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Invited review: Genetics and claw health: Opportunities to enhance claw health by genetic selection

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ABSTRACT

Routine recording of claw health status at claw trimming of dairy cattle has been established in several countries, providing valuable data for genetic evaluation. In this review, we examine issues related to genetic evaluation of claw health; discuss data sources, trait definitions, and data validation procedures; and present a review of genetic parameters, possible indicator traits, and status of genetic and genomic evaluations for claw disorders. Different sources of data and traits can be used to describe claw health. Severe cases of claw disorders can be identified by veterinary diagnoses. Data from lameness and locomotion scoring, activity information from sensors, and feet and leg conformation traits are used as auxiliary traits. The most reliable and comprehensive information is data from regular hoof trimming. In genetic evaluation, claw disorders are usually defined as binary traits, based on whether or not the claw disorder was present (recorded) at least once during a defined time period. The traits can be specific disorders, composite traits, or overall claw health. Data validation and editing criteria are needed to ensure reliable data at the trimmer, herd, animal, and record levels. Different strategies have been chosen, reflecting differences in herd sizes, data structures, management practices, and recording systems among countries. Heritabilities of the most commonly analyzed claw disorders based on data from routine claw trimming were generally low, with ranges of linear model estimates from 0.01 to 0.14, and threshold model estimates from 0.06 to 0.39. Estimated genetic correlations among claw disorders varied from −0.40 to 0.98. The strongest genetic correlations were found among sole hemorrhage (SH), sole ulcer (SU), and white line disease (WL), and between digital/interdigital dermatitis (DD/ID) and heel horn erosion (HHE). Genetic correlations between DD/ID and HHE on the one hand and SH, SU, or WL on the other hand were, in most cases, low. Although some of the studies were based on relatively few records and the estimated genetic parameters had large standard errors, there was, with some exceptions, consistency among studies. Various studies evaluate the potential of various data soureces for use in breeding. The use of hoof trimming data is recommended for maximization of genetic gain, although auxiliary traits, such as locomotion score and some

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conformation traits, may be valuable for increasing the reliability of genetic evaluations. Routine genetic evaluation of direct claw health has been implemented in the Netherlands (2010); Denmark, Finland, and Sweden (joint Nordic evaluation; 2011); and Norway (2014), and other countries plan to implement evaluations in the near future.

Key words: claw disorder, genetic parameter, genetic evaluation

INTRODUCTION

Foot and claw disorders are among the major reasons for dairy cows leaving the herd, with lameness accounting for 10 to 15% of all involuntary culls (Green et al., 2002; Cha et al., 2010). German data show that involuntary culling due to feet and leg problems has increased over time (Vit, 2016). Unfavorable genetic correlations between production and functional traits have had obvious drawbacks for the health of the dairy cow (Veerkamp et al., 2003; Gernand et al., 2012).

A wide range of estimates are found in the literature for the frequencies of lameness and claw disorders in dairy cows, with substantial inter-herd variation. However, different data sources, classification systems, and definitions of reference groups and time periods make it difficult to compare results between studies. Mean frequencies of lameness in dairy herds in Europe and North America range between 23 and 70% (Green et al., 2002; Cook, 2003; Van der Waaij et al., 2005; Dippel et al., 2009; Rouha-Mülleder et al., 2009; Solano et al., 2015; Burgstaller et al., 2016), although some studies report lower prevalence (7.7% in dairy cows with lameness score $\geq$3; Fjeldaas et al., 2011). Incidence rates of claw disorders based on veterinarian diagnoses are below 10% (Egger-Danner, 2015; Zottl et al., 2016). In Norway, the number of cases of veterinary treatment of claw disorders per 100 cow-years at risk was 1.5 (Tine, 2015).

Discomfort and pain from claw disorders have been identified as an important animal welfare issue (von Keyserlingk et al., 2001; Logue and Bergsten, 2007; van Gastelen et al., 2011; Bruijnis et al., 2013; Huxley, 2013; de Vries et al., 2015). Despite increased awareness of lameness in relation to welfare and lost productivity, no studies have reported a reduction in the prevalence of lameness over the last 20 yr.

Cattle lameness has a great economic impact on the dairy industry, and it is the third-ranked health condition in frequency and cost after mastitis and reproduction disorders (Green et al., 2002; Hernandez et al., 2002; Cha et al., 2010; Bruijnis et al., 2013; Huxley, 2013). Lame cows are more frequently affected with mastitis, metabolic disorders, and reduced fertility. Nonspecific findings that accompany lameness include low BCS and reduced milk yields (Green et al., 2014). Annual costs for lame cows range from $206 to $412 per year (Enting et al., 1997; Greenough et al., 1997). Costs for individual disorders range from $120 for foot rot to $216 for sole ulcers, whereby the 40% of the costs are due to milk loss, 26% from decreased fertility, and 34% from treatment costs (Cha et al., 2010). Greater awareness and more thorough action by farmers concerning dairy cow foot health could reduce the economic consequences and improve health and welfare (Bruijnis et al., 2013).

The objective of this paper was to examine opportunities to enhance claw health in dairy cattle by genetic selection. We discuss the definition of the breeding goal, possible data sources (phenotyping), data validation procedures, trait definitions, models for genetic evaluation, aspects of direct and indirect selection, and prospects for achieving genetic improvement for claw health traits, and we present a review of genetic parameters and status of genetic and genomic evaluations for claw disorders.

BREEDING GOAL

Every genetic improvement program has an overall objective—the breeding goa—that guides selection decisions made by participants in the program. In the past, the breeding goal was often milk or fat yield, but over the last 30 yr, most countries have adopted total merit indices (**TMI**; Miglior et al., 2005; Egger-Danner et al., 2014), which focus instead on lifetime profitability. A TMI is a mathematical tool used to combine information about many economically important traits into a single breeding value for ranking animals. Heritabilities, genetic and phenotypic correlations, reliabilities of breeding values, and economic weights are used to construct the TMI (Cameron, 1997). If claw health is to be improved genetically, traits related to claw health should be included in the TMI with appropriate weights.

DATA SOURCES

Phenotypes

Both direct and indirect (auxiliary) traits may be used for genetic evaluation of claw health. Direct traits include veterinary diagnoses and claw disorders recorded by hoof trimmers. Indirect or auxiliary traits include locomotion and lameness scores, type traits from conformation recording, and traits derived from advanced sensors (e.g., activity-related sensors or mid-infrared spectral data).

Claw Trimmer Data. Several studies have shown that data recorded by hoof trimmers are the most promising for genetic improvement of claw health (Koenig et al., 2005; Häggman et al., 2013; Van Pelt, 2015). To produce high-quality evaluations, phenotypes must be clearly defined and consistently recorded. Hoof trimmers, veterinarians, and others who record data should be trained to use a consistent set of diagnoses and comparable scores so that data are comparable across recorders over time. An advantage of recording claw status at hoof trimming is that diseases may be recognized in their early stages, which avoids bias from recording only clinical cases and allows for early interventions that reduce costs and improve cow welfare. A survey conducted by the International Committee for Animal Recording (**ICAR**) Working Group on Functional Traits identified a broad range of recording practices and documentation schemes (Figure 1). The Working Group then collaborated with a group of international experts on foot health to develop the ICAR Claw Health Atlas (Egger-Danner et al., 2015), which provides standardized descriptions of 27 different claw disorders (Table 1). This atlas will support the collection of high-quality data within and across countries to support management and genetic evaluation programs.

Veterinary Diagnoses. In addition to information from claw trimming, veterinary diagnoses are potentially valuable sources of information, particularly for more severe cases. This information is available in countries with routine recording of diagnoses in connection with veterinary interventions and medical treatments, including the Nordic countries, Austria, and some parts of Germany (Aamand, 2006; Østerås et al., 2007; Egger-Danner et al., 2012). Analyses exclusively based on veterinary diagnoses of claw disorders are expected to have much lower frequencies than those based on hoof trimming data and may be biased toward diseases that result in lame cows. The inclusion of data from regular preventive trimming will provide more data about mild (early) cases.

Lameness. Several studies (Berry et al., 2010; Parker Gaddis et al., 2014; Koeck et al., 2016) used lameness observations, coded 0 (not lame) or 1 (lame), in a manner comparable to other health disorders recorded by farmers. The severity of lameness may also be described using a clinical gait score (Sprecher et

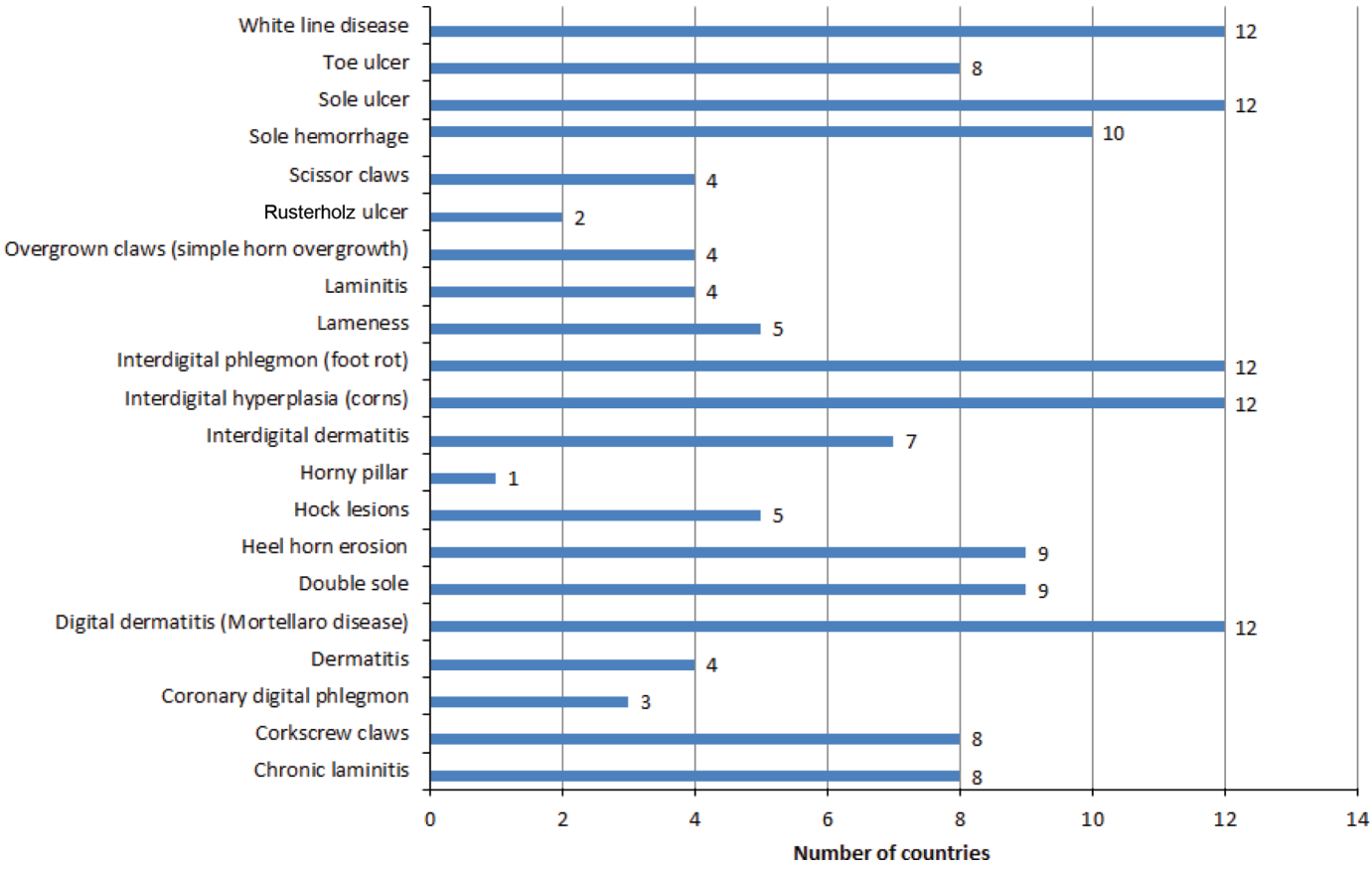

Figure 1. Overview of claw disorders recorded by different countries (Christen et al., 2015). Color version available online.

Table 1. Abbreviations and harmonized descriptions of foot and claw disorders (Egger-Danner et al., 2015)

Name	Code	Description	Synonymous terms
Asymmetric claws	AC	Significant difference in width, height and/or length between outer and inner claw that cannot be balanced by trimming.	—
Corkscrew claw	CC	Any torsion of either the outer or inner claw. The dorsal edge of the wall deviates from a straight line.	—
Concave dorsal wall	CD	Concave shape of the dorsal wall.	—
Digital dermatitis	DD	Infection of the digital and/or interdigital skin with erosion, mostly painful ulcerations and/or chronic hyperkeratosis/proliferation.	Mortellaro disease, Strawberry disease
Interdigital/superficial dermatitis	ID	All kind of mild dermatitis around the claws that is not classified as digital dermatitis.	—
Double sole	DS	Two or more layers of under-run sole horn.	Underrun sole
Heel horn erosion	HHE	Erosion of the bulbs, in severe cases typically V-shaped, possibly extending to the corium.	Slurry heel, erosio ungulae
Horn fissure	HF	Crack in the claw wall.	—
Axial horn fissure	HFA	Vertical (longitudinal) crack in the inner claw wall.	—
Horizontal horn fissure	HFH	Horizontal crack in the claw wall.	—
Vertical horn fissure	HFV	Vertical (longitudinal) crack in the outer or dorsal claw wall.	—
Interdigital hyperplasia	IH	Interdigital growth of fibrous tissue.	Corns, tyloma, interdigital fibroma
Interdigital phlegmon	IP	Symmetric painful swelling of the foot commonly accompanied with odorous smell with sudden onset of lameness.	Foot rot, foul in the foot, interdigital necrobacillosis
Scissor claws	SC	Tip of toes crossing each other.	—
Sole hemorrhage	SH	Diffused and/or circumscribed red or yellow discoloration of the sole and/or white line.	Sole bruising
Sole hemorrhage diffused form	SHD	Diffused light red to yellowish discoloration.	—
Sole hemorrhage circumscribed form	SHC	Clear differentiation between discolored and normal colored horn.	—
Swelling of coronet and/or bulb	SW	Uni- or bilateral swelling of tissue above horn capsule, which may be caused by different conditions.	—
Ulcer	U	Ulceration of the sole area specified according to localization (zones) such as bulb ulcer, sole ulcer, toe ulcer/necrosis.	—
Sole ulcer	SU	Penetration through the sole horn exposing fresh or necrotic corium.	—
Bulb ulcer	BU	Ulcer located at the bulb.	Heel ulcer
Toe ulcer	TU	Ulcer located at the toe.	—
Toe necrosis	TN	Necrosis of the tip of the toe with affection of bone tissue.	—
Thin sole	TS	Sole horn yields (feels spongy) when finger pressure is applied.	—
White line disease	WL	Separation of the white line with or without purulent exudation.	—
White line abscess	WLA	Necro-purulent inflammation of the corium.	—
White line fissure	WLF	Separation of the white line that remains after balancing both soles.	—

al., 1997; Flower and Weary, 2006; Koeck et al., 2016; Egger-Danner et al., 2017), which quantifies lameness on a scale from absent to very severe. Such scoring can be used for detection of claw health problems on the individual animal and herd levels, and is also useful in assessing welfare. The results from Egger-Danner et al. (2017) indicate the usability for breeding purposes.

Locomotion Scoring. Locomotion scoring is part of the conformation assessment used by Holstein breed societies. Trained breed society classifiers score the use of legs and feet, and commonly judge both length and direction of the step on a scale of 1 to 9, where 1 is "poor" and 9 is "excellent" (ICAR, 2017). Tadich et al. (2010) reported that locomotion scoring may not be sensitive enough to detect slight gait alterations or newly developing claw pathologies. For early detection of lameness or claw disorders, more frequent scoring is necessary (Bicalho and Oikonomou, 2013).

Conformation Traits Describing Feet and Legs. The conformation of feet and legs is recorded routinely in linear type classification systems used by breeding societies. Studies have found that some conformation traits may be useful indicators of claw health (van der Linde et al., 2010; Fuerst-Waltl et al., 2015), whereas others (e.g., Koenig and Swalve, 2006; Häggman and Juga, 2013; Ødegård et al., 2014) found limited value in those traits. Most cows are scored only once in their life, so little information is available about changes in conformation over time or the relationship of those changes to claw health. Some measurements of claw characteristics, such as dorsal wall length, heel depth, and heel density, have been measured on bulls and their daughters for use in claw health predictions (Anacker and Gernard, 2006).

Automated Data Collection. Methods of objective analysis of cattle locomotion could provide useful information for early and more accurate detection of lameness and foot pathologies (Alsaaod et al., 2015; Beer et al., 2016; Nechanitzky et al., 2016). Increasing numbers of farms have sensors and automatic systems for milking and feeding, but little research is available on how well measurements from those systems can detect claw disorders. Activity sensors measure the movement, including the number and duration of lying bouts, which can be used to predict the risk of lameness (de Mol et al., 2013). Miguel-Pacheco et al. (2014) found that lameness resulted in a change of behavior in automatic milking systems, with lame cows moving less, spending less time feeding, and visiting the milking robot less frequently. Mangweth et al. (2012) showed that it is possible to predict lameness scores using accelerometers to measure motion. Cows with sole ulcers or white line disease were detected with a sensitivity of 97% and specificity of 80% using a 4-scale weighing system (Nechanitzky et al., 2016). Beer et al. (2016) found that models based on only two 3-dimensional accelerometer variables (walking speed and standing bouts) identified slightly lame cows with sensitivity and specificity both exceeding 90%.

Infrared thermography (**IRT**) has been used to detect inflammation or injury associated with conditions such as foot lesions (Alsaaod and Büscher, 2012; Stokes et al., 2012; Alsaaod et al., 2014; Wilhelm et al., 2015). For example, Oikonomou et al. (2014) reported a negative association between digital cushion thickness at the typical ulcer site of the lateral claw of the hind feet and the sole temperature as measured by IRT. Positive correlations have been found between sole temperature and locomotion score, suggesting that additional research should focus on clarifying relationships of temperature with claw health.

Milk composition can be predicted from mid-infrared (**MIR**) spectral data (De Marchi et al., 2014) and used for management purposes (Gengler et al., 2016). High postpartum blood BHB is associated with increased risk of lameness in dairy cows (Suthar et al., 2013), and Gengler et al. (2016) demonstrated that MIR can be used to predict milk BHB as well as other metabolites (e.g., acetone and citrate) linked to negative energy balance. Functional claw integrity has been linked to calcium (Tomlinson et al., 2004) and can be monitored using MIR (Soyeurt et al., 2009). There are ongoing efforts to transfer laboratory-based MIR to near-infrared based predictions (e.g., Coppa et al., 2014) that can be deployed as on-farm and in-line technologies in milking parlors or robots to obtain real-time measurements at every milking (e.g., Kaniyamattam and De Vries, 2014).

Recording Practices and Data Quality

Claw care practices differ widely across countries, as does the percentage of hoof trimmings carried out by professionals. In countries with routine genetic evaluations for claw health, data from claw trimmings are stored in a central database and used for herd management as well as genetic improvement. Successful genetic evaluation programs for claw and leg health require electronic systems for documenting and recording claw trimming data (Kofler et al., 2011, 2013; Miglior et al., 2014; Nielsen, 2014; Van Pelt, 2015). Kofler (2013) published an overview of available computerized database programs for this purpose. Data quality is influenced by several factors, including recorder bias (intra- and inter-observer variation) that can differ based on who made the recording (claw trimmer, veterinarian, farmer, or other), the claw trimmer's level of education

and focus or interest, time available, and cleaning routines. Manske (2002) found differences in the recording of claw lesions among claw trimmers, including underreporting of mild and common lesions.

Some countries with established infrastructures to collect and store data from claw trimming centrally for breeding purposes also organize regular training sessions or undertake other measures to ensure comparability of the results between the different claw trimmers (e.g., Charfeddine and Pérez-Cabal, 2014; Van Pelt, 2015). Detailed information on measures to improve quality of claw health data can be found in Charfeddine et al. (2016).

GENETIC EVALUATION

Data Validation

Data validation and editing criteria are needed to ensure reliable and accurate data. Charfeddine et al. (2016) suggested a 2-step for process for validating claw health data. The first step includes simple plausibility checks such as valid animal ID, valid codes for claw disorders, and birth date checks. The second step focuses on the correctness of the data by applying editing criteria at the trimmer, herd, animal, and record levels. Data from claw trimming are used for many purposes, such as herd management, benchmarking, and genetic evaluation, and editing criteria will vary accordingly. Here we discuss data validation issues related to genetic studies.

Many studies include claw health information only from professional or certified claw trimmers (van der Linde et al., 2010; Buch et al., 2011; van der Spek et al., 2013), whereas others include records from other trimmers and farmers (Ødegård et al., 2013). Pérez-Cabal and Charfeddine (2015) restricted the data to trimmers with at least 2,000 records, and they omitted data at the start of recording for each trimmer (training period). Data validation could also include checking whether the trimmer's use of claw disorder diagnoses are reasonable and comparable with those of others. Using data only from professional trimmers may ensure more consistent recording. If the number of records is limited, less-strict editing may be preferred. Some of these effects can be accounted for by including trimmer effects in the model (Ødegård et al., 2013).

Herd-level validation is needed to determine if claw trimming records are reliable for a certain herd and time period. Johansson et al. (2011) excluded herd-year-season classes with no claw disorder records (all normal claws) as uninformative. Ødegård et al. (2013) excluded herds reporting less than 10% or fewer than 10 normal (healthy) claw records. Van der Waaij et al. (2005) included only herds with at least 75% of cows trimmed, whereas van der Linde et al. (2010) required that at least 50% of herd mates and at least 20 cows per herd were trimmed. Pérez-Cabal and Charfeddine (2015) included only herds with at least 50% of the cows trimmed during a full year, and excluded herds with less than 10 records in total, as well as herds with known high prevalence rate (due to specific management procedures). To keep only routine trimmings, Häggman and Juga (2013) and Malchiodi et al. (2017) omitted herd trimming dates with fewer than 5 trimmed cows; Pérez-Cabal and Charfeddine (2015) required at least 10 records per herd and 5 trimmed cows per herd visit; and van der Spek et al. (2015b) required at least 2 trimmed cows per herd visit. Herd-level edits could also include edits to ensure continuity of data flow over time.

At the animal and record levels, editing criteria related to age, days in milk, parity, and minimum opportunity period to express the disorder are common. Buch et al. (2011) included cows with age at first calving from 20 to 38 mo, Häggman and Juga (2013) deleted records before age 21 mo and after 165 mo, van der Linde et al. (2010) included parities 1 through 5 and required a minimum age of 640 d at first calving. To ensure a minimum number of days at risk, Koenig et al. (2005) excluded cows present in the herd <8 wk. To avoid left-censoring, it is common to include only cows that had been in the herd since (first) calving. Van der Linde et al. (2010) included records from rear legs only because, for two-thirds of the cows, only rear legs were trimmed. Van der Spek et al. (2013) also included information only from hind legs.

Different strategies have been chosen for data editing and validation at the trimmer, herd, animal, and record levels, which illustrates the need to adapt validation criteria according to herd size, data structure, management practices, and recording systems for claw health data, which vary among countries. Experiences and best practices from several different countries have been reported by Charfeddine et al. (2016). Recommendations are under preparation and will be published in the forthcoming ICAR guidelines for claw health (http://www.icar.org/).

Trait Definition

Claw disorders are usually defined as binary traits, based on whether or not the claw disorder was present (recorded) at least once during a defined time period, which varies among studies. Van der Linde et al. (2010) included records from 0 to 305 d after calving; Johansson et al. (2011) used 0 to 430 d after calving; Ødegård et al. (2013) included records from calving to 365 d

later or to next calving; and Buch et al. (2011) included the first trimming after calving restricted to events within 1 yr of calving.

Binary coding can be based on single disorders (i.e., each diagnosis is one trait) or groups or composite traits (Buch et al., 2011; Gernand et al., 2012; Chapinal et al., 2013; Dhakal et al., 2015). In most cases, traits are grouped according to etiology and pathogenesis. Infectious lesions mostly affect the skin and are related to environmental hygiene [e.g., digital dermatitis (**DD**) and interdigital dermatitis (**ID**), foot rot/interdigital phlegmon (**IP**), and heel horn erosion (**HHE**)]. Noninfectious lesions affect the claw horn [e.g., sole ulcer (**SU**), toe ulcer (**TU**), sole hemorrhage (**SH**), and white line disease (**WL**)], which are caused primarily by a combination of metabolic and mechanical factors (Greenough, 2008; Rouha-Mülleder et al., 2009; Solano et al., 2015).

Alternatively, claw disorders can be defined as ordered categorical traits by counting the number of cases during a set time period to account for multiple occurrences. This requires clear definitions of new cases, and the minimum number of days between occurrences used to tell cases apart may vary between disorders. Recording at the level of individual legs may be needed to accurately define new cases. Pérez-Cabal and Charfeddine (2015) included only the first record when there was more than one record of the same disorder, in the same cow, in the same claw within 15 d. Van der Linde et al. (2010) and Häggman and Juga (2013) considered records within 7 d of each other as the same case.

Chapinal et al. (2013) found a genetic correlation of 0.55 between "any hoof lesion" in front legs and "any hoof lesion" in rear legs. This suggests that claw disorders in front and rear legs are not exactly the same genetically, so information on individual legs, if available, could be useful in genetic evaluations.

Parities can be treated as repeated records or as multiple traits. High genetic correlations justify treating claw disorders as the same trait across parities. Van der Linde et al. (2010) estimated genetic correlations between claw health traits in first and later parities, which ranged from 0.72 to 1. Van der Spek et al. (2015a) estimated genetic correlation (standard error in parentheses) between claw disorders in first and later parities of 0.29 (0.31) for SH and 0.66 (0.15) for dermatitis, while the correlations for double sole, interdigital hyperplasia (**IH**), WL, and SU were not different from 1.

It is also unclear whether the same disease occurring at different stages of lactation should be assumed to be the same or different traits. Van der Spek et al. (2015a) estimated genetic correlations (SE) between claw disorders in early and late lactation of 0.69 (0.13) for dermatitis and 0.53 (0.20) for WL, whereas correlations for double sole, IH, SH, and SU did not differ from 1. The latter was in agreement with Gernand et al. (2013), who found genetic correlations close to 1 among test days from 50 to 305 d in lactation. These results suggest that claw disorders at different stages of lactation may be treated as the same trait.

The identification of cows free of claw disorders (i.e., healthy herdmates) may be challenging because herd trimming strategies and recording practices vary across farms and countries. The status of all cows, including those with normal or healthy claws, should ideally be recorded at claw trimming. In this case, the best solution is to include only those cows with information from claw trimming in the analyses. Another approach is to include all cows present in the herd on trimming day in the analysis and assume that all cows with possible claw problems were selected for trimming (i.e., those not trimmed can be assumed healthy). However, assuming that all untrimmed cows were healthy underestimates the incidence of claw disorders (mild cases could be present, but not detected), whereas including only trimmed cows may overestimate the incidence (untrimmed cows are more likely to be unaffected). The inclusion or omission of untrimmed cows did not affect heritabilities of claw disorders on the underlying scale (van der Spek et al., 2013; Malchiodi et al., 2017).

Croué et al. (2017) analyzed 3 different scenarios (1 = only trimmed cows, 2 = trimmed cows and untrimmed contempories at the farms considered healthy, and 3 = including a 0/1 trimming status trait). The results showed a bias if untrimmed cows were considered healthy with a negligible effect on heritability but an important effect on the genetic correlations between infectious and noninfectious traits. Van der Spek et al. (2013) showed also minor changes in heritability if untrimmed cows were assumed healthy. The variable trimming status indicates a genetic background for this trait. Cows that are more likely to be trimmed are also more likely to be affected by a claw disorder.

Models

Claw disorders are usually defined as binary traits and analyzed by linear animal models (e.g., van der Linde et al., 2010; Ødegård et al., 2015). This approach ignores multiple incidences of a disease throughout a cow's lactation. Alternatively, an ordinal threshold model may be applied to analyze the number of cases (e.g., Chang et al., 2006; Heringstad et al., 2006), or a longitudinal threshold model can be used to include multiple cases and account for changes over time (Heringstad et al., 2003). Censoring is a challenge, especially if later lactations are included. Relevant models

that allow for censoring have been applied to analyses of mastitis data, including survival models (Carlén et al., 2006) and ordinal censored threshold models (Heringstad et al., 2006). Structural equation models (Gianola and Sorensen, 2004; Wu et al., 2010) can be used to reveal possible causal relationships between phenotypes; that is, whether or not the occurrence of one claw disorder increases susceptibility to other problems. Koenig et al. (2008) applied recursive models to infer relationships between claw disorders and milk yield in Holstein cows. Although more advanced models may be advantageous because they use more of the available information, linear models may often be the model of choice for routine genetic evaluation because they are fast, easy to implement, and provide very similar results to more advanced models in most cases. Malchiodi et al. (2017) analyzed claw heath data using either a threshold or a linear model, and the resulting EBV were highly correlated. Pérez-Cabal and Charfeddine (2015) found that linear models gave smaller mean squared errors and tend to predict affected cows better than threshold models

Effects to consider in the model, in addition to standard effects such as age, contemporary group, and lactation number, include effects of time (lactation stage) at trimming and trimmer. The latter requires that a unique ID be recorded for each trimmer. Lactation stage at trimming can be the number of days or weeks between calving and trimming. The timing of the occurrence of disease is probably less accurate when based on claw trimming rather than on veterinary treatment data. Depending on the herd's claw-trimming routine, some time may elapse between the occurrence of a problem and the trimming day, and milder cases may go unnoticed until trimming.

Genetic Parameters

Heritability of Claw Disorders Based on Data from Claw Trimming. Table 2 summarizes heritability estimates for the most commonly analyzed claw disorders based on data from claw trimming. Heritability estimates from linear models were generally low, ranging from 0.01 to 0.14. Heritabilities of liability to claw disorders from threshold models were higher, ranging from 0.06 to 0.39. Some studies combined DD and ID into one trait, whereas other studies estimated heritabilities individually for DD and ID. Interdigital hyperplasia had the highest heritability in many studies, including both linear and threshold model estimates. Although some studies included relatively few records and the estimated genetic parameters had large standard errors, there was generally consistency among studies.

Heritability estimates for less-common claw disorders (fewer estimates were available) are presented in Table 3. The heritability estimates for these traits ranged from 0.06 to 0.34 using threshold models, and from 0.01 to 0.20 using linear models. Wall ulcer and double sole had the lowest heritability, and interdigital growth had the highest heritability, among these traits.

Schöpke et al. (2015) investigated the genetic background of DD using improved definitions of clinical status, accounting for the dynamics of the disease. They demonstrated that more accurate recording yielded higher heritability. Estimates of heritability (SE) for DD in their study ranged between 0.19 (0.11) and 0.52 (0.17), which is much higher than the value in Table 2. However, for routine genetic evaluations, large-scale recording is needed and it may be challenging to obtain this detailed recording routinely.

These results show that there is sufficient genetic variability for traits based on claw trimming data to support genetic evaluations for improved claw health. The results from routine genetic evaluation (e.g., from the Netherlands and the Nordic countries) show that although heritabilities for claw disorder are in the range between 0.01 and 0.20, breeding values with high reliabilities can be produced using data currently available. Genetic selection is an important component of a long-term program to improve foot health in dairy cattle populations, but improvements in management also should be considered for the greatest benefit to cows and farmers.

Heritability of Groups of Traits and Composite Traits. Some claw disorders have low frequencies and similar biological causes, so grouping them into composite traits to increase the number of records available for evaluation is an option. Heritability estimates of claw health defined as grouped or composite trait are given in Table 4. Linear model estimates of heritability of overall claw health (any lesion) ranged from 0.05 to 0.07, whereas estimates from threshold models ranged from 0.07 to 0.13. Heritability estimates from linear models were, as expected, higher for group traits (Table 4) than for specific disorders (Table 2) due to higher frequencies.

Although the definition of groups and composite traits varied between studies, categories were, in most cases, defined according to etiology. Buch et al. (2011) suggested that hygiene-related (dermatitis and HHE) and feed-related (SH and SU) claw disorders be grouped together, as genetic correlations were high within groups and low between groups. Ødegård et al. (2013) grouped claw disorders as laminitis-related (SU, WL, SH) and infectious (dermatitis, HHE, IP) claw disorders. Johansson et al. (2011) suggested grouping into infection-related (dermatitis, HHE, and skin prolif-

Table 2. Heritability estimates (standard error or standard deviation) of the claw disorders digital or interdigital dermatitis (DD/ID), heel horn erosion (HHE), interdigital hyperplasia (IH), sole hemorrhage (SH), sole ulcer (SU), and white line disease (WL)

Reference	Model[1]	Breed[2]	N[3]		DD/ID	HHE	IH	SH	SU	WL
Buch et al. (2011)	LM	SRB	314		0.03 (0.006)	0.03 (0.005)	—	0.05 (0.007)	0.03 (0.006)	—
Johansson et al. (2011)	LM	HF	297		0.04	0.04	—	0.04	0.04	0.01
		RDC	179		0.04	0.07	—	0.05	0.02	0.01
Malchiodi et al. (2017)	LM	HF	53	DD	0.07 (0.007)	—	0.04	0.02	0.04	0.02
				ID	0.01 (0.003)		(0.005)	(0.003)	(0.006)	(0.004)
	TM			DD	0.16 (0.02)	—	0.19	0.09	0.14	0.06
				ID	0.13 (0.03)		(0.02)	(0.02)	(0.02)	(0.01)
van der Linde et al. (2010)	LM	HF	62	DD	0.09	—	0.13	0.06	0.12	0.03
				ID	0.11	—	—	—	—	—
van der Spek et al. (2013)	LM	HF	20		0.04 (0.01)	—	0.14 (0.01)	0.02 (0.01)	0.03 (0.01)	0.04 (0.01)
van der Spek et al. (2015b)	LM	MB	5		0.01 (0.01)	—	0.05 (0.02)	0.02 (0.01)	0.03 (0.02)	0.09 (0.02)
van der Waaij et al. (2005)	LM	HF	22	DD	0.10 (0.02)	—	0.10 (0.02)	0.08 (0.02)	0.01 (0.01)	0.02 (0.01)
				ID	0.05 (0.01)	—	—	—	—	—
Häggman et al. (2013)	Log	FA	52	DD	0.10 (0.06)	0.01 (0.004)	—	0.03 (0.01)	0.15 (0.03)	0.11 (0.01)
				ID	0.11 (0.03)	—	—	—	—	—
Häggman and Juga (2013)	Log	HF	25	DD	0.13 (0.05)	0.02 (0.01)	—	0.02 (0.01)	0.08 (0.03)	0.04 (0.02)
				ID	0.03 (0.04)	—	—	—	—	—
Koenig et al. (2005)	Log	HF	5	DD	0.07 (0.009)	—	0.11 (0.02)	—	0.09 (0.006)	—
Koenig et al. (2008)	LM	HF	5		0.07 (0.05)	—	0.11 (0.05)	—	0.10 (0.07)	—
	TM				0.09 (0.06)	—	0.19 (0.05)	—	0.14 (0.07)	—
	SEqM				0.05 (0.05)	—	0.16 (0.06)	—	0.13 (0.06)	—
Gernand et al. (2012)	TM	HF	19	DD	0.09 (0.02)	—	0.22 (0.04)	—	0.07 (0.02)	0.09 (0.02)
Ødegård et al. (2013)	TM	NR	123		0.20 (0.03)	0.09 (0.02)	—	0.07 (0.01)	0.18 (0.02)	0.06 (0.02)
Pérez-Cabal and Charfeddine (2015)	LM	HF	35		0.02 (0.004)	—	0.01 (0.002)	—	0.04 (0.004)	0.02 (0.003)
	TM				0.14 (0.03)	—	0.39 (0.07)	—	0.15 (0.02)	0.09 (0.02)
Swalve et al. (2008)	LM	HF	17	DD	0.08 (0.01)	—	—	—	0.07 (0.01)	0.05 (0.01)
				ID	0.09 (0.01)	—	—	—	—	—
	TM			DD	0.13 (0.02)	—	—	—	0.17 (0.02)	0.10 (0.02)
				ID	0.20 (0.02)	—	—	—	—	—
Range	LM	All			0.01–0.11	0.03–0.07	0.01–0.14	0.02–0.08	0.01–0.12	0.01–0.09
Range	TM	All			0.09–0.20	0.09	0.19–0.39	0.07–0.09	0.07–0.18	0.06–0.10

[1]LM = linear model, TM = threshold model, log = logistic model, SEqM = structural equation model.

[2]HF = Holstein, MB = Montbéliarde, NR = Norwegian Red, RDC = Red Dairy Cattle, SRB = Swedish Red, FA = Finnish Ayrshire.

[3]Number of cows with records given in thousands.

Table 3. Heritability (h^2) estimates, with standard error (SE) or standard deviation (SD), of claw disorder

Claw health trait	Model[1]	Heritability	SE or SD	Breed[2]	Reference
Corkscrew claw	Log	0.09	0.03	HF	Häggman and Juga, 2013
		0.20	0.02	FA	Häggman et al., 2013
	TM	0.23	0.02	NR	Ødegård et al., 2013
	LM	0.02		HF	Johansson et al., 2011
		0.03		RDC	
Double sole	LM	0.02	0.01	HF	Van der Spek et al., 2013
Interdigital phlegmon	TM	0.08	0.02	HF	Gernand et al., 2013
		0.06	0.02	HF	Pérez-Cabal and Charfeddine, 2015
		0.14	0.06	NR	Ødegård et al., 2013
Interdigital growth	TM	0.34	0.03	HF	Swalve et al., 2008
	LM	0.20	0.01		
Laminitis	TM	0.06	0.01	HF	Gernand et al., 2013
		0.20	0.02	HF	Swalve et al., 2008
	LM	0.13	0.01	HF	Swalve et al., 2008
Chronic laminitis	Log	0.13	0.03	FA	Häggman et al., 2013
		0.02	0.04	HF	Häggman and Juga, 2013
	TM	0.07	0.02	HF	Pérez-Cabal and Charfeddine, 2015
	LM	0.01	0.01	HF	van de Waaij et al., 2005
Rotation	TM	0.20	0.02	HF	Swalve et al., 2008
	LM	0.14	0.01		
Skin proliferation	LM	0.02		HF	Johansson et al., 2011
		0.03		RDC	
Thick hocks	TM	0.15	0.03	HF	Swalve et al., 2008
	LM	0.06	0.01		
Toe ulcer	TM	0.06	0.02	HF	Malchiodi et al., 2017
	LM	0.01	0.002		
Wall disorders	Log	0.10	0.001	HF	Koenig et al., 2005
	LM	0.10	0.05	HF	Koenig et al., 2008
	TM	0.13	0.05		
	SEqM	0.13	0.06		
Wall ulcer	LM	0.01		HF	van der Linde et al., 2010

[1]LM = linear model, TM = threshold model, log = logistic model, SEqM = structural equation model.
[2]HF = Holstein, FA = Finnish Ayrshire, NR = Norwegian Red, RDC = Red Dairy Cattle.

Table 4. Heritability (h^2) estimates, with standard error (SE) or standard deviation (SD), of claw health defined as groups or composite traits

Claw health trait	h^2	SE or SD	Frequency, %	Breed[1]	N[2]	Model[3]	Reference
Any lesion	0.075	0.010	38.3	HF	27	LM	Chapinal et al. (2013)
Horn lesion	0.015	0.004	7.0				
Front lesion	0.015	0.004	7.0				
Rear lesion	0.079	0.010	34.5				
Infectious lesion	0.092	0.011	—				
Any lesion	0.07	0.007	37.8	HF	53	LM	Malchiodi et al. (2017)
	0.12	0.01				TM	
Combined	0.07	—	69	HF	62	LM	van der Linde et al. (2010)
Trimming status	0.02	0.01	43.6–57.7	HF	24	LM	van der Spek et al. (2015a)
Trimming status	0.06	0.02	50	MB	5	LM	van der Spek et al. (2015a)
Combined	0.05	0.01	54.8	HF	20	LM	van der Spek et al. (2013)
Overall	0.08	0.01	24.7	FA	52	Log	Häggman and Juga (2013)
Infectious	0.11	0.05	—	HF	23	TM	Dhakal et al. (2015)
Noninfectious	0.08	0.05	—				
Claw disorders	0.07	0.01	22.6	HF	19	TM	Gernand et al. (2012)
Laminates related	0.10	0.01	6.8	NR	123	TM	Ødegård et al. (2013)
Infectious	0.10	0.02	5.7				
All	0.13	0.01	21.3				
Overall claw disorder	0.05	0.004	21.4	HF	35	LM	Pérez-Cabal and Charfeddine (2015)
	0.11	0.007	21.4			TM	

[1]FA = Finnish Ayshire, HF = Holstein, MB = Montbéliarde, NR = Norwegian Red.
[2]Number of cows with records given in thousands.
[3]LM = linear model, TM = threshold model.

Table 5. Estimates of genetic correlation (standard error or standard deviation) among the claw disorders digital or interdigital dermatitis (DD/ID), heel horn erosion (HHE), interdigital hyperplasia (IH), sole hemorrhage (SH), sole ulcer (SU), and white line disease (WL)

Trait	HHE	IH	SH	SU	WL	Reference
DD/ID	0.87 (0.05)		−0.04 (0.11)	−0.19 (0.12)		Buch et al. (2011)
		0.11 (0.02)				Gernand et al. (2012)
	0.58 to 0.77					Johansson et al. (2011)
		0.39 (0.10)		0.56 (0.07)		Koenig et al. (2005)
		0.57 (0.08)	0.04 (0.11)	0.07 (0.09)	−0.30 (0.10)	Malchiodi et al. (2017)
	0.65 (0.09)			0.19 (0.11)	0.04 (0.14)	Ødegård et al. (2013)
		0.10 (0.02)		−0.08 (0.06)	−0.30 (0.04)	Pérez-Cabal and Charfeddine (2015)
				0.12 to 0.42	−0.05 to 0.17	Swalve et al. (2008)
		0.26 to 0.65	−0.14 to 0.12	−0.12 to 0.15	−0.33 to 0.02	van der Linde et al. (2010)
		0.66 (0.08)	−0.15 (0.14)	0.07 (0.16	0.07 (0.14)	van der Spek et al. (2013)
		0.47 (0.12)	−0.12 (0.16)	−0.18 (0.25)	0.08 (0.20)	van der Waaij et al. (2005)
HHE			0.23 (0.11)	0.13 (0.12)		Buch et al. (2011)
			−0.07 (0.20)	−0.05 (0.21)	−0.36 (0.12)	Häggman and Juga (2013)
				0.42 (0.10)	0.22 (0.14)	Ødegård et al. (2013)
IH				0.50 (0.11)		Koenig et al. (2005)
			0.04 (0.12)	0.20 (0.10)	−0.15 (0.12)	Malchiodi et al. (2017)
				0.00 (0.02)	−0.23 (0.11)	Pérez-Cabal and Charfeddine (2015)
			−0.11 to 0.18	−0.08 to 0.07	−0.35 to 0.02	van der Linde et al. (2010)
			−0.40 (0.13)	0.04 (0.13)	0.22 (0.11)	van der Spek et al. (2013)
			0.13 (0.16)	0.18 (0.26)	0.34 (0.18)	van der Waaij et al. (2005)
SH				0.73 (0.07)		Buch et al. (2011)
				0.38 (0.15)	0.39 (0.12)	Häggman and Juga (2013)
				0.68 to 0.74	0.62 to 0.73	Johansson et al. (2011)
				0.80 (0.08)	0.52 (0.13)	Malchiodi et al. (2017)
				0.58 to 0.79	0.06 to 0.51	van der Linde et al. (2010)
				0.90 (0.10)	0.10 (0.17)	van der Spek et al. (2013)
				0.81 (0.26)	0.30 (0.21)	van der Waaij et al. (2005)
SU					0.31 (0.13)	Häggman and Juga (2013)
					0.74 to 0.78	Johansson et al. (2011)
					0.75 (0.08)	Malchiodi et al. (2017)
					0.79 (0.08)	Ødegård et al. (2013)
					0.98 (0.05)	Pérez-Cabal and Charfeddine (2015)
					0.01	Swalve et al. (2008)
					0.41 to 0.60	van der Linde et al. (2010)
					0.49 (0.13)	van der Spek et al. (2013)
					0.95 (0.15)	van der Waaij et al. (2005)

eration), feed-related (SH, SU, WL), and malformation (CC) traits. Chapinal et al. (2013) grouped claw disorders into infectious, horn, and other lesions; they also distinguished between front and rear lesions. Dhakal et al. (2015) grouped traits as infectious and noninfectious. Groups of infectious claw disorders tended to show higher heritability than noninfectious (Table 4).

Some traits do not fit into well-defined groups, but may provide useful information about claw health. Chapinal et al. (2013) estimated higher heritability for rear leg than for front leg claw disorders, which may be due to higher frequency. The heritability of trimming status, whether the cow was trimmed (score 1) or not (score 0) (van der Spek et al. (2015a), was 0.02 to 0.06.

Genetic Correlations Among Claw Disorders. Estimated genetic correlations among claw disorders are given in Table 5 and the range of estimates is summarized in Table 6. Genetic correlations varied from −0.40 to 0.98 (Table 5). The strongest genetic correlation were found among SH, SU, and WL (noninfectious), and between dermatitis (DD/ID) and HHE (infectious). Genetic correlations between DD/ID, HHE, or IH on the one hand and SH, SU, or WL on the other were low for most cases. For example, Buch et al. (2011) estimated a genetic correlation of 0.87 between DE and HHE, whereas genetic correlations of SU with DE (−0.19) and HHE (0.13) were not different from zero. Although some studies were based on relatively few records and estimates had large standard errors, there was generally good consistency among most studies, with some exceptions (Table 5).

Chapinal et al. (2013) reported strong positive genetic correlations between front and rear infectious lesions (0.77) and front and rear horn lesions (0.61), whereas the genetic correlation between infectious and horn lesions was close to zero (0.08). Positive and strong

Table 6. Range of genetic correlation estimates[1] among digital or interdigital dermatitis (DD/ID), heel horn erosion (HHE), interdigital hyperplasia (IH), sole hemorrhage (SH), sole ulcer (SU), and white line disease (WL)

Item	HHE	IH	SH	SU	WL
DD/ID	0.58–0.87	0.10–0.66	−0.15–0.12	−0.19–0.56	−0.33–0.08
HHE			−0.07–0.23	−0.05–0.50	0.22–0.36
IH			−0.40–0.13	−0.08–0.50	
SH				0.38–0.90	0.10–0.62
SU					0.01–0.98

[1]Buch et al. (2011), Gernand et al. (2012), Häggman and Juga (2013), Johansson et al. (2011), Koenig et al. (2005), Ødegård et al. (2013), Pérez-Cabal and Charfeddine (2015), Swalve et al. (2008), van der Linde et al. (2010), Van der Spek et al. (2013), Van der Waaij et al. (2005).

genetic correlations are favorable in the sense that selection for one trait will result in an indirect selection response for others. Strong genetic correlations support grouping as a strategy for trait definition for genetic evaluation, whereas lack of genetic correlation implies the need for multiple traits.

Heritability of Other Measures of Claw Health. In addition to the information from claw trimming, other direct and indirect traits are used to measure claw health. For example, data from locomotion and lameness scoring are examples of indicator traits, whereas veterinary treatment data are direct measures of claw health. Table 7 gives an overview of the heritabilities of such traits. Heritability estimates of lameness observations were low (0.02–0.04). If lameness was recorded according to Sprecher et al. (1997) with repeated lameness scoring, heritabilities ranged between 0.07 and 0.10 for linear models. Heritability estimates for locomotion score were between 0.09 and 0.14 (Table 7). Negative correlations between locomotion and claw health are favorable, with high locomotion score being associated with better claw health. Correlations of claw health with lameness scores are expected to be positive. Several studies have concluded that lameness and locomotion score may be useful indicator traits for claw health (e.g., Laursen et al., 2009; Weber et al., 2013; Egger-Danner et al., 2017). Veterinary treatment data tend to include only very severe cases of claw disorders.

Table 7. Heritability (h^2) estimates (standard error or standard deviation) of claw health traits other than from claw trimming

Trait	Breed[1]	h^2 (SE/SD)	Model[2]	Reference	Genetic correlation with claw health[3]
Lameness obs.	HF	0.04 (0.005)	LM	Berry et al. (2010)	
(0,1)	HF	0.02 (0.004)	LM	Koeck et al. (2014)	
	HF	0.02 (0.005)	TM	Parker Gaddis et al. (2014)	
Lameness[4]	HF	0.08	LM	Weber et al. (2013)[5]	0.94 to 0.95
		0.15	TM		0.60 to 0.72
	FL	0.07 (0.02)	LM	Koeck et al. (2016)[6]	
	FL	0.095 (0.092)	LM	Zottl et al. (2016)[7]	
Locomotion[8]	HF	0.09 (0.003)	LM	Laursen et al. (2009)	−0.60 to −0.11
	HF	0.11 (0.007)	LM	Onyiro et al. (2008)	
	HF	0.14 (0.02)	LM	van der Linde et al. (2010)	−0.58 to 0.06
	HF	0.10 (0.04)	LM	Van der Waaij et al. (2005)	−0.91 to 0.13
	HF	0.029 (0.015)	LM	Chapinal et al. (2013)	−0.46 to −0.35
Veterinarian diagnoses (0,1)	FL	0.02 (0.003)	LM	Fuerst-Waltl et al. (2012)	
	HF	0.01 (0.001)	LM	Laursen et al. (2009)	
Claw measurements	HF	0.02–0.38	LM	Anacker and Gernard (2006)	

[1]FL = Fleckvieh, HF = Holstein.

[2]LM = linear model, TM = threshold model.

[3]Negative correlations between claw health and locomotion are favorable, indicating that better locomotion is correlated with better claw health.

[4]Lameness scoring according to Sprecher et al. (1997) with 5 possible scores (1 = normal gait, 2 = mildly lame, 3 = moderately lame, 4 = lame, and 5 = severely lame).

[5]According to Sprecher et al. (1997), but treated as 0/1 (1 = lameness score ≥3).

[6]According to Sprecher et al. (1997) repeated.

[7]According to Sprecher et al. (1997), but lactation lameness score taking frequency of different severity cases into account.

[8]Locomotion scored from 1 (lame) to 9 (no abduction).

The incidence is typically low, as are the heritability estimates from linear models, which range from 0.01 to 0.02 (Table 7).

Anacker and Gernard (2006) estimated heritabilities between 0.02 and 0.38 for claw measurements based on station data from young Holstein bulls. The highest heritabilities were derived for dorsal wall length (0.17–0.28), heel depth (0.19–0.20), and diverging claws (0.27–0.38). Based on traits measured on daughters, heel density had one of the highest heritabilities (0.25–0.37) among claw measurements. Direct measures of claw health have rather high heritabilities, but results demonstrate that availability of data may limit their use (Koenig and Swalve, 2006).

Genetic Correlations Between Claw Disorders and Feet and Leg Conformation Traits. Several studies have estimated genetic correlations between claw health and feet and leg conformation traits; estimates vary between breeds and populations. Ødegård et al. (2014) estimated low to moderate genetic correlations between feet and leg conformation traits and both infectious- and laminitis-related claw disorders. Rear leg rear view (**RLRV**) had a negative genetic correlation with infectious-related claw disorders (−0.20) and positive with laminitis-related claw disorders (0.26). Ødegård et al. (2014) concluded that selection for feet and leg conformation would not be an efficient approach for genetic improvement of claw health in Norwegian Red. Häggman and Juga (2013) estimated genetic correlations between claw disorders and feet and leg confirmation traits in Finnish Holstein ranging from −0.51 to 0.45. However, most of the correlations were low, many were not different from zero, and indirect selection for claw health using feet and leg conformation would, therefore, not be efficient. This is in agreement with Uggla et al. (2008), who 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. Also, Swalve et al. (2008) and Dhakal et al. (2015) found weak genetic relationships between claw health and conformation traits. Chapinal et al. (2013) estimated low to moderate genetic correlations between claw lesions and conformation traits, ranging from −0.39 (0.20) for RLRV to 0.26 (0.16) for rear leg side view (**RLSV**). van der Linde et al. (2010) estimated genetic correlations between claw health and conformation traits ranging from −0.58 to 0.41. They concluded that feet and leg conformation traits were useful indicator traits for claw health but could not replace direct claw health information. Onyiro et al. (2008) estimated moderate to high genetic correlations of DD with bone quality, locomotion, and leg and feet composite, respectively, but the genetic correlations of DD with RLSV and foot angle were not different from zero. Laursen et al. (2009) studied associations between overall claw health, based on veterinary records, and feet and leg conformation traits. The estimated genetic correlation (SE) was 0.21 (0.10) with RLRV, and not different from zero with any of the other feet and leg conformation traits (RLSV, foot angle, hock quality, or bone structure).

The size and direction of correlations may vary between breeds and populations due to differences in genetic level or population mean of conformation traits. Many feet and leg composites are traits with an intermediate optimum, and a crucial question is whether the association between claw health and feet and leg conformation traits can be assumed to be linear. Pérez-Cabal and Charfeddine (2016) found that cows with intermediate scores for feet and leg type traits had a lower incidence of claw disorders. Possible nonlinear relationships are not taken into account in estimation of genetic correlations, and may explain varying results. For example, if both too-steep and too-loose foot angles are bad for claw health, linear scores analyzed with a linear model may find a correlation close to zero. Selection for claw health using feet and legs type traits only would not be efficient but the inclusion of some feet and leg conformation traits (e.g., RLRV) as auxiliary traits in genetic evaluation for the claw health enables more accurate selection and can increase genetic gain for claw and leg health.

Genetic Correlation Between Claw Disorders and Other Traits. Buch et al. (2011) estimated genetic correlations between 4 claw disorders (DD, HHE, SH, and SU) and protein yield (**PY**), udder health, and female fertility in Swedish Red cows. Genetic correlations were significantly different from zero between PY and HHE, SH, and SU (0.24, 0.11, and 0.20, respectively), between clinical mastitis and SH (0.35) and SU (0.32), between number of inseminations and DD/ID and HH (0.22 and 0.32), and between interval from calving to first insemination and SU (0.33). Koenig et al. (2005) estimated unfavorable genetic correlations between test-day milk yield in early lactation and DD (0.24), SU (0.06), wall disorder (0.27), and IH (0.34), respectively, whereas genetic correlations between SCS and individual claw disorders ranged from 0.15 to 0.24. Gernand et al. (2012) estimated genetic correlations close to zero between claw disorders (DD and IH) and test-day milk production traits, and a genetic correlation of 0.23 (0.12) between lameness and SCS. The estimated genetic correlations between claw disorders and other diseases, clinical mastitis, endometritis, and ovarian cysts were all close to zero. Dhakal et al. (2015)

reported close-to-zero genetic correlations between claw lesion traits and both productive life and net merit. Pryce et al. (1997) estimated a genetic correlation of 0.29 between 305-d milk yield and lameness. Correlations between breeding values for claw health and other breeding values for other traits in the TMI in Simmental (Egger-Danner, 2015) confirm this antagonistic relationship.

There was a lack of consistency in genetic correlations of claw disorders with other traits. The limited number of studies, which mainly consisted of small data sets, produced estimates with large standard errors. However, precise estimates of genetic and phenotypic correlations are needed to construct TMI. Consequently, there is a need to re-estimate these genetic correlations in large data sets.

Complex Associations Between Milk Production and Claw Health. The relationship of lameness and claw health with milk production and composition is complex, and it is difficult to distinguish causes from effects. For example, locomotive problems (and health problems in general) appear to occur more frequently for cows with high milk yield within the first third of lactation (Collard et al., 2000; Green et al., 2014). On the other hand, locomotive problems result in reduced reproductive efficiency, increased culling rates, and decreased production (e.g., Green et al., 2002; Bicalho and Oikonomou, 2013; Burgstaller et al., 2016). Hamann and Krömker (1997) found that changes in milk yield often reflect clinical problems, and that changes in milk composition are linked to subclinical challenges to claw health. There are several indicators that fine milk composition may contain even more relevant biomarkers for claw health. Several studies (e.g., Collard et al., 2000) reported effects on locomotive problems, in particular laminitis-related claw lesions, of long and extreme periods of negative energy balance. Another study established that higher body condition scores were positively associated with digital cushion thickness (Bicalho et al., 2009). Negative energy balance is known to affect milk composition because mobilization of body fat also affects lipid metabolism into milk fatty acids (Gross et al., 2011). Iqbal et al. (2016) reported links between digital cushion fatty acid composition and lipid metabolism by analyzing gene network expression in Holstein cows fed a high-energy diet. A second process that links milk composition to claw health can be traced to the formation of keratin proteins in claw horn (Tomlinson et al., 2004). Nutritional and hormonal factors were reported to affect claw keratin formation, and several of these factors, especially minerals, are known to be partially related to their content in milk (e.g., Wegner and Stull, 1978). Koenig et al. (2008) reported genetic correlations between test-day milk production and individual claw disorders ranging from 0.17 to 0.44. They pointed out that these results suggest that breeding strategies focusing on increased milk yield will increase incidences of claw disorders as a correlated response. Landmann and Koenig (2008) predicted that a 1-unit increase in the incidence of any claw disorder results in a reduction of milk yield at the following test-day of up to 0.67 kg. However, Onyiro et al. (2008) found the opposite, reporting favorable associations of DD with milk and fat yields (−0.31 and −0.43, respectively) based on approximate genetic correlations calculated from sire EBV. Telezhenko and Johansson (2013) showed that for the Nordic Holstein population, increased production did not cause declining hoof health, despite the generally observed antagonistic relationship. They concluded that this could be explained by correlated positive effect of long-term improvement of the other health traits in Nordic Holsteins.

Predictions of Genomic Breeding Values for Claw Health

Dhakal et al. (2015) found that including genomic data in a single step evaluation increased reliabilities of breeding values for young bulls for infectious and non-infectious claw lesions by 0.24 and 0.18, respectively. Stoop et al. (2015) reported that genomic information added 32% reliability to the claw health index for Dutch Holstein young bulls without daughters. A Norwegian study reported little effect of including conformation traits in genomic evaluation of claw disorders for Norwegian Red (Ødegård et al., 2014). Including foot and leg conformation traits marginally improved predictive ability of genomic breeding values for CC but had no effect on predictive ability for infectious- and laminitis-related claw disorders. Results from a 10-fold cross validation showed that predictive ability for claw disorders in Norwegian Red, calculated as the correlation between genomic EBV (GEBV) and deregressed proofs, varied between 0.27 and 0.37 (Ødegård et al., 2014). Claw health traits based on data from routine claw trimming are challenging in genomic selection. These are new traits with limited historical data; thus, a smaller reference population is available to be used in genomic predictions compared with other traits. Genotyping cows in herds with reliable claw trimming records may be one strategy to enhance the accuracy of genomic predictions for these traits. The genetic evaluation for claw health in the Nordic countries includes cows in the reference population. In 2014, 10,000 cows were added to 7,800 bulls, which resulted in an increase in reliability for Norwegian Red cattle of 0.09 (NAV, 2017).

Table 8. Status[1] of genetic evaluations for claw health based on different data sources from selected countries

Country	Claw trimmer	Veterinarian diagnoses	Feet and legs conformation	Locomotion	Automation/ sensor
Australia	—	R&D	Eval	R&D	—
Austria (+ Germany): Fleckvieh, Brown Swiss	R&D	Pre	R&D	R&D	—
Canada	Eval	R&D	Eval	R&D	—
Denmark, Finland, Sweden	Eval	Eval	Eval	—	—
France	Pre	—	—	—	—
Germany (+ Austria): Holstein	Pre	Pre	—	—	R&D
The Netherlands	Eval	—	Eval	—	—
Norway	Eval	—	Eval	—	—
Spain	Pre	—	—	—	—

[1]R&D = research underway (research and development); Pre = preliminary evaluations (including project internal evaluations); Eval = official routine genetic evaluations.

QTL and Single Genes Affecting Claw Disorders

A few studies have detected QTL for claw health. Buitenhuis et al. (2007) detected 4 QTL associated with lameness. Swalve et al. (2014) identified a strong association between the *IQGAP1* gene and sole hemorrhage in German Holstein. Van der Spek et al. (2015a) detected some suggestive SNP associations for claw disorders and trimming status in French Holstein. In a small study based on 23 cases and 24 controls, Scholey et al. (2012) identified SNP on chromosomes 6 and 26 associated with DD. According to Scholey et al. (2013), DD skin has higher levels of gene expression for cytokines, which can suppress the immune response. Numerous keratin proteins are found to be downregulated in DD. Wu et al. (2016) identified 5 and 3 QTL regions, respectively, associated with feet and leg disorders in Danish Holstein and Nordic Red dairy cattle, but no QTL for this trait in Danish Jersey. They did not identify any QTL in common among the 3 breeds.

Swalve et al. (2013) revealed a strong association of one SNP on chromosome 21 with laminitis status and presumed that genetic selection for improved resistance for laminitis is possible. The authors also noted that a careful planning of a field study is required to obtain informative data. Molano et al. (2017) showed that for IH, DD, SU, and digital cushion thickness, significant and suggestive regions are found in the genome (e.g., IH on chromosomes 6 and 10, DD on chromosomes 11 and 27, SU on chromosome 12, and digital cushion thickness on chromosome 12).

International Developments in Genetic Evaluation

Implementation. Routine genetic evaluations of claw health based on data from regular claw trimming are established in some countries. The Netherlands has had genetic evaluation of claw health since April 2010 (Stoop et al., 2010). A claw health index based on data from claw trimmers and linear scoring has been published. Denmark, Finland, and Sweden have published breeding values for claw health since May 2011 as part of the Nordic Cattle Genetic Evaluation system, and a claw health index based on 7 traits and data from 3 lactations has been included in the Nordic Total Merit since August 2011 (Häggman and Juga, 2013). Norway has had routine genetic evaluation of claw health since 2014. The current evaluation includes 3 traits: CC, laminitis-related claw disorders, and infectious claw disorders, and the claw health index is included in TMI for Norwegian Red with 4% relative weight (Ødegård, 2015). In Canada, the Canadian Dairy Network has released genomic EBV for digital dermatitis in December 2017 using a single-step genomic evaluation (Jamrozik et al., 2017).

Research and Development. Several countries have ongoing projects to establish an infrastructure for routine electronic recording of claw trimming data and central data store with the aim of genetic evaluation (van der Linde et al., 2010; Charfeddine and Pérez-Cabal, 2014; Thomas and Leclerc, 2014; Miglior et al., 2016). An overview of the current status of claw health evaluations in selected countries is provided in Table 8.

SELECTION, MATING, AND GENETIC GAIN

Genetic gain is determined by the heritability of the trait, the selection intensity, the reliability of the breeding values, and the generation interval. Even if heritability is low, genetic differences do exist. Genetic studies on foot and claw disorders have shown the advantage of using direct claw health data when breeding for improved claw health (Koenig and Swalve, 2006; van der Linde et al., 2010), and heritability estimates were generally higher when data from claw trimming were used (Koenig et al., 2005; Boelling et al., 2008; Laursen et al., 2009; van der Linde et al., 2010). Boelling et al. (2008) suggested an index where the different relevant

data sources are combined. To achieve the highest genetic gain for claw health in routine applications, claw health indexes are used. Different data sources and traits are combined in the claw health index (van der Linde et al., 2010; Ødegård, 2015; NAV, 2017).

Koenig and Swalve (2006) analyzed the use of claw measurements, information from linear scoring, and claw trimming information. For the deterministic calculation, the trait laminitis was used with a frequency of 32%. Genetic gain was calculated for various combinations of traits and available information. If the number of daughters with laminitis information increased from 10 to 20 and 50 daughters per bull, the reliability of the breeding value increased respectively from 58 to 68 and 81%. If only laminitis information was used in the index and 50 daughters were available per bull, the frequency of laminitis could be reduced by up to 14%. Swalve et al. (2011) ranked the sires according to their EBV. Daughters of the top 10 sires according to EBV had prevalence of laminitis of 24.9%, whereas daughters of the lowest-ranked sires had a prevalence of 46.3%. Chawala et al. (2011) showed a significant effect of breed and heterosis on lameness incidence in New Zealand dairy cattle and suggested that these effects should be explored within a breeding program.

The use of claw measurements from bulls and information from linear scoring had a minor effect on the genetic gain. Van Pelt (2015) showed the effect of different information sources on the reliability of the claw health index. In the Netherlands, an average bull with 150 daughters has available linear scoring data from around 60% and claw trimming data from about 10% of the daughters. This results in a reliability for the claw health index of 59%. If no data from linear scoring were used, reliability would drop to 53%. If only data from linear scoring were used, reliability would drop to 24%. If the percentage of daughters with claw trimming data increased to 20%, reliability would increase to 69%. Boelling et al. (2008) analyzed the use of claw trimming data and locomotion and veterinary diagnoses in genetic evaluation and concluded that the use of additional information from indicator traits has the potential to increase reliability and is therefore recommended. All studies show that the most effective way to improve claw health genetically is to use the information from professional claw trimming. Additional information has the potential to increase reliability of the claw health index.

CONCLUSIONS

Claw disorders and lameness are the third most frequent and costly health issue in dairy cattle, and the associated discomfort and pain is an important welfare issue. Both management and genetic selection can be used to improve foot and claw health, but only genetic improvement provides permanent gains. Several different sources of claw health data are now available, with the information recorded by claw trimmers showing particular promise. Many observations are needed to produce genetic evaluations with high reliability due to the low heritability of most claw health traits, so the use of auxiliary traits that have positive genetic correlations with direct measures of claw health may be necessary. It is important to establish recording systems that use common trait definitions and recording standards to ensure that evaluations are based on high-quality data. Incentives, such as an easy-to-use electronic recording system, will help to motivate claw trimmers to participate in data collection efforts. Claw health traits must be added to total merit indices with sufficient economic weight to enable genetic improvement. Reference populations for genomic evaluation may need to include cows due a lack of bulls with high-reliability traditional evaluations.

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