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Short communication: Genetic relationships between claw disorders, protein yield, and somatic cell score by days in milk

E. Gernand* and S. König†[1]
*Thuringian State Institute of Agriculture, 07743 Jena, Germany
†Department of Animal Breeding, University of Kassel, 37213 Witzenhausen, Germany

ABSTRACT

The aim of the present study was to infer daily genetic relationships between the selected claw disorders digital dermatitis, sole ulcer (SU), and interdigital hyperplasia (IH) and protein yield and the udder health indicator somatic cell score (SCS). Data were from 26,651 Holstein cows kept in 15 selected large-scale herds located in the region of Thuringia in the eastern part of Germany. Herds are characterized by organized data recording for novel health traits, and for the present study, claw disorders from the years 2008 to 2012 were used. A longitudinal and binary health data structure was created by assigning claw disorders to adjacent official test days. No entry of a claw disorder within a given interval of approximately 30 d implied a score of 0 (healthy), and otherwise, a score of 1 (diseased). Threshold random regression models (RRM) were applied to binary health data, and linear RRM to Gaussian-distributed protein yield and SCS. Genetic correlations between protein yield and SCS for identical days in milk (DIM) only revealed a tendency for genetic antagonisms between DIM 40 and DIM 180, with a maximal genetic correlation (r_g) of 0.14 at DIM 100. With regard to protein yield and claw disorders, the largest and moderate values of r_g (~0.30), indicating a genetic antagonism between productivity and claw health, were found when correlating protein yield from DIM 300 with SU from DIM 160. Especially for SU and protein yield, time-lagged relationships were more pronounced than genetic relationships from the same test days. Genetic correlations between IH and protein yield were favorable and negative from calving to DIM 300. Generally, on the genetic scale, we found heterogeneous associations between protein yield and claw disorders (i.e., different r_g at identical test days for different claw disorders, and also an alteration of r_g for identical traits at different DIM). The SCS measured at d 20, 160, and 300 was genetically positively correlated with SU over the whole trajectory of 365 d, indicating a common genetic background for claw and udder health. A maximal value of 0.36 was found for the r_g between SCS from d 300 and SU early in lactation. Additionally, a recursive effect was observed (i.e., $r_g = 0.26$ between SCS from d 20 and SU from d 340). Genetic correlations between SCS and IH, and between SCS and digital dermatitis, were close to zero and partly negative during lactation. Results showed the feasibility of threshold RRM applications to binary claw health data, and a changing genetic background in the course of lactation. From a practical perspective, and with regard to the herds used in this study, continuation of breeding on productivity will have different effects on incidences of different claw disorders, with the highest susceptibility to SU.
Key words: random regression model, claw disorder, protein yield, somatic cell score

Short Communication

Genetic associations between claw health, productivity, and udder health have been studied by using single test-day observations for production traits from different lactation stages (e.g., König et al., 2008), using an average from several test days (e.g., Koenig et al., 2005), or using lactation records (e.g., Lyons et al., 1991). In those studies, mostly antagonistic relationships between claw disorders and milk or protein yield were identified. Furthermore, genetic correlations ($\mathbf{r_g}$) between claw disorders and the udder health indicator SCS were positive, indicating that the same cows are susceptible to both categories claw and udder infections. Nevertheless, interpretation of r_g between health and productivity is complicated due to the role of cause and effect. To infer relationships by depicting the physiological background, recursive models based on only 2 observations for test-day data and a single observation for claw health per cow were used (König et al., 2008). The application of random regression models (**RRM**) to both types of traits Gaussian-distributed test-day production records and binary claw disorders implies the consideration of all available observations in the course of lactation. Genetic correlations within

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[1]Corresponding author: sven.koenig@uni-kassel.de

Table 1. Mean incidences for claw disorders and means for protein yield and SCS for different test days[1] in the course of lactation

	Test day											
Item[2]	1	2	3	4	5	6	7	8	9	10	11	12
Claw disorder												
DD	2.78	0.72	0.77	0.87	0.91	0.95	0.99	0.99	0.97	0.90	0.84	0.72
SU	1.55	1.77	1.93	1.83	1.95	1.61	1.53	1.50	1.30	1.24	0.98	0.78
IH	2.38	0.89	0.69	0.63	0.75	0.70	0.71	0.72	0.69	0.80	0.71	0.68
Protein yield	1.03	1.11	1.13	1.12	1.09	1.05	1.00	0.95	0.88	0.73	0.55	0.47
SCS	2.54	2.08	2.09	2.19	2.28	2.38	2.49	2.58	2.71	2.88	3.00	3.12

[1]Test day in the sense of official milk recording dates in monthly intervals: test d 1 = first official milk recording after calving, test d 2 = second official milk recording after calving, and so on.

[2]DD = digital dermatitis; SU = sole ulcer; IH = interdigital hyperplasia.

and between traits for all combinations of DIM allow a differentiated interpretation of associations on the genetic scale (e.g., to study the effect of high genetic merit for protein yield directly after calving on disease susceptibility, or to analyze the effect of a claw disorder on productivity in the ongoing lactation).

Recently, a changing genetic background with changes in variances and variance ratios for claw disorders by DIM was shown by Gernand et al. (2013). Additionally, they estimated r_g between claw disorders and linear type traits. The largest, but only moderate estimates were found when correlating measurements from the same day. Genetic correlations between claw disorders and linear type traits from test days further apart were close to zero. Results indicated that type traits routinely recorded approximately 2 mo after calving are only weak predictors for claw health in very early or late lactation. In consequence, the aim of our present study was the extension of the RRM approach by additionally including test-day protein yield and test-day SCS. In detail, we studied genetic associations between claw disorders with test-day protein yield, between claw disorders and test-day SCS, and between test-day protein yield and test-day SCS for all combinations of DIM over a period of 365 d.

Data recording included 26,651 Holstein cows from parities 1, 2, and 3, and spanned a period from 2008 to 2012. Cows were kept in 15 large-scale cooperator herds in the region of Thuringia located in the eastern part of Germany. Data preparation for creating a longitudinal data structure by assigning claw disorders to the nearest official test day was identical, as described by Gernand et al. (2013). Such a strategy for data preparation resulted in 406,327 test-day records for all traits, including 184,404 test-day records from parity 1, 135,685 test-records from parity 2, and 86,234 test-day records from parity 3. Sires had, on average, 21 daughters per sire, and 74 sires had more than 60 daughters. Recording of claw disorders was based on the diagnosis key by Feucker and Staufenbiel (2003). The focus of the current study was on the purulent claw disorders digital dermatitis (**DD**) and sole ulcer (**SU**), and on the nonpurulent claw disorder interdigital hyperplasia (**IH**). Decision of claw disorder selection was based on incidences and heritabilities. In the study by Gernand et al. (2013), SU and DD had the highest incidences, with 10.54 and 12.52% on a lactation level, respectively, and heritabilities were low to moderate. For IH, the lactation incidence was quite low (5.62%), but the highest heritabilities, with estimates up to 0.35, were found. Mean incidences on the test-day scale for the 3 claw disorders DD, SU, and IH are summarized in Table 1.

Threshold RRM for binary health traits and linear RRM for protein yield and SCS were used to infer genetic (co)variance components for all combinations of test-day traits with claw disorders, and for protein yield with SCS, resulting in 7 bivariate runs (6 bivariate threshold-linear models, and 1 linear-linear model). The statistical models in matrix notation were defined as follows:

$$\mathbf{l} = \mathbf{X\beta} + \mathbf{Zu} + \mathbf{Wpe} + \mathbf{e};$$

$$\mathbf{y} = \mathbf{X\beta} + \mathbf{Zu} + \mathbf{Wpe} + \mathbf{e},$$

where $\mathbf{l}$ = vector of unobserved liabilities for claw disorders with the binary outcome 1 = diseased or 0 = healthy; $\mathbf{y}$ = vector of phenotypic observations for the Gaussian traits protein yield and SCS, and vector of liabilities for binary traits DD, SU, and IH; $\boldsymbol{\beta}$ = vector of fixed effects, including the combined effect of herd-test date-milking frequency and regressions on DIM within parity using fourth-order Legendre polynomials; $\mathbf{u}$ = vector of random additive genetic effects, with regressions on DIM using fourth-order Legendre polynomials; $\mathbf{pe}$ = vector of permanent environmental effects, with regressions on DIM using fourth-order Legendre polynomials; $\mathbf{e}$ = vector of random residual effects; and $\mathbf{X}$, $\mathbf{Z}$, and $\mathbf{W}$ are the associated incidence matrices, respectively. For the application of Legendre polynomials,