Claw Health Index for Dutch Dairy Cattle

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Introduction

Claw health is an important issue in dairy herds in the Netherlands. More than 70% of the cows in the Netherlands has at least one claw disorder (Van der Waaij et al., 2005). Claw disorders affect the welfare of the animal and also 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 on € 104 per case of clinical lameness and ranked third after mastitis and fertility problems (Enting et al., 1997).

Claw health is affected by both management and genetics. Several studies showed that claw health is heritable, estimated heritabilities ranged from 0.01 to 0.12 (Koenig et al. (2005); Naeslund et al. (2008); Van der Waaij et al. (2005)).

From 2006 onwards, claw health data have been routinely recorded in the Netherlands by professional hoof trimmers of the Agrarische Bedrijfsverzorging in the so-called "Digiklauw" scheme. The data recorded per year (about 80,000 trimmings in 600 herds) in the Netherlands is still limited. The reliability of the estimated breeding value of young bulls could potentially be increased by use of conformation data to predict claw health. Therefore, use of conformation data to predict claw health might be beneficial.

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 traits and claw health traits and (3) to develop an index combining estimated breeding values of claw health traits and possibly feet and leg conformation traits.

Material and methods

Data. Trimmed cows and observed claw disorders were recorded by professional hoof trimmers in the period October 2006 through January 2009. Data comprised 141,262 trimmings and 241,065 claw disorders of 62,187 unique cows in 686 herds, scored by 95 hoof trimmers. Only rear leg claw disorders were included. Scored claw disorders were: sole haemorrhage (SH), digital dermatitis (DD), interdigital dermatitis (ID), sole ulcer (SU), interdigital hyperplasia (IH), and white line disease (WL). Data were scored as categorical trait (0 = no disorder, 1 = slight disorder, 2 = moderate disorder, 3 = severe disorder) or as binary trait (0 = no disorder, 1 = disorder). Animals had at least 75% Holstein Friesian genes, a lactation stage at recording between 0 and 365 days, minimum age at first calving of 640 days and a maximum parity at recording of 5. Trimmings and claw disorders within 7 days in one herd were combined on animal level, one trimming per cow per day and one case per claw disorder was included, at least 50% of the herd mates and at least 20 cows in a herd needed to be trimmed, the number of average claw disorders per cow per trimming per herd-day had to be between 0.1 and 3.0. Claw health scores were transformed to a standard normal

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distribution per hoof trimmer-year combination. After editing, 69,281 records of 40,536 cows with 79,210 claw disorders were available for parameter estimations. The number of records per parity ranged from 23,020 (parity 1) to 5,354 (parity 5). The percentage of disorders per trait ranged from 22% to 38% for SH, DD, and ID and from 5% to 11% for the other traits.

Conformation data on feet and leg traits from the national conformation evaluation were available from 2003 onwards 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). Only first observations per cow in the first parity were included. Data edits on conformation data were applied as in the national genetic evaluation for conformation traits in the Netherlands and Flanders. After editing, 41,048 animals with conformation records were included, of which 25,559 animals had an observation for claw health.

Statistical analyses. The model for claw health traits included fixed effects for parity, age at calving, stage of lactation at trimming, herd - date and hoof trimmer - half year and a random sire, permanent environment and error effect. The model for conformation traits included fixed effects for herd-date-classifier, age at calving, stage of lactation at classification, classification standard - year and a random sire 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.

Claw health traits were analysed univariate and bivariate (parity 1 and parities ≥2) using ASREML (Gilmour et al., 2002). Correlations between claw health traits and conformation traits were estimated in bivariate analyses.

Claw health index. The breeding goal was defined as reducing costs due to claw disorders. Claw health traits were combined into an economic selection index based on economic values per claw disorder (unpublished). In the selection index calculations genetic variances and heritabilities were taken from univariate analyses, genetic correlations between traits were taken from bivariate analyses.

Claw health and conformation traits were added to the index as long as the added trait increased the reliability 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. The participation in hoof trimming recording was assumed to be 10% and in the conformation recording 60% of the lactating daughters.

Results and discussion

Genetic parameters. Heritabilities and repeatabilities of parity 1 and ≥2 and genetic and permanent enviromental correlations between parity 1 and ≥2 per claw health trait are in Table 1. Heritabilities of parity 1 and parities ≥2 were quite comparable for most traits, 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, highest repeatabilities were found for IH (0.42 in parity 1 and 0.62 in parities ≥2).

Table 1: Heritability[α] (h^2) and repeatability[α] (r) for parity 1 and ≥2 and genetic (r_g) and permanent environmental correlation (r_{perm}) between parity 1 and ≥2 per trait

Trait	Parity 1		Parities ≥2		Parity 1 - ≥2	
	h^2	r	h^2	r	r_g	r_{perm}
Sole haemorrhage	0.07	0.15	0.05	0.17	0.93	1.00
Digital dermatitis	0.09	0.36	0.08	0.30	0.88[β]	0.72
Interdigital dermatitis	0.08	0.21	0.11	0.27	1.00	1.00
Sole ulcer	0.08	0.30	0.12	0.30	0.89	1.00
Interdigital hyperplasia	0.08	0.42	0.14	0.62	0.83[β]	0.96
White line disease	0.03	0.14	0.03	0.17	0.90	0.87

[α] Standard errors on h^2 and r ranged from 0.004 to 0.017, [β] r_g significantly different from 1.00.

The low repeatabilities found for claw health traits make repeated observations very valuable for the genetic evaluation, resulting in higher reliabilities of breeding values. Genetic correlations between parity 1 and parities ≥2 were ≥ 0.83 for all traits, the genetic correlation between parity 1 and parities ≥2 was significantly different from 1.00 for DD and IH. Permanent environmental correlation between parity 1 and parities ≥2 was 0.72 for DD and ≥ 0.87 for all other traits. Estimated genetic correlations between claw health traits and conformation traits are in Table 2.

Table 2: Estimated genetic correlations[α] between claw health traits[β] and conformation traits[χ]

	FL	RLRV	RLSV	FA	LOC
Sole haemorrhage	-0.20	0.16	0.13	-0.05	-0.21
Digital dermatitis	-0.51	-0.32	0.11	-0.18	-0.58
Interdigital dermatitis	-0.44	-0.23	0.25	-0.25	-0.49
Sole ulcer	-0.16	-0.15	0.41	-0.20	-0.24
Interdigital hyperplasia	-0.40	-0.26	0.05	-0.18	-0.38
White line disease	0.05	-0.01	-0.07	0.24	0.02

[α] Standard errors ranged from 0.08 to 0.15, [β] claw health traits in parity 1,

[χ] Feet and legs (FL), rear leg rear view (RLRV), rear leg side view (RLSV), foot angle (FA) and locomotion (LOC).

The genetic correlations between claw health and conformation traits (Table 2) were low to moderate, most claw health traits had moderate maximum correlations (0.40 to 0.58) with conformation traits, SH and WL had lower maximum genetic correlations with conformation traits (0.24 or lower). Absolute genetic correlations between claw health traits (not shown) were low to high (0.00 to 0.88). Claw health traits may be separated into two groups based on mutual correlations, hygiene related and laminitis related claw disorders. DD, ID, and IH (hygiene related claw disorders) had mutual correlations (parity 1 and parities ≥2) between 0.26 and 0.88. SH, SU, and WL (laminitis related claw disorders) had mutual correlations between 0.06 and 0.79. The genetic correlations between hygiene- and laminitis-related traits were between -0.35 and 0.18.

Claw health index. The standard deviation of the breeding goal was € 10.56. The reliability of the claw health index of a progeny-tested bull was 53%. Adding feet and leg conformation traits to the index increased the reliability of the claw health index by 6% to 59%. WL and RLSV were not included in the index, because these traits did not add 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 (24% vs. 59%). Therefore, recording claw health data is essential for effective selection on claw health. Including claw health and conformation traits in the index resulted in a reduction up to 0.7% prevalence per claw disorders per year. In monetary terms, the genetic response per year was a reduction of costs due to claw disorders of € 1.29 per cow present per year in case of selection on claw health only.

Conclusions

Results from this study showed that individual claw health traits are heritable (heritabilities ranged from 0.03 to 0.14). Repeatabilities of claw health traits were low to moderate (0.14 to 0.62), meaning that repeated observations on claw health traits are valuable information for genetic improvement of claw health. Estimated absolute genetic correlations between different claw health traits ranged from low to high (0.00 to 0.88) and ranged from low to moderate between claw health traits and conformation traits (0.01 to 0.58). A claw health index including claw health traits resulted in a reliability of the index of 53% for a progeny-tested bull. Feet and leg conformation traits added 6% extra reliability to the claw health index. The selection response based on an claw health index with 59% reliability is a decrease up to 0.7% prevalence of claw disorders per year.

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