



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

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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

Abstract

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

Introduction

Undisturbed locomotion is a major criterion of animal welfare, and for a dairy cow it is also prerequisite to function as part of her herd. Impaired locomotory health and in particular claw conditions which are clearly dominating among the locomotory disorders have accordingly substantial impact on the efficiency and sustainability of dairy farming (Cha *et al.*, 2010, Charfeddine & Pérez-Cabal, 2017). Furthermore, alterations in the claws are often very painful and therefore causing lameness, high frequencies of which in modern livestock keeping are seen as significant animal welfare issue.

Great differences between farms regarding the prevalences of lame cows and underlying causes of lameness indicate the potential of measures to improve the health of feet and legs in dairy cattle (e.g. Cramer *et al.*, 2008, Foditsch *et al.*, 2016). Claw health is accordingly an important, though complex component of health monitoring projects and programs. Besides strong impact of management, studies have shown the relevant genetic background of claw conditions in dairy cows (e.g., König & Swalve 2006, Malchiodi *et al.*, 2015), implying that breeding can valuably contribute to reducing the proportions of affected animals in the population. However, different potential data sources and related technical and logistical challenges, lacking standardization and harmonization as well as concerns regarding overall data quality have hampered the increase of the number of routine genetic and genomic applications for claw health in dairy cattle worldwide (Heringstad *et al.*, 2017).

Through records from routine hoof trimming, highly valuable information on the claw health status of all cows trimmed becomes available. However, information on the more severe cases of foot and leg disorders may originate from veterinary medical treatment data, and observations of farmers may supplement to both of the aforementioned data sources. Accordingly, data integration concepts should be most appropriate for ensuring sufficient amount and quality of phenotypic data as basis of reliable genetic and genomic evaluations. The comprehensive and integrated system for health monitoring in dairy cattle in Germany is including veterinary diagnoses, observations of farmers, screening records (e.g. for reproduction disorders) and documentation from routine hoof trimming. This is enabled by ensured standardizing coding of health events across data sources and documentation systems as supported by the internationally agreed recording standard (Stock *et al.*, 2012). 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.

Major tasks of the German Innovation Partnership GKUHplus, supported by funds of the German Government's Special Purpose Fund held at Landwirtschaftliche Rentenbank, were extending the collection and use of health data and strengthening routine applications for direct health traits in dairy cattle. Strong regional partners and close interdisciplinary collaboration have contributed to the success of the project, and since 2016 health records for German Holstein dairy cattle from all federal states and Austria are considered in the prototype genetic evaluation for direct health traits.

For this study, health data collected in dairy farms from 2009 to 2016 were available. Claw health traits were defined in line with the internationally harmonized standard for claw data recording (ICAR 2015) and based on the hierarchical codes of the central key (ICAR 2016). 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 pool of phenotypic information 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.

Considering only health records for German Holsteins, 269,439 lactations of 134,917 cows were informative for claw health traits and provided the basis of the genetic evaluation. 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 phlegmon, 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.

Pearson correlation coefficients and Spearman rank correlations were determined between EBV of Holstein AI bulls from the prototype genetic evaluation for claw health and the official routine genetic evaluation for dairy cattle (vit 2017). Statistical analyses were performed using the SAS software package (Statistical Analysis System, SAS version 9.3; SAS Institute Inc., Cary, NC, USA, 2017). PEST software (Prediction Estimation; Groeneveld & Kovac 1990) was used for the genetic evaluation.

Descriptive statistics and heritability estimates of the six claw health traits considered are given in Table 1. With restrictive definition of control animals (presence in the herd, i.e. under health monitoring, without respective diagnosis records for at least 75% of 305 days standard lactation), lactation incidences of 5 to 20 percent were calculated, illustrating the quantitative importance of claw conditions of dairy cows. However, additional information on locomotion (lameness) was not available for the cows and severity of alterations were not considered, so no direct conclusions can be drawn on the clinical relevance of these findings.

With estimates of between 0.06 and 0.11, heritabilities 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. However, thorough data processing is crucial when linking different sources of data, and demands increase the more heterogeneous recording intervals and overall data structure are.

Material and methods

Results and discussion

Table 1. Claw health traits in the genetic evaluation with frequencies (lactation incidences, LI) and heritabilities (h^2), with additional information on the composition and heritability of the claw health index.

Trait	Number of lactations	LI	h^2	Index weight	Index h^2
Interdigital hyperplasia, IH	240,312	5.0 %	0.11	10 %	0.08
Laminitis, LA	242,160	8.7 %	0.06	15 %	
White line disease, WL	241,257	7.6 %	0.06	15 %	
Claw ulcers, UL	203,344	14.5 %	0.09	15 %	
Digital phlegmon, PH	199,342	12.8 %	0.07	15 %	
Digital dermatitis, DD	217,817	20.2 %	0.07	30 %	

Standard error of $SE_{h^2} < 0.01$

Table 2: Correlations (Pearson correlation coefficients) between breeding values for claw health and results of routine genetic evaluation for dairy cattle (April 2017) referring to conformation of feet and legs in 436 Holstein AI bulls with at least 50% reliability of the claw health index.

Trait	RZ Spr	RZ KW _i	RZ HB _s	RZ HB _w	RZ Bew	RZ Fun
Claw health index	0.07	0.04	0.08	-0.16	0.36	0.27
Interdigital hyperplasia, IH	0.09	0.06	0.16	-0.11	0.31	0.27
Laminitis, LA	0.05	0.02	0.01	-0.07	0.22	0.16
White line disease, WL	0.13	-0.03	-0.02	-0.03	0.22	0.17
Claw ulcers, UL	0.06	0.06	0.07	-0.17	0.34	0.26
Digital phlegmon, PH	0.12	-0.06	0.06	-0.12	0.27	0.21
Digital dermatitis, DD	0.00	0.05	0.09	-0.16	0.29	0.21

Spr = Sprunggelenk / hock quality, KW_i = Klauenwinkel / foot angle, HB_s = Hinterbeinstellung / rear leg set rear view, HB_w = Hinterbeinwinkelung / rear leg set side view, Bew = Bewegung / locomotion, Fun = Fundament / feet

Table 3. Correlations (Pearson correlation coefficients) between breeding values for claw health and results of routine genetic evaluation for dairy cattle (April 2017) for the total merit index and major trait complexes in N=436 Holstein AI bulls with at least 50% reliability of the claw health index.

Trait	RZG	RZM	RZS	RZR	RZN	RZE
Claw health index	0.36	0.21	0.17	0.17	0.38	0.03
Interdigital hyperplasia, IH	0.20	0.07	0.11	0.05	0.26	0.11
Laminitis, LA	0.29	0.20	0.11	0.10	0.27	-0.01
White line disease, WL	0.37	0.18	0.19	0.23	0.40	0.13
Claw ulcers, UL	0.42	0.23	0.23	0.20	0.43	0.10
Digital phlegmon, PH	0.19	0.02	0.16	0.08	0.32	0.02
Digital dermatitis, DD	0.24	0.18	0.08	0.11	0.21	-0.07

RZG = total merit index, RZM = production, RZS = somatic cell score, RZR = fertility, RZN = longevity, RZE = conformation

In the genetic evaluation for claw health traits performed in the GKUHplus project in January 2017 and considering health data from January 2009 to December 2016, 5,955 Holstein AI bulls were represented with on average 19 daughters (range 1 to 2,052). However, 73 percent of these bulls had between one and ten daughters and only 412 bulls had 50 or more daughters with claw health information. Average reliabilities of EBV were therefore low, and further extension of the phenotypic data basis will be needed to increase the number of bulls with reliably estimated conventional breeding values for claw health traits.

Nevertheless, analyses of distributions of individual EBV and Claw health index showed significant phenotypic differentiation between progeny groups of sires, implying substantial opportunities to reduce the frequencies of claw disorders in dairy cattle through routine genetic evaluation. Correlation analyses with the currently available genetic proofs clearly showed the limitations of using conformation related indicator traits (Table 2). At the same time, selection for improved claw health should not interfere with genetic progress in other trait complexes (Table 3).

Claw health requires particular attention in dairy production and should be seen as essential part in initiatives for monitoring and improving health of dairy cows. Challenges related to routine access and use of claw data do exist, but comprehensive concepts with integrative approaches make it possible to efficiently increase information density and by this strengthen routine applications. However, awareness of remaining challenges related to phenotyping (harmonization and standardization of data recording), logistics, data quality management and definition of traits may be crucial to ensure long-term success of the engagement for improving the health of feet and legs in dairy cattle.

Results from the German R&D project GKUHplus demonstrate feasibility of integrated use of claw data for genetic evaluation for claw health traits in Holstein dairy cattle. Furthermore, they also indicate the potential of using cow phenotypes on claw health collected broadly in the field as basis for developing genomic applications for new traits, as it is done in the new R&D project KuhVision which is a joint initiative of the German Holstein breeding organizations and aims at setting up a female reference population.

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Cha, E., Hertl, J.A., Bar, D., and Y.T. Grohn. 2010. The cost of different types of lameness in dairy cows calculated by dynamic programming. *Prev. Vet. Med.* 97, 1-8.

Charfeddine, N., and M.A. Pérez-Cabal. 2017. Effect of claw disorders on milk production, fertility, and longevity, and their economic impact in Spanish Holstein cows. *J. Dairy Sci.* 100, 653-665.

Conclusions

Acknowledgements

List of references

- Cramer, G., Lissemore, K.D., Guard, C.L., Leslie, K.E., and D.F. Kelton.** 2008. Herd- and cow-level prevalence of foot lesions in Ontario dairy cattle. *J. Dairy Sci.* 91, 3888-3895.
- Foditsch, C., Oikonomou, G., Machado, V.S., Bicalho, M.L., Ganda, E.K., Lima, S.F., Rossi, R., Ribeiro, B.L., Kussler, A., and R.C. Bicalho.** 2016. Lameness prevalence and risk factors in large dairy farms in upstate New York. Model development for the prediction of claw Horn disruption lesions. *PLoS One* 11(1), e0146718.
- Heringstad, B., Egger-Danner, C., Stock, K.F., Pryce, J.E., Gengler, N., Charfeddine, N., and J.B. Cole.** 2017. Genetic evaluation of claw health - challenges and recommendations. 68th Annual Meeting of the European Federation of Animal Science, 28 August - 1 September 2017, Tallinn, Estonia; S06-2.
- ICAR (International Committee for Animal Recording).** 2015. ICAR Claw Health Atlas. Available online at <http://www.icar.org/wp-content/uploads/2016/02/ICAR-Claw-Health-Atlas.pdf> (assessed 17 September 2017).
- ICAR (International Committee for Animal Recording).** 2016. ICAR Recording Guidelines. Appendix Section 07 Recording of functional traits. Available online at <http://www.icar.org/Guidelines/07-Bovine-Functional-Traits.pdf> (assessed 27 October 2017).
- Koenig, S., and H.H. Swalve.** 2006. Modellkalkulationen zu züchterischen Möglichkeiten auf Klauengesundheit beim Milchrind. *Züchtungskunde* 78, 345-356.
- Malchiodi, F., Koeck, A., Chapinal, N., Sargolzaei, M., Fleming, A., Kelton, D., Schenkel, F., and F. Miglior.** 2015. Genetic analyses of hoof lesions in Canadian Holsteins using an alternative contemporary group. *Interbull Bull.* 49, 64-68.
- Stock, K.F., Cole, J., Pryce, J.E., Gengler, N., Bradley, A., Andrews, L., Heringstad, B., and C. Egger-Danner.** 2013. Standardization of health data - ICAR guidelines including health key. In: Challenges and benefits of health data recording in the context of food chain quality, management and breeding, Egger-Danner, C., Hansen, O.K., Stock, K.F., Pryce, J.E., Cole, J., Gengler, N., and B. Heringstad (Editors), ICAR Technical Series No. 17, ICAR, Rome, Italy, p. 75-81.
- VIT (IT Solutions for Animal Production).** 2017. Dairy cattle breeding values - Description of genetic evaluation. Available online at: http://www.vit.de/index.php?id=milchrinder-zws-online&no_cache=1&L=1 (assessed 17 September 2017).