

Genetic evaluation of claw health – challenges and recommendations

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Routine recording of claw health status at claw trimming of dairy cattle have been established in several countries, providing a valuable database for genetic evaluation. In this review, issues related to genetic evaluation of claw health are examined; data sources, trait definitions, and data validation procedures are discussed; and a review of genetic parameters, possible indicator traits, and status of genetic and genomic evaluations for claw disorders are presented. Different sources of data and traits can be used to describe claw health, including veterinary diagnoses, data from lameness and locomotion scoring, activity-related information from sensors, and foot and leg conformation traits. The most reliable and comprehensive information is probably data from claw trimming. Heritability of the most commonly analyzed claw disorders based on data from routine claw trimming were in general low, with linear (threshold) model estimates ranging from 0.01 to 0.14 (0.06-0.39). 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 low in most cases. Although some studies were based on relatively few records and the estimated genetic parameters had large standard errors, results were generally consistent across studies. Routine genetic evaluations of direct claw health have been implemented in The Netherlands (2010), Denmark, Finland and Sweden (joint Nordic evaluation; 2011), and Norway (2014), and other countries plan to implement this in the near future.

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Various studies worldwide have shown the need to work on genetic improvement of claw health. The challenge is the availability of phenotypes. Within the Austrian project 'Efficient Cow' various different phenotypes related to claw health have been recorded in 167 farms and about 3.500 Fleckvieh (Simmental), 1.000 Brown Swiss and 1.000 Holstein cows during the observation period of 1 year. Within the project claw trimming was documented and recorded. Additionally lameness was assessed at each time of milk recording by the trained staff of the milk recording organizations using the scoring system of ZINPRO. Within the health monitoring in Austria veterinarian diagnoses are recorded on routine bases. The same is true for culling data. Heritabilities and genetic correlations between the traits have been estimated for veterinarian diagnoses, lameness scores, claw health based on claw trimming data and culling information with a linear animal model. The heritability based on veterinarian diagnoses is 0.025 for Fleckvieh (Simmental) and 0.013 for Brown Swiss. The respective values based on claw trimming data are 0.042 for Fleckvieh (Simmental) and 0.075 for Brown Swiss. The trait was defined as 0/1 or including the number of events as the second value of the results. Based on the lameness score a lactation lameness value was calculated taking the frequency of different severity cases into account. The heritability for this value is 0.092 for Fleckvieh and 0.109 for Brown Swiss. The genetic correlations between veterinarian diagnoses, claw trimming data and lactation lameness value are in the range of 0.3-0.9. The results confirm the usability of various data sources for genetic improvement of claw health.