J. Dairy Sci. 101:1–21
https://doi.org/10.3168/jds.2017-13531

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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Received July 20, 2017.
Accepted January 8, 2018.
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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 ≥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).