategy of selecting cows for genotyping and the number of genotyped cows may be crucial. Jiménez-Montero et al. (2012) concluded that genotyping cows with lower and upper extreme values within the distribution of yield deviations provided the highest gain in accuracy of predicted GEBV in small reference populations. In a simulation study, accuracy of genomic predictions improved when increasing the number of

genotyped cows from 0 to 3,000, whereas additional genotyped cows gave no further improvement (Luan et al., 2014). However, a study on 5,593 genotyped cows by Koivula et al. (2014) concluded that more cows should be genotyped to obtain higher accuracy of GEBV. In the present study, genotypes of both random cows and a few selected cows for claw health were included in the analyses. The selection of herds were based on having routine claw trimmings and high incidence of claw disorders, with the intention to get informative genotypes. The results showed no differences when including a random sample of genotyped cows or selected genotyped cows. However, to conclude a larger amount of cows should be selected for genotyping based on claw health records and included in the analyses. The possible improvement though, should be evaluate against the cost of genotyping cows specially selected for claw health. More realistic is to utilize already genotyped cows in the Norwegian Red population. Among the 198,899 cows with claw health records, only 1,726 have been genotyped so far. This leaves a huge potential for future improvements in genomic predictions of claw disorders.

Validation

Single-step GBLUP have shown better performance than the two-step approach in several studies (e.g. Gao et al., 2012; Koivula et al., 2012) and should be preferred when including genomic information for genetic evaluation of claw health in Norwegian Red. However, correct validation is challenging because claw health is a novel trait with limited historical data. A validation set including the youngest sires born in 2008 and 2009 would imply excluding about 2/3 of the claw health records available, because most of the records are from 2008 and later. Another option for validation could be to use cows in the validation set, but then more cows with claw health records need to be genotyped. A 10-fold cross-validation avoids the problems with excluding nearly all of

the recent data. However, older sires closely related to several animals in the reference population may be included in the validation set. Gaining a lot of information from relatives in the prediction of EBV could lead to overestimation of predictive ability. Number of animals in the validation set may also affect the results. Erbe et al (2010) found largest variation in the correlations of GEBV in a cross-validation with small validation sets (100 sires) compared to larger validation sets (up to 1500 sires). The present study showed small standard deviations of mean correlations from the 10-fold cross-validation using validation sets of 120 sires. Indicating that, at present, the 10-fold cross-validations were a good option in the analyses of claw health in Norwegian Red.

Another issue is how to calculate accuracy, reliability or predictive ability of the EBV when the true breeding values is unknown. To assess predictive ability in the present study the EBV from 10-fold cross-validations were correlated to EBV using full dataset and REL_{all}, which should not be interpreted as accuracy or reliability. This should be used solely to compare the 4 alternatives. The results showed how much the prediction of EBV changed when including additional genotype information, relative to include all known information in the prediction, i.e. how much pedigree information, genotyped sires, randomly genotyped cows and selected genotyped cows contributed to the predictions. As expected, adding more information to the analyses increased the correlations.

CONCLUSION

Including genotypes of sires in the genetic evaluation of claw disorders improved the genetic predictions compared to using pedigree information only. Including genotypes of cows, in addition to genotyped sires, had no effect on the predictive ability in the present study, neither when including randomly genotyped cows or selected genotyped cows in the relationship matrix. The

lack of improvement may be due to the small number of genotyped cows, and it would be of interest to investigate this further when more cows with claw health records are genotyped.

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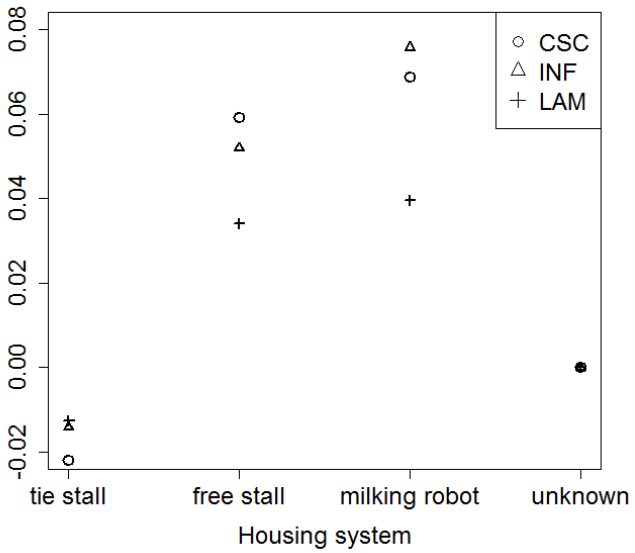
Table 1. Heritability of and genetic correlations (standard error) among corkscrew claw (CSC), infectious claw disorder (INF) and laminitis-related claw disorder (LAM) from linear animal model analyses with pedigree based relationship matrix (REL_{ped}) or single-step analysis using all genotype information (REL_{all}).

			Genetic correlations	
		Heritability	CSC	INF
REL_{ped}	CSC	0.09		
	INF	0.04	0.12 (0.05)	
	LAM	0.03	0.38 (0.05)	0.29 (0.06)
Single-step REL_{all}	CSC	0.10		
	INF	0.04	0.10 (0.05)	
	LAM	0.04	0.36 (0.05)	0.31 (0.05)

Table 2. Mean, standard deviation (SD), minimum value (Min) and maximum value (Max) of correlation between EBV from 10-fold cross-validation and EBV from the full dataset for corkscrew claw (CSC), infectious claw disorder (INF) and laminitis-related claw disorder (LAM). Four different relationship matrices were used: pedigree (REL_{ped}); genotyped sires and pedigree (REL_{sire}); genotyped sires, randomly genotyped cows and pedigree (REL_{rand}); and genotyped sires, randomly genotyped cows, selected genotyped cows and pedigree (REL_{all}).

	CSC				INF				LAM			
	Mean	SD	Min	Max	Mean	SD	Min	Max	Mean	SD	Min	Max
REL_{ped}	0.67	0.04	0.58	0.71	0.67	0.04	0.61	0.75	0.68	0.05	0.60	0.77
REL_{sire}	0.77	0.03	0.72	0.81	0.79	0.04	0.74	0.85	0.80	0.04	0.72	0.85
REL_{rand}	0.78	0.03	0.73	0.82	0.79	0.04	0.74	0.85	0.81	0.04	0.72	0.86
REL_{all}	0.78	0.03	0.73	0.83	0.79	0.04	0.75	0.85	0.81	0.04	0.72	0.85



368

369 **Figure 1.** The systematic effect solution (BLUE) for housing system, from single-step GBLUP

370 analysis using full dataset, for a cow's risk of having corkscrew claw (CSC), infectious claw

371 disorder (INF) and laminitis-related claw disorder (LAM).

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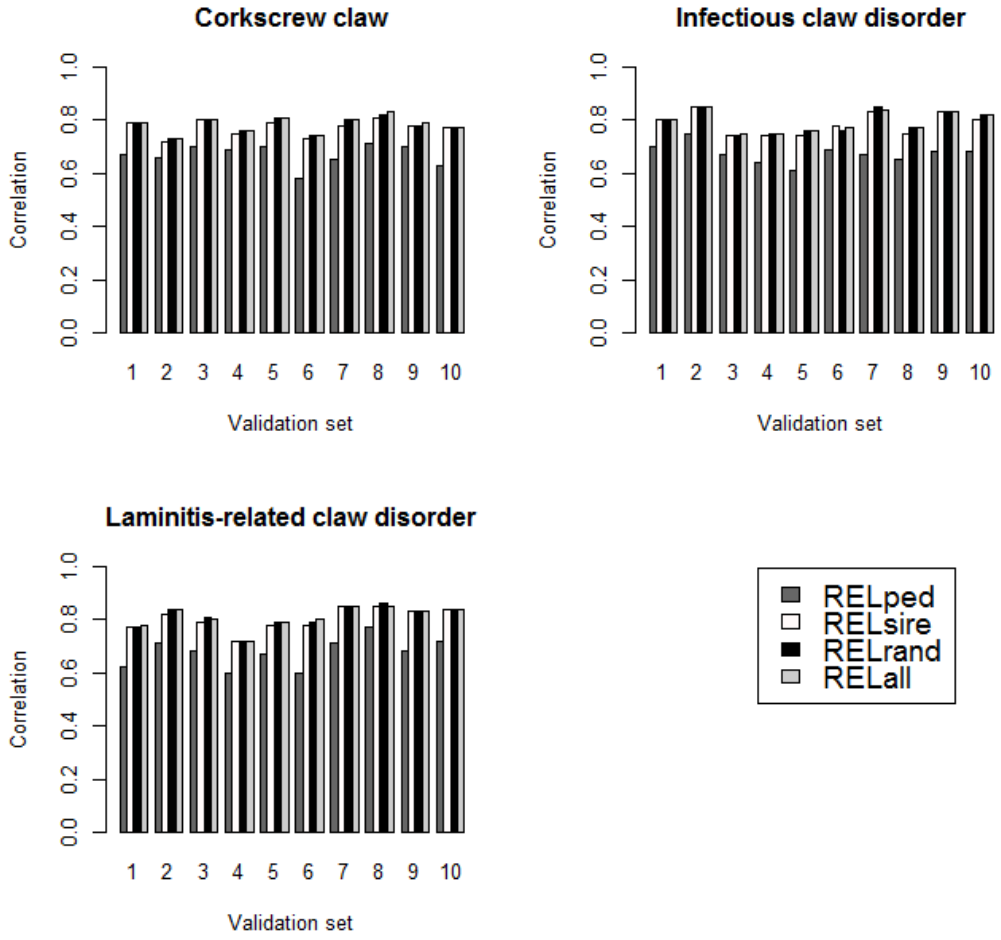

374

375 **Figure 2.** Correlations between EBV from the 10 validation sets and EBV from the ssGBLUP
376 using full dataset for corkscrew claw, infectious claw disorder and laminitis-related claw
377 disorder. By use of four relationship matrices: pedigree (REL_{ped}); genotyped sires and pedigree
378 (REL_{sire}); genotyped sires, randomly genotyped cows and pedigree (REL_{rand}); and genotyped
379 sires, randomly genotyped cows, selected genotyped cows and pedigree (REL_{all}).

380

381