Claw health index for Dutch dairy cattle based on claw trimming and conformation data

C. van der Linde,¹ G. de Jong, E. P. C. Koenen, and H. Eding

CRV BV, PO Box 454, 6800 AL Arnhem, the Netherlands

ABSTRACT

The purpose of this study was to develop a model for a routine genetic evaluation of claw health traits and to develop an index including data on claw health and conformation traits. Claw health data comprised observations on 40,536 dairy cows of claw traits recorded by claw trimmers. Claw health traits scored were sole hemorrhage (SH), digital dermatitis (DD), interdigital dermatitis (ID), wall ulcer (WU), sole ulcer (SU), interdigital hyperplasia (IH), and white line disease (WL). A combined claw health trait was added as a trait to the data, combining all claw disorders. Observations on 5 feet and leg conformation traits on 41,048 animals were evaluated as predictive traits for claw health. These conformation traits were rear leg side view, rear leg rear view, foot angle, locomotion, and feet and legs. Prevalence of claw disorders ranged from 3% (WU) to 38% (SH). Overall, 69% of the animals had at least one claw disorder. Estimated heritabilities for claw health traits ranged from 0.01 (WU) to 0.13 (IH), and repeatabilities (within and across lactation) ranged from 0.15 (WU) to 0.57 (IH). Genetic correlations of claw health traits in parity 1 and parities ≥ 2 ranged from 0.72 to 1.00. Estimated genetic correlations among claw health traits ranged from -0.35 to 0.88 and between claw health and conformation traits ranged from -0.58 to 0.41 . The breeding goal for claw health was to reduce costs due to claw disorders. The economic index for claw health, which included claw health and feet and leg conformation traits, had a reliability of 59% for an average progeny-tested bull in the Netherlands. The prevalence of claw disorders can be reduced up to 0.7% per year with selection on claw health only.

Key words: claw health, genetic parameters, selection index, conformation

INTRODUCTION

Claw health is an important issue in dairy herds in the Netherlands. More than 70% of Dutch cows have at least one claw disorder (Somers et al., 2003; Van der Waaij et al., 2005). Claw disorders affect the welfare of the animal and have economic implications due to costs of treatment, earlier culling, and production losses. The economic losses due to claw disorders in the Netherlands were estimated at €104 per case of clinical lameness and ranked third after mastitis and fertility problems (Enting et al., 1997). Ettema and Ostergaard (2006) estimated the costs per case of clinical lameness at €192 for Danish circumstances.

Claw health is affected by both management and genetics. Several studies have shown that claw health is heritable, with estimated heritabilities ranging from 0.01 to 0.20 (Koenig et al., 2005; Van der Waaij et al., 2005; Naeslund et al., 2008; Swalve et al., 2008). Although the heritabilities of claw health traits are low, long-term improvement of claw health traits may be achieved by breeding for improved claw health.

Breeding on claw health requires the collection of enough good quality data to obtain an EBV with a reasonable reliability. From 2006 onward, claw health data have been routinely recorded in the Netherlands by professional claw trimmers from the Farm Relief Services (Agrarische Bedrijfsverzorging). Trimmed cows and observed claw disorders of cows trimmed by claw trimmers were digitally recorded in the “Digiklauw” scheme (Agrarische Bedrijfsverzorging, Almen, the Netherlands). The number of herds participating in this scheme is about 600, with about 80,000 trimmings performed by claw trimmers per year. The number of cows with observations for claw health per year in the Netherlands is still limited. The reliability of the EBV of young bulls could be increased by use of conformation data to predict claw health. Several studies showed considerable genetic correlations between feet and leg conformation and claw health traits (Koenig et al., 2005; Van der Waaij et al., 2005; Onyiro et al., 2008), whereas other studies (Swalve et al., 2008; Uggle et al., 2008) concluded that these genetic correlations were small. Genetic correlations between feet and leg

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¹Corresponding author: rene.van.der.linde@crv4all.com

conformation and claw health traits differ depending on the conformation traits and the population studied. Therefore, the potential of conformation data to predict claw health needs to be investigated.

The objectives of this study were (1) to develop a model for a routine genetic evaluation of claw health traits, (2) to investigate the relationship between feet and leg conformation and claw health traits, and (3) to develop an index combining EBV of claw health traits and possibly feet and leg conformation traits.

MATERIALS AND METHODS

Data

Claw health data were recorded by professional claw trimmers in the period from October 2006 to January 2009. Trimmed cows and observed claw disorders were recorded. Data comprised 141,262 trimmings and 241,065 claw disorders from 62,187 cows in 686 herds, scored by 95 claw trimmers. Cows could have repeated observations within lactation as well as across lactations. Only rear leg claw disorders were included, because in two-thirds of the cows only rear leg claws were trimmed. Scored claw disorders were sole hemorrhage (**SH**), digital dermatitis (**DD**), interdigital dermatitis (**ID**), wall ulcer (**WU**), sole ulcer (**SU**), interdigital hyperplasia (**IH**), and white line disease (**WL**). Data were scored as categorical traits (0 = no disorder, 1 = slight disorder, 2 = moderate disorder, 3 = severe disorder) or, for IH and WL, as binary traits (0 = no disorder, 1 = disorder). An extra trait (combined claw health trait, **CT**) was defined as a binary trait, indicating whether a cow had one or more claw disorders or not.

Cows had at least 75% Holstein-Friesian genes, a lactation stage at recording between 0 and 365 d, minimum age at first calving of 640 d, and a maximum parity at recording of 5. Individual cow trimmings and claw disorders recorded within a period of 7 d in a herd were combined. At least 50% of the herd mates and at least 20 cows in a herd had to be trimmed. The number of average claw disorders per cow per trimming per herd visit had to be between 0.1 and 3.0. Edits on percentage of cows trimmed in a herd showed that, in most herds, either ≤ 30 or $\geq 80\%$ of the cows were being trimmed (24 and 63% of the trimmings before data edits, respectively). The number of claw disorders per trimming was comparable across different percentages of cows trimmed in a herd. Claw health scores were transformed to a standard normal distribution $\sim N(0,1)$ per claw trimmer-year combination. The fractions of the different classes were calculated and these fractions were transformed to the corresponding x-coordinate of the standard normal distribution. Trimmings and claw

disorders recorded by claw trimmers with fewer than 100 observations per year were merged into one class within year of trimming. After editing, 69,281 records of 40,536 cows with 79,210 claw disorders were available for parameter estimation. These data were collected in 572 herds by 92 claw trimmers. The number of records per parity ranged from 23,020 in parity 1 to 5,354 in parity 5. The prevalence of claw disorders per parity is shown in Figure 1. Prevalence was defined as the percentage of cows trimmed that had a claw disorder.

Conformation data on feet and leg traits from the national conformation evaluation were available from 2003 on for herds with trimmings in the data set. Feet and leg conformation traits were rear leg side view (**RLSV**), rear leg rear view (**RLRV**), foot angle (**FA**), locomotion (**LOC**), and feet and legs (**FL**). Feet and legs is a descriptive trait, whereas the others are linear traits. Not all herds with claw health data participated in the national conformation classification program. Only first observations per cow in the first parity were included. Stage of lactation at classification was between 14 and 365 d and age at first calving between 640 and 1,095 d; a minimum of 5 classified cows and at least one cow with claw health data were required per herd visit. After editing, 41,048 animals with conformation records were included, of which 25,559 animals had an observation for claw health. Conformation records were scored in 434 herds by 21 classifiers, during 3,074 herd visits.

Statistical Analyses

Fixed effects to include in the model for claw health traits were tested for significance ($P < 0.01$) using a general linear model and the statistical software package SPSS (SPSS Inc., Chicago, IL). Tested fixed effects were parity, age at calving, stage of lactation, year-season of calving, herd-date of visit, and claw trimmer-half year of trimming. The significance test of the fixed effects was based on the first observation per animal for SH (trait with the highest prevalence). There were 32,975 trimmings of as many cows, with 12,537 claw disorders due to SH. The fixed effects of parity, stage of lactation, age at calving, herd-date of visit, and claw trimmer-half year of trimming were found to be significant. Year-season of calving ($P = 0.04$) was not significant. The percentage of explained variation (R^2) by significant fixed effects was 33.4%.

The model for analysis of the claw health traits was

$$Y_{ijklmnop} = \mu + P_i + A_j + L_k + HV_l + TY_m + PERM_n + S_o + E_{ijklmnop}, \quad [1]$$

Figure 1. Prevalence of claw disorders by parity.

where $Y_{ijklmnop}$ is the score of one of the claw disorders, μ is the overall mean, P_i is parity ($i = 1$ to 5), A_j is age at calving (62 monthly classes, $j = 21$ to 82), L_k is stage of lactation at trimming (monthly classes, $k = 1$ to 12), HV_l is herd-date of visit ($l = 1$ to $1,270$), TY_m is claw trimmer-half year of trimming ($m = 1$ to 222), $PERM_n$ is the random permanent environmental effect of animal ($n = 1$ to $40,536$), S_o is the random sire effect ($o = 1$ to $7,221$), and $E_{ijklmnop}$ is the error effect.

Fixed effects in the model for conformation traits were not tested for significance, because the model was very similar to that used for the national genetic evaluation for conformation traits (<https://www.cr-delta.nl/nl/fokwaarden/pdf/E8.pdf>). The model for analysis of the conformation traits was

$$Y_{ijklmn} = HVC_i + A_j + L_k + CY_l + S_m + E_{ijklmn}, [2]$$

where Y_{ijklmn} is the score of one of the conformation traits, HVC_i is herd-date of visit-classifier ($i = 1$ to $3,074$), A_j is age at calving (15 monthly classes, $j = 21$ to 35), L_k is stage of lactation at classification (monthly classes, $k = 1$ to 12), CY_l is classification standard by year ($l = 1$ to 14), S_m is the random sire effect ($m = 1$ to $7,221$), and E_{ijklmn} is the error effect.

The relationship matrix was added to both models using sire and maternal grandsire. Three generations of pedigree data of all cows with claw health or conformation observations were included. Variance associated with the permanent environmental effect was included in the heritability and repeatability estimates for claw health.

Claw health traits were analyzed with univariate and bivariate (parity 1 and parities ≥ 2) models using ASREML (Gilmour et al., 2002). Traits were regarded as different traits if genetic correlations between parities were significantly different from 1.00 ($P < 0.05$) or when genetic variance estimates in different parities were significantly different ($P < 0.05$). Correlations between claw health and conformation traits were estimated in bivariate analyses.

Claw Health Index

The breeding goal was defined as reducing costs due to claw disorders. Traits included in the breeding goal were weighted according to costs per disorder (Brujinis et al., 2010). Scores of claw health traits in the analysis were on the scale of a standard normal distribution $\sim N(0,1)$ and costs per disorder were on the binary scale. Therefore, the trait unit in the analysis had to be converted to the binary scale to be able to include costs per disorder as weight per claw health trait in the selection index calculations. The percentage of healthy cows and the genetic standard deviation resulting from the analysis were expressed on the binary scale. The area under the normal curve of the density formula bound by the ordinates of population mean ± 1 genetic standard deviation was determined and divided by 2. This resulted in the prevalence per genetic standard deviation in the analysis. The economic values per genetic standard deviation were calculated by multiplying the prevalence per genetic standard deviation by the costs per claw disorder. On the binary scale, no distinction

was made between different categories of severity of claw disorders. In the selection index calculation, one observation per animal was included, genetic variances and heritabilities were taken from univariate analyses, and genetic correlations between traits were taken from bivariate analyses. Genetic correlations among claw health traits in parities ≥ 2 were used. Results based on genetic correlations among traits in parity 1 were calculated and were very comparable to results based on parities ≥ 2 traits.

The need to include all claw health traits in the selection index was evaluated. Claw health traits were added to the index as long as the added trait increased the reliability of the index (described below) by at least 1%. Index calculations were based on a scenario where a progeny-tested bull had 150 lactating daughters and the sire of the bull had 1,000 lactating daughters. Ten percent of these daughters were assumed to participate in claw trimming recording.

We also tested whether CT could replace the other claw health traits as an index trait. The advantage of CT compared with the other claw health traits is the inclusion of one instead of several traits in the genetic evaluation for claw health. Variance of the index with CT included and the index with the other claw health traits included were compared. The variance of the claw health index including CT was required to explain at least 98% of the variance of the index including all other claw health traits for CT to replace the other claw health traits in the index.

Conformation traits were added to the index as long as they increased the reliability of the index by at least 1%. Sixty percent of sire daughters were assumed to participate in conformation recording. The reliability of a claw health index including only conformation traits was calculated to determine the increase in reliability by including claw trimming data in the index.

Genetic responses per claw health trait were also calculated. The genetic response was based on 4 selection paths (Rendel and Robertson, 1950): sires of bulls (SB), sires of cows (SC), dams of bulls (DB), and dams of cows (DC). The selected proportion of SB was 5%, of SC 10%, and of DB and DC 100% (no selection). The generation interval for SB was assumed to be 10 yr, for SC 7 yr, for DB 3 yr, and for DC 4 yr. The genetic response (R) per selection path was calculated using equation [3]. The genetic progress per year (ΔG) was calculated using equation [4]. The accuracy (r_{IH}) was calculated using equation [5] and the reliability was calculated as r_{IH}^2 .

$$R = i \times r_{IH} \times \sigma_H, \quad [3]$$

$$\Delta G = \frac{R_{SB} + R_{SC} + R_{DB} + R_{DC}}{L_{SB} + L_{SC} + L_{DB} + L_{DC}}, \quad [4]$$

$$r_{IH} = \frac{\sigma_I}{\sigma_H}, \quad [5]$$

where i is the selection intensity, σ_I is the standard deviation of the index, σ_H is the standard deviation of the breeding goal, and L is the generation interval in years per selection path.

RESULTS AND DISCUSSION

Genetic Parameters

Prevalence, genetic variance, heritability, and repeatability per trait estimated univariately are in Table 1. The highest percentages of disorders were found for SH, DD, and ID, and ranged from 22 to 38% for all traits except CT, which combined all disorders, resulting in the highest percentage (69%). The remaining traits accounted for 11% of disorders or less. Estimated heritabilities ranged from 0.01 (WU) to 0.13 (IH), and repeatabilities (within and across lactation combined) ranged from 0.15 (WU) to 0.57 (IH). Low repeatabilities found for claw health traits make repeated observations very valuable for the genetic evaluation, resulting in higher reliabilities of EBV. Estimated heritabilities of claw health traits in this study (0.01 to 0.13 from univariate analysis) were comparable to results found in other studies, such as 0.01 to 0.10 (Van der Waaij et al., 2005), 0.05 to 0.20 (Swalve et al., 2008), 0.05 to 0.07 for combined claw health traits including DD and heel horn erosion or SH and SU (Naeslund et al., 2008), and 0.07 to 0.12 (Koenig et al., 2005).

Results of bivariate analyses between parities for each claw health trait are in Table 2. Heritabilities of parity 1 and parities ≥ 2 were quite comparable for most traits; the largest differences (parities ≥ 2 minus parity 1) were found for ID (+0.03), SU (+0.04), and IH (+0.06). Repeatabilities of parity 1 and parities ≥ 2 were generally low; the highest estimates were found for IH (0.42 in parity 1 and 0.62 in parities ≥ 2). Genetic correlations between parity 1 and parities ≥ 2 were ≥ 0.72 for all traits; the genetic correlation between parity 1 and parities ≥ 2 was significantly different from 1.00 for DD, SU, and IH. Genetic variances of parity 1 and parities ≥ 2 were significantly different for ID, SU, and IH. Permanent environmental correlation between parity 1 and parities ≥ 2 was 0.72 for DD and ≥ 0.87 for all other traits. The permanent environmental correlation

Table 1. Prevalence, genetic variance¹ (σ_g^2), heritability¹ (h^2), and repeatability¹ (r) per claw health trait

Trait	Prevalence (%)	σ_g^2	h^2	r
Sole hemorrhage	38	0.0334	0.06	0.16
Digital dermatitis	22	0.0430	0.09	0.31
Interdigital dermatitis	29	0.0534	0.11	0.26
Wall ulcer	3	0.0021	0.01	0.15
Sole ulcer	7	0.0307	0.12	0.30
Interdigital hyperplasia	5	0.0247	0.13	0.57
White line disease	11	0.0082	0.03	0.16
Combined claw health trait	69	0.0316	0.07	0.22

¹Significantly ($P < 0.05$) different from zero for all traits.

between parity 1 and parities ≥ 2 was not significantly ($P < 0.05$) different from 1.00 for all traits except DD.

Table 3 gives the trait description, number of records, average, standard deviation, genetic variance, and heritability of conformation traits. Estimated heritabilities largely agreed with heritabilities used in the national genetic evaluation in the Netherlands and Flanders (maximum absolute differences per trait of 0.02), indicating that this conformation subset was representative of the national conformation data set.

Estimated genetic correlations between claw health and conformation traits are in Table 4. Parities 1 and ≥ 2 were regarded as different traits for all claw traits and analyzed separately in this case. Genetic correlations between claw health traits WU and CT and conformation traits are not shown. Wall ulcers were discarded from this analysis, because in additional analyses (results not shown), a genetic correlation of 0.98 between WU and WL was estimated. Results for CT are not shown because this trait was meant to investigate whether the other claw health traits could be substituted with one trait combining all claw disorders. Genetic correlations between CT and conformation traits ranged from -0.56 (LOC) to 0.14 (RLSV).

Genetic correlations between claw health and conformation traits ranged from -0.58 (DD and LOC) to 0.41 (SU and RLSV). Most claw health traits had moderate maximum correlations (0.40 to 0.58) with conformation traits, whereas SH and WL had smaller maximum genetic correlations with conformation traits (0.24 or smaller). Conformation traits FL and LOC had the highest number of genetic correlations with claw health traits being significantly ($P < 0.05$) different from 0, 7, and 8, respectively. Absolute genetic correlations between claw health and conformation traits tended to be stronger in the first than in the second parity, particularly for DD. Genetic correlations of DD in first and later parities with FL were -0.51 and -0.27 , respectively, and with LOC they were -0.58 and -0.31 , respectively. Possible reasons for stronger genetic correlations in parity 1 than in parities ≥ 2 were that conformation traits were scored in the first parity only and were influenced by the claw condition of the animal. Sole ulcer had stronger genetic correlations with some of the conformation traits in parities ≥ 2 compared with parity 1; for example, genetic correlations with FL were -0.16 and -0.34 , respectively, and with LOC they were -0.24 and -0.30 , respectively.

Table 2. Genetic variance¹ (σ_g^2), heritability¹ (h^2), and repeatability¹ (r) for parity 1 and ≥ 2 and genetic (r_g) and permanent environmental correlation (r_{perm}) between parity 1 and ≥ 2 per claw health trait

Trait	Parity 1			Parities ≥ 2			Parity 1 – ≥ 2	
	σ_g^2	h^2	r	σ_g^2	h^2	r	r_g	r_{perm}
Sole hemorrhage	0.0386	0.07	0.15	0.0271	0.05	0.17	0.93	1.00
Digital dermatitis	0.0491	0.09	0.36	0.0361	0.08	0.30	0.88 ³	0.72 ³
Interdigital dermatitis	0.0323 ²	0.08	0.21	0.0570 ²	0.11	0.27	1.00	1.00
Wall ulcer	0.0014	0.02	0.14	0.0025	0.01	0.16	0.72	1.00
Sole ulcer	0.0134 ²	0.08	0.30	0.0366 ²	0.12	0.30	0.89 ³	1.00
Interdigital hyperplasia	0.0079 ²	0.08	0.42	0.0338 ²	0.14	0.62	0.83 ³	0.96
White line disease	0.0056	0.03	0.14	0.0091	0.03	0.17	0.90	0.87
Combined claw health trait	0.0377	0.07	0.20	0.0305	0.07	0.23	0.92	1.00

¹Significantly ($P < 0.05$) different from zero for all traits.

²Genetic variances of parity 1 and parities ≥ 2 significantly ($P < 0.05$) different.

³Correlation significantly ($P < 0.05$) different from 1.00; SE on r_g was between 0.03 and 0.12 for all traits except wall ulcer (0.21).

Table 3. Trait description, number of records, average, standard deviation, genetic variance (σ_g^2), and heritability¹ (h^2) of conformation traits

Trait	Trait description	Records (n)	Mean	SD	σ_g^2	h^2
Feet and legs	70 = poor, 89 = very good	41,048	80.0	3.5	1.67	0.16
Rear leg rear view	1 = hock in, 9 = straight	41,048	4.9	1.6	0.41	0.17
Rear leg side view	1 = straight, 9 = sickled	41,048	5.1	1.5	0.57	0.26
Foot angle	1 = low angle, 9 = steep	41,048	4.8	1.5	0.43	0.21
Locomotion	1 = lame, 9 = even gait, long strides	40,711	4.7	1.6	0.33	0.14

¹SE on heritability ranged from 0.016 to 0.022.

This result suggests that feet and leg traits seem to be a better predictor of SU occurring in higher parities than in parity 1. This might be due to a higher prevalence of SU in higher parities (4% in parity 1 vs. 14% in parity 5). Genetic correlations between claw health and conformation traits might be nonlinear, because some conformation traits have intermediate optima (RLSV and FA). However, analyses of single-trait EBV did not reveal any evidence for non-linearity of genetic correlations (results not shown).

Absolute genetic correlations among claw health traits (Table 4) were small to large (0.00 to 0.88). Claw health traits may be separated into 2 groups based on first- and later-parity correlations; namely, hygiene-related and laminitis-related claw disorders. Digital dermatitis, ID, and IH (hygiene-related claw disorders) had correlations between parity 1 and parities ≥ 2 ranging between 0.26 and 0.88; 11 of 12 such correlations were significantly ($P < 0.05$) different from zero. Sole hemorrhage, SU, and WL (laminitis-related claw disorders) had first- to later-parity correlations ranging between 0.06 and 0.79; 9 of 12 such correlations were significantly ($P < 0.05$) different from zero. The genetic correlations between hygiene- and laminitis-related traits were between -0.35 and 0.18 , and only 1 of them was significantly ($P < 0.05$) different from zero. Swalve et al. (2008) estimated genetic correlations among claw health traits as high as 0.49 . Only a few correlations between claw health and conformation traits in that study were significantly different from zero.

Different results of correlations between claw health and conformation traits were described in the literature. Van der Waaij et al. (2005) estimated absolute genetic correlations between claw health and conformation traits in the Netherlands as high as 0.91 between LOC and chronic laminitis. Genetic correlations with other feet and leg conformation traits were 0.64 (FA with WL) or lower. Locomotion seemed to be a good indicator for claw health in the Netherlands, but those results were not confirmed in this study. The main difference between Van der Waaij et al. (2005) and the present study was the lower number of records for LOC

(4,469 vs. 40,711 respectively) and claw health (21,611 vs. 69,281 respectively). Onyiro et al. (2008) estimated the heritability of DD and correlations between DD and feet and leg type traits. Their heritability estimate for DD (0.03) was lower than estimated in this study (0.09). This might be due to scoring DD by type classifiers, without visual claw inspection, instead of claw trimmers. The correlations between DD and type traits (LOC, -0.67 ; FL, -0.63 , both $P < 0.05$) were only slightly stronger than correlations estimated in this study (LOC, -0.58 ; FL, -0.51). Koenig et al. (2005) estimated genetic correlations between claw disorders and type traits of -0.61 (FA and DD), 0.48 (RLSV and SU), -0.81 (wall disorder and FL), and -0.72 (IH and FL). In contrast to other studies, Swalve et al. (2008) and Ugglä et al. (2008) concluded that genetic correlations between claw health and feet and leg conformation traits were small and mostly not significantly different from zero. The reason for the small correlations found by Ugglä et al. (2008) might be that they did not study LOC and FL, the traits with the largest genetic correlation with claw health traits in this study.

The number of records included for parameter estimation in the present study was substantially lower than the number of records in the original data set. This lower number of records was mainly caused by strict data edits implemented to ensure accurately estimated parameters. Data edits for the routine genetic evaluation procedure will be changed compared with the parameter estimation described in this study to include more records. The criteria on percentage of cows trimmed will be lowered from 50 to 20% and the data edit on minimum number of trimmed cows per herd visit will be lowered from 20 to 10. In the parameter estimation step of this study, almost 70,000 records were included; changing the 2 aforementioned data edits would have resulted in almost 20,000 additional records. In addition to the analyses described in this study, an analysis with data edits for the routine genetic evaluation was conducted. Sire variances for the 6 claw traits were between 88 and 117% compared with results in Table 1. Variance estimates of random

Table 4. Estimated genetic correlations between claw health traits¹ and conformation traits

Item	SH1	SH2	DD1	DD2	ID1	ID2	SU1	SU2	IH1	IH2	WL1	WL2	FL	RRLV	RLSV	FA	LOC
Sole hemorrhage 1 (SH1)																	
Sole hemorrhage 2 (SH2)	0.93*		0.06	-0.14	0.14	0.12	0.58*	0.60*	0.18	0.06	0.24	0.06	-0.20	0.16	0.13	-0.05	-0.21
Digital dermatitis 1 (DD1)			0.11	0.02	0.09	0.01	0.70*	0.79*	-0.11	0.09	0.31	0.51*	-0.12	0.09	-0.07	0.10	-0.14
Digital dermatitis 2 (DD2)				0.88*	0.75*	0.88*	0.02	0.06	0.46*	0.60*	-0.29	-0.33*	-0.51*	-0.32*	0.11	-0.18	-0.58*
Interdigital dermatitis 1 (ID1)					0.41*	0.56*	-0.09	0.15	0.26	0.65*	-0.23	-0.13	-0.27*	-0.17	0.08	0.19*	-0.31*
Interdigital dermatitis 2 (ID2)						1.00*	0.09	-0.12	0.34*	0.54*	-0.14	-0.29	-0.44*	-0.23*	0.25*	-0.25*	-0.49*
Sole ulcer 1 (SU1)							-0.10	0.03	0.46*	0.64*	-0.24	0.02	-0.34*	-0.15	0.10	-0.06	-0.37*
Sole ulcer 2 (SU2)								0.89*	0.07	-0.08	0.51*	0.41*	-0.16	-0.15	0.41*	-0.20	-0.24*
Interdigital hyperplasia 1 (IH1)									-0.02	0.00	0.45*	0.60*	-0.34*	-0.09	0.09	-0.12	-0.30*
Interdigital hyperplasia 2 (IH2)										0.83*	-0.05	-0.15	-0.40*	-0.26*	0.05	-0.18	-0.38*
White line disease 1 (WL1)											-0.35*	0.02	-0.36*	-0.30*	0.11	-0.15	-0.33*
White line disease 2 (WL2)												0.90*	0.05	-0.01	-0.07	0.24	0.02
Feet and legs (FL)													0.07	0.16	-0.11	0.14	0.06
Rear leg rear view (RLRV)														0.82*	-0.45*	0.48*	0.96*
Rear leg side view (RLSV)															-0.23*	0.26*	0.82*
Foot angle (FA)																-0.77*	-0.31*
Locomotion (LOC)																	0.34*

¹Claw health trait in parity 1 (1) and parities ≥ 2 (2).*Genetic correlations significantly different from zero ($P < 0.05$).

components (genetic, error, and permanent environment) ranged from 94 to 104%. It can be concluded that changing data edits resulted in slightly different estimates of variance components.

The claw health traits were separated into 2 correlated traits for parity 1 and parities ≥ 2 . Analyzing these traits as 3 different traits (parity 1, parity 2, and parity ≥ 3) was not possible because of severe convergence problems. It is expected, however, that genetic correlations between parity 2 and parities ≥ 3 be close to 1, because genetic correlations between parity 1 and ≥ 2 were already strong and genetic correlations between parity 2 and ≥ 3 are generally even stronger.

Claw Health Index

Claw health traits included in the claw health index calculations were SH, DD, ID, SU, IH, and WL. Table 5 gives the costs per case of a claw disorder (Brujinis et al., 2010), the prevalence per genetic standard deviation, and the economic value per genetic standard deviation of claw health traits. Economic values per genetic standard deviation were highest for the traits SH, DD, and ID (about €4 per trait) and were €1 to €2 per trait for SU, IH, and WL. The standard deviation of the breeding goal was €10.56. The reliability of the claw health index of a progeny-tested bull was 53%. The reliability of the claw health index based on CT only was 27%. Therefore, CT could not replace the 6 individual claw health traits in the index without losing a substantial amount of information.

Adding feet and leg conformation traits to the index resulted in 6% extra reliability (59%) of the claw health index compared with including claw health traits only. The reliability of 59% was achieved by including the claw health traits SH, DD, ID, SU, IH, and the feet and leg conformation traits FL, RLRV, FA, and LOC as index traits. White line disease and RLSV did not add extra reliability to the claw health index of a progeny-tested bull. Including only conformation traits instead of claw health and conformation traits in the index resulted in a much lower reliability of the index (24 vs. 59%). Including only conformation data in the index reduced the prevalence per claw disorder up to 0.5% per year (for ID) as response of selection (Table 6). Including both claw health and conformation traits in the index reduced the prevalence per claw disorder up to 0.7% per year (for ID). Table 6 shows that the genetic response for claw health traits increases considerably when including claw health and conformation traits compared with including only conformation traits in the index. Therefore, recording claw health data is essential for effective selection on claw health. This is in agreement with previous studies. Koenig et al. (2005)

Table 5. Costs per case, prevalence per genetic standard deviation (σ_g), and economic value (EV) per σ_g of claw health traits

Trait	Costs per case ¹ (€)	Prevalence per σ_g (%)	EV per σ_g (€)
Sole hemorrhage	55	6.9	3.81
Digital dermatitis	68	6.1	4.16
Interdigital dermatitis	57	7.9	4.48
Sole ulcer	79	2.4	1.87
Interdigital hyperplasia	66	1.6	1.08
White line disease	58	1.7	0.99

¹Values from Bruijnjs et al. (2010).

concluded that genetic progress could be tripled by direct selection using observations on claw disorders instead of using conformation data only for selection on claw health. Koenig and Swalve (2006) found that the selection response in laminitis resistance per generation could be doubled when laminitis observations of 50 daughters were included as an index trait. Results from selection index calculations in this study might be slightly underestimated because one observation per animal was included instead of repeated observations.

In monetary terms, the genetic response per year (ΔG) using an index including claw health and conformation traits was a reduction of costs due to claw disorders of €1.29 per cow per year.

The relative importance of claw health compared with milk production was assessed using equation [3]. Both traits were compared assuming that selection was only for one trait, either milk production or claw health, and bulls had daughters at the end of the first lactation. The selection intensity was assumed equal for both traits. The assumed r_{IH} for milk production was 0.95 and for claw health 0.77 ($\sqrt{0.59}$). The used σ_H was €66 for milk production (<https://www.cr-delta.nl/nl/fokwaarden/pdf/E7.pdf>) and €10.56 for claw health. Using equation [3], the ratio of the economic importance of milk production compared with claw health is roughly 8:1.

The number of herds participating in the Digiklauw program has been constant at about 600 herds in recent years, but is expected to increase to 1,500 in 2010 by merging the Digiklauw and the Dutch Animal Health Service (GD, Deventer, the Netherlands) program for claw trimming. The assumption of 10% participation in the claw trimming program is based on this expected increase of the number of participating herds.

CONCLUSIONS

Results from this study showed that individual claw health traits are heritable, enabling genetic selection on improved claw health. Repeatabilities of claw health traits were low to moderate, meaning that repeated observations on claw health traits are valuable information for genetic improvement of claw health. Estimated genetic correlations among different claw health traits ranged from small to large, indicating that observations on claw health cannot be regarded as observations on the same trait. Claw health traits could be separated into 2 groups based on first- and later-parity correlations; namely hygiene-related (DD, ID, and IH) and laminitis-related (SH, SU, and WL) claw disorders. Genetic correlations between claw health and feet and leg conformation traits ranged from small to moderate. Feet and leg conformation traits were useful indicator traits for claw health, but could not replace claw

Table 6. Annual genetic response in prevalence (PR) and genetic standard deviation (σ_g) per claw health trait of an index of conformation traits excluding and including claw health data

Trait	Index without claw health data		Index with claw health data	
	PR (%)	σ_g	PR (%)	σ_g
Sole hemorrhage	−0.3	−0.04	−0.4	−0.06
Digital dermatitis	−0.4	−0.06	−0.6	−0.09
Interdigital dermatitis	−0.5	−0.06	−0.7	−0.09
Sole ulcer	−0.1	−0.05	−0.2	−0.07
Interdigital hyperplasia	−0.1	−0.04	−0.1	−0.08
White line disease	−0.0	−0.01	−0.1	−0.03

health traits as index traits because of lower selection responses using conformation traits only.

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