

Genetic evaluation for claw health traits as part of the integrated system for health monitoring in German Holstein dairy cattle

K. F. Stock¹, H. H. Swalve², R. Schafberg², V. Müller-Rätz² & F. Reinhardt¹

¹*IT Solution for Animal Production (vit), Heinrich-Schroeder-Weg 1, D-27283 Verden (Aller), Germany*

²*Martin-Luther-University Halle-Wittenberg, Institute of Agricultural and Nutritional Sciences (IANS), Animal Breeding, Theodor-Lieser-Strasse 11, D-06120 Halle (Saale), Germany*

Abstract

The important role of claw health and its management has motivated installation of monitoring and improvement programs for dairy cattle worldwide. Significant genetic variation implies that breeding measures can valuably contribute to keeping prevalences and incidences of lameness and claw disorders low. However, new concepts are required for ensuring sufficient amount and quality of phenotypic data as basis of reliable genetic and genomic evaluations. The aim of this study was to use data and results from the genetic evaluation prototype for claw health traits from the German R&D project GKUHplus for illustrating the potential of integrated use of trimming and treatment data.

Health data collected in dairy farms from 2009 to 2016 were available for this study. Considering only health records for German Holsteins, approximately 269,000 lactations of 134,917 cows were informative for claw health traits and provided the basis of the genetic evaluation. Standardized recording that included the affected claw or limb was safeguarded across documentation systems used on the farms and by the claw trimmers. Direct electronic transfer of information from hoof trimming was enabled for approximately 30% of the lactation records. Treatment data and manually entered claw health data from trimming completed the data pool for the genetic analyses. Dates when animals entered and left the herd were available for all participating farms and allowed, in combination with the integrated claw health data, definition of comparison groups. For maximum differentiation between individuals, the number of distinct claw health events per lactation was analyzed using linear animal repeatability models. Genetic parameters and breeding values (EBV) were estimated univariately for six individual claw health traits: interdigital hyperplasia, IH; laminitis, LA; white line disease, WL; claw ulcers, UL; digital phlegmona, PH; digital dermatitis, DD. Weight of traits for the derived Claw health index were 30% for DD, 10% for IH, and 15% each for LA, WL, UL and PH. With heritability estimates ranging between 0.06 and 0.11, results were consistent with literature and routine applications most of which referred to trimming records as exclusive data basis. Full integration of treatment and trimming data was therefore seen as feasible approach to increase coverage and avoid bias of available information on claw health from commercial dairy herds. In total, 5,955 Holstein AI bulls were represented with on average 19 daughters in the genetic evaluation for claw health traits, but the proportion of bulls with up to 10 daughters was high (73%) and only 412 bulls had 50 or more daughters with claw health information. Analyses of distributions of individual EBV and Claw health index showed significant phenotypic differentiation between progeny groups of sires, implying substantial opportunities to reduce frequencies of claw disorders in dairy cattle through routine genetic evaluation which integrates treatment and trimming data and that way makes optimal use of available claw health information.

Keywords: standardized claw data recording, heritability, estimated breeding values, genetic evaluation for claw health traits