Post print version
DOI: http://dx.doi.org/10.3168/jds.2012-650

INTERPRETIVE SUMMARY

Genetic analyses of claw health in Norwegian Red cows. *By Ødegård et al., page 000.* Claw health is important both from an economical point of view and for animal welfare reasons. In Norway, claw health data has been recorded since 2004. Normal (healthy) claws and 9 defined claw disorders are recorded at claw trimming. Records from 141,659 Norwegian Red cows were analyzed. Claw disorders were analyzed as single traits and as grouped traits. Heritability ranged from 0.04 (lameness and acute trauma) to 0.23 (corkscrew claw). Results show that claw disorders are heritable and possible to include in a breeding scheme.

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. There are 9 defined claw disorders recorded: corkscrew claw (CSC), heel horn erosion (HH), dermatitis (DE), sole ulcer (SU), white line disorder (WLD), haemorrhage 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 one 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 (OVERALL). 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, were 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 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 WLD and SU (0.79) were highest. Genetic correlations between INFEC and CSC was close to zero (0.06) and between LAMIN and CSC and INFEC it was 0.31 and 0.24, respectively. 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 an increased number of free stalls (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 had claw lesions in free stall and tie stall, respectively. Lameness cause economic losses to the farmer (Enting et al., 1997), because it influence 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 number of lame cows. Environmental factors, such as herd, flooring and feeding, affects claw disorders (e.g. Bielfeldt et al., 2005; Fjeldaas et al., 2011; Buttchereit et al., 2012). Experience of detecting claw disorders may vary between claw trimmers. Holzhauer et al. (2006) found differences between trained claw trimmers in ability to diagnose chronic laminitis, interdigital dermatitis/heel horn erosion, sole heamorrhage 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, 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 authors (e.g. van der Waaij et al., 2005; Laursen et al., 2010; Häggman et al., 2012). Laursen et al. (2010) found highest genetic correlation between overall claw health and locomotin (0.46) and rear leg rear view (0.21). Among single claw disorders and leg and conformation traits, van der Waaij et al. (2005) estimated highest genetic correlations between foot angel and white line disease (0.64) and between locomotion and interdigital hyperplasia (0.82). Uggla et al. (2008) concluded that the 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, 2011). Recording corkscrew claw at claw trimming will 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 was used in the analyses. There were in total 309,885 claw health records from 178,452 cows recorded at claw trimming. The claw trimmers record whether the cow has normal (healthy) claws or if one or more of 9 claw disorders are present (Table 1). Identification of claw trimmer, date for claw trimming and other disorders or remarks are also recorded. Claw trimmers were categorized into professional claw trimmers, other claw trimmers, farmers and other persons like veterinarians or veterinarian 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 they can be identified when recording claw health, whereas other claw trimmers and farmers use a universal group code. A cow may have several claw disorder reported at the same day, however which leg (front or rear) is 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 all cows are not 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 1 claw health record and 23 % of the claw health records were a claw disorder. Frequencies of each 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). Veterinary treated cases of IDP were not reported in the claw

health recording, and therefore not included in this 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 records for both elite- and young sires), herd and cow, respectively, with 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, 2002). Only cows with claw health data were included in the analyses. Herds reporting less than 10 % or less than 10 normal claw records from 2004 to 2011 were excluded; cows should have a Norwegian Red A. I. sire; and age at calving should be within defined intervals. The intervals for calving age in months were: 1st calving between 16 and 48; 2nd calving between 26 and 61; 3rd calving between 36 and 74; and 4th calving between 45 and 87. After editing, the dataset contained 204,892 claw health records from 141,659 cows, 1,904 sires and 6,156 herds. There were no records of HSW before 2007, so the dataset 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 low frequency (Table 3) grouping them is an option. Overall claw disorder (**OVERALL**) was defined based on whether or not the cow had at least one claw disorder

(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) range 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.

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 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:

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

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 4th class included lactation 4 to 13. Calving year and month had 93 classes from April 2004 to December 2011, where the 1st 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 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 $\mathbf{s} \sim N(0, \mathbf{A}\sigma_s^2)$, $\mathbf{h} \sim N(0, \sigma_h^2)$ and $\mathbf{e} \sim N(0, 1)$ where, σ_s^2 is sire variance, σ_h^2 is herd variance, and the residual variance (σ_e^2) 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 var(**s**) = **G** $\otimes$ **A**, var(**h**) = **H** $\otimes$ **I**, and var(**r**) = **R** $\otimes$ **I** where, **I** is a identity matrix and **G**, **H** and **R** are the 5×5 matrices containing genetic-, herd-, and residual variances and covariance among the 5 traits. Heritability was calculated using:

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

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 (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 number of iteration 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 frequency when farmers performed claw trimming, whereas for CSC there were almost no differences between the four categorizes of claw trimmers. Calving year and month had effect but showed no clear trend for any of the claw disorders. Stage of lactation showed a peak 3 to 5 months 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 OVERALL 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 0 for any of the disorders. The widest 95 % HPD were found for DE and IDP, and the narrowest interval 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 were 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 that 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 correlation among CSC, DE and WLD were all close to 0 (≤ 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 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 claw loose hardness (Webster, 1993) and become more available for infectious bacteria in such environment. A high concentrate feeding regime will increases the risk of capsule disruption of the claw that will increase the risk for SU and WLD (Webster, 1993). Van der Linde et al. (2010) estimated genetic correlations among sole haemorrhage, 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 correlations between SU and DE (-0.19) and HH (0.13) were not different from 0.

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 (Table 4 and Table 6). For OVERALL the posterior mean of heritability of liability was 0.13 with SD 0.01 and the 95 % HPD ranged from 0.10 to 0.15. The heritability of OVERALL was higher than 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 OVERALL was in accordance with Buttchereit et al. (2012) but higher than the heritability on the underlying scale found by Häggman et al. (2012).

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 and 0.24, respectively (Table 6). The 95 % HPD for the genetic correlation between INFEC and CSC contained 0 (-0.12 to 0.23), whereas between LAMIN and CSC 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 or LAMIN, were high within groups and lower between groups (Table 5). Other authors found moderate to high genetic correlations among single claw disorders grouped similarly 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 haemorrhage, 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 haemorrhage 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 haemorrhage 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 disorders 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 become reasonable to assume they are almost the same trait or 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) (Table 7 and Table 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 five 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 like types of flooring, cubicle, nutrition and feeding system can affect claw disorders. For example, small or not well

formed cubicles can reduce the lying time and thereby increase the risk of claw disorders (Leonard et al., 1996) like SU and WLD.

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

Claw health data

Not every cow in a herd had a claw health record, because it may have been considered that claw trimming was not needed. These cows may be healthy, but not necessarily, because some of the claw disorders can only be observed at claw trimming. To define healthy cows, one alternative is to only include cows with claw health records in the analyses, another is to include all cows in a herd and assume cows without claw health records to be 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 in general lower compared to the 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 to results from other studies (e.g. Koenig et al., 2005; Swalve et al., 2008; Häggman et al., 2012) where 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 that only perform claw trimming in their own herd may have less experience in diagnosis of claw disorders. The group other claw trimmers have the largest amount of claw

health records, but individual claw trimmers cannot be distinguished within the group. The 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 to 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 between breeds (Holstein and RDC) and countries from 11 to 59 (Johansson et al., 2011).

Claw health status recorded at claw trimming provide 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 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 a long-term perspective.

ACKNOWLEDGMENTS

The authors would like to thank all claw trimmers and farmers that report claw health data, the Norwegian Dairy Herd Recording System and the Norwegian Cattle Health Service (Ås,

344 Norway) for access to data, the Norwegian Research Council and Geno for funding, and Åse
345 Margrethe Sogstad (Norwegian Cattle Health Service, Ås, Norway) for help to interpret the
346 claw health data.
347

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441 **Table 1**. Definitions of normal claws and claw disorders included in the Norwegian claw

442 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, if severe cases it can reach the corium
Haemorrhage of sole and white line	HSW	Haemorrhage of more than 20 percent 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 ≥ 3
Acute trauma	AT	E.g. fractures and dislocation of joint

443

444 **Table 2.** Development of normal (healthy) claws and claw disorders in Norway from 2004 to

445 2011, as percentage of all claw trimming records

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
Haemorrhage 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

446

447 **Table 3.** Mean frequency of single and grouped claw disorders analyzed, were cows have 1
448 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
Haemorrhage 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

449

450 **Table 4.** Posterior mean, standard deviation (SD), and 95 % highest probability density
451 interval (95 % HPD) of heritability of liability and posterior mean and SD of sire variance
452 (σ_s^2) and herd variance (σ_h^2) from 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
Haemorrhage 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

453

Table 5. Posterior mean (standard deviation) [95 % highest probability density intervals] 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]

459 **Table 6.** Posterior mean (standard deviation) [95 % highest probability density intervals] of
460 heritability of liability (on diagonal) and genetic correlation (below diagonal) among
461 corkscrew claw (CSC), infectious claw disorders (INFEC), and laminitis related claw
462 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]

463

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

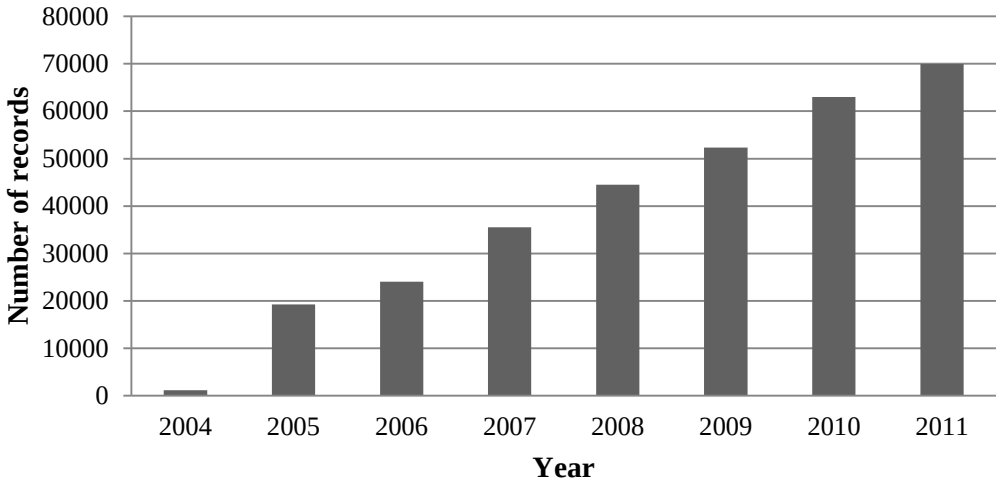
	CSC	HH	DE	SU	WLD
CSC		0.40 (0.02)	0.26 (0.03)	0.37 (0.02)	0.46 (0.02)
HH	-0.06 (0.01)		0.65 (0.02)	0.44 (0.02)	0.54 (0.02)
DE	-0.14 (0.02)	0.34 (0.02)		0.47 (0.03)	0.52 (0.03)
SU	0.06 (0.01)	0.11 (0.02)	0.07 (0.02)		0.51 (0.02)
WLD	0.01 (0.01)	0.08 (0.02)	0.00 (0.02)	0.14 (0.02)	

467

468 **Table 8.** Posterior mean (standard deviation) of herd correlation (above diagonal) and residual
469 correlation (below diagonal) among corkscrew claw (CSC), infectious claw disorders
470 (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)	

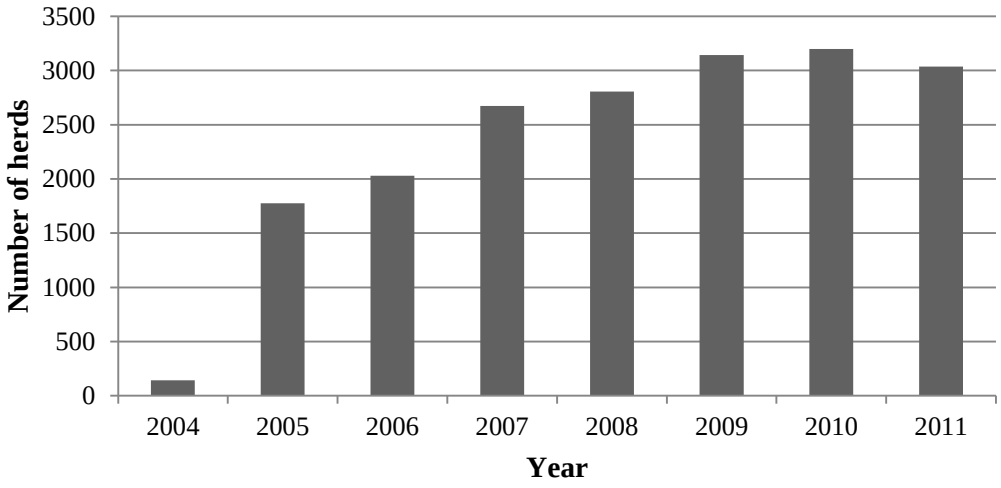
471



472

473 **Figure 1.** Number of claw health records per year.

474



475

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

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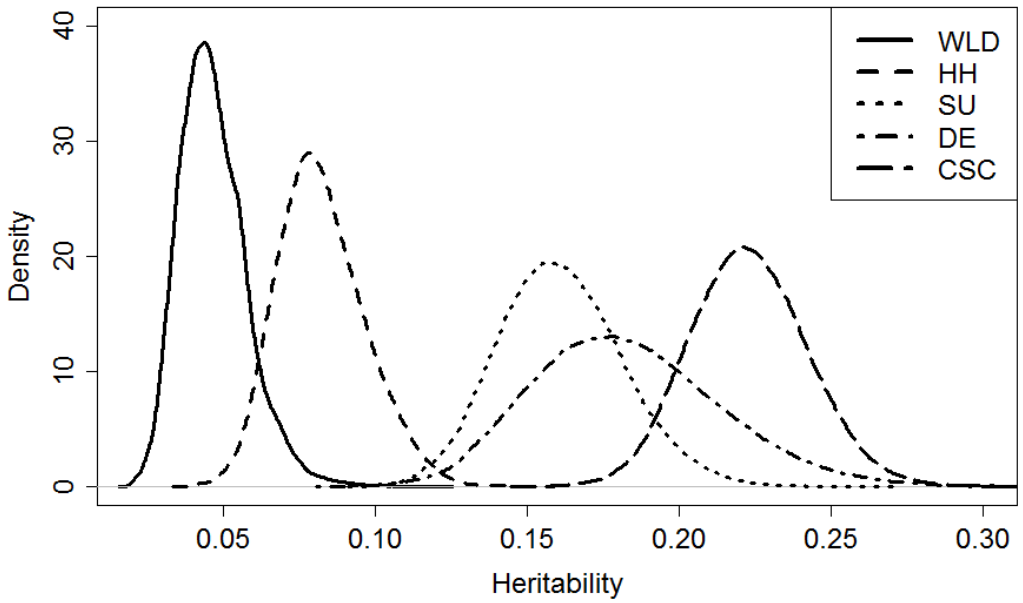

478

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

482

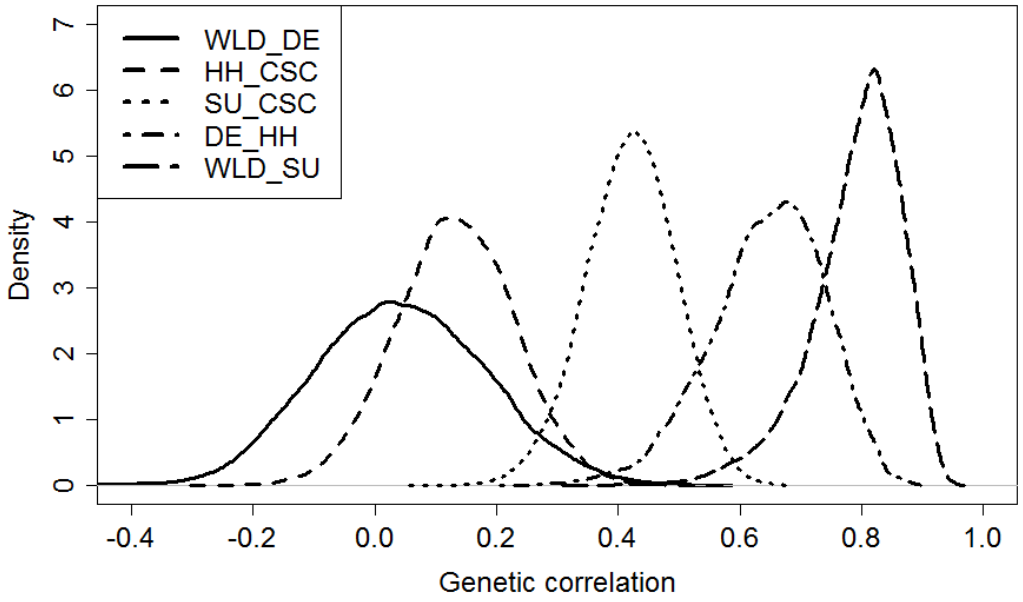

Figure 4. Posterior distribution of genetic correlation between (from the left) white line disorder and dermatitis (WLD_DE), heel horn erosion and corkscrew claw (HH_CSC), sole ulcer and corkscrew claw (SU_CSC), dermatitis and heel horn erosion (DE_HH), and white line disorder and sole ulcer (WLD_SU).