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Estimation of heritability of hoof and leg disorders and their genetic relationships with longevity and feet and leg conformation traits in Holstein cows

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Introduction

In Japan, approximately 30% of Holstein cows are culled due to disease, and more than 20% of these cases are attributable to hoof and leg problems. Hoof and leg disorders negatively affect milk production and animal welfare, in addition to increasing treatment costs, thereby resulting in substantial economic losses (Malchiodi *et al*. 2015). Therefore, hoof and leg disorders present major health challenges for dairy farms. Furthermore, Hoof and leg disorders are the primary causes of lameness in dairy cows (Van Nuffel *et al*. 2015), which is associated with reduced productivity and an increased risk of culling (Booth *et al*. 2004; Garvey 2022).

Against this background, clarifying the genetic relationships between hoof and leg disorders, longevity, and feet and leg conformation traits in Holstein cattle is important for developing breeding strategies that take disease resistance into account. Therefore, the objectives of this study were to estimate the genetic parameters of hoof and leg disorders in Holstein cows and to elucidate their genetic relationships with longevity and feet and leg conformation traits.

Materials & Methods

Data. The clinical records used in this study comprised of hoof and leg disorder data collected by the Agricultural Mutual Relief Association from seven regions of Japan. The dataset included lactations 1 to 3 of 379,098 Holstein cows that calved after 2004. The age at calving ranged from 18 to 36 months the first lactation, 30 to 55 months for the second lactation, and 42 to 75 months for the third lactation. The disorders analyzed included arthritis (AR), interdigital dermatitis (ID), interdigital phlegmon (IP), digital dermatitis (DD), purulent pododermatitis (PP), white line lesion (WL), and sole ulcer (SU). In this study, each disease was defined as a binary trait (0 = affected, 1 = unaffected) based on the occurrence of disease within 305 days after calving. For all diseases, the proportion of cases occurring within 305 days after calving in each lactation period (365 days) was ≥86% in the first lactation, ≥89% in the second lactation, ≥90% in the third lactation. Although treating cases occurring after 305 days postpartum as unaffected may introduce censoring effects, the impact is considered to be small because the proportion of cases occurring after this period is low.

Model. Heritabilities for hoof and leg disorders were estimated by a linear repeatability animal model based on multiple lactation records, in accordance with the national genetic evaluation method of mastitis and metabolic disorders such as ketosis and displaced abomasum in Japan. The equation of this model is as follows:

$$y_{ijklmn} = hy_i + BYM_j + PAGE_k + u_l + pe_m + e_{ijklmn} \quad (1)$$

where y_{ijklm} is a binary variable indicating the disease status for each disorder; hy_i is the random effect of the i-th herd-year of calving; BYM_j is the fixed effect of the j-th region-year-month of calving, where the region effect consists of two levels: Hokkaido and other prefectures; $PAGE_k$ is the fixed effect of the k-th parity-calving age class with 15 subclasses

for the first lactation (with classes grouped at 18 - 20 and 21 - 22 months), 25 subclasses for the second lactation (with classes grouped at 30 - 31 months), and 28 subclasses for the third lactation (with classes grouped at 42 - 43, 68 - 69, 70 to 72, and 73 to 75 months); u_l is the random effect of the l-th cow for additive genetic; pe_m is the random effect of the m-th permanent environment effect; and e_{ijklmn} is the random residual associated with each record. Genetic correlations between hoof and leg disorders, longevity, and feet and leg conformation traits were estimated using a two-trait animal model fitted to first lactation records. The feet and leg conformation traits included rear legs side view (SV), rear legs rear view (RV), foot angle (FA), bone quality of the rear legs (BQ), heel depth (HD), and locomotion (LOC), all of which were scored on a linear scale from 1 to 9. Longevity was evaluated using stayability (STY) scores, defined by dividing the period within each lactation into three intervals: from calving to 49 days in milk (DIM), from 50 to 249 DIM, and from 250 DIM to the next calving date. A continuous linear score ranging from 1 to 9 was assigned to each interval. The model equations for each trait are as follows.

$$y_{ijklm} = hy_i + BYM_j + AGE_k + u_l + e_{ijklm} \quad (2)$$

$$y_{ijklm} = HY_i + BYM_j + AGE_k + u_l + e_{ijklm} \quad (3)$$

$$y_{ijklm} = HCY_i + CAGE_j + LS_k + u_l + e_{ijklm} \quad (4)$$

where y_{ijklm} represents the observed value of each trait. In Eq.2 for hoof and leg disorders, AGE_k is the fixed effect of the k-th calving age at first parity. Other effects are the same as those included in the Eq.1. In Eq.3 for STY, HY_i is the fixed effect of the i-th herd-year of calving. In Eq.4 for feet and leg conformation traits, HCY_i is the fixed effect of the i-th herd–classification date–classifier; $CAGE_j$ is the fixed effect of the j-th classification age; and LS_k is the fixed effect of the k-th lactation stage.

Genetic parameters were estimated using the GIBBSF90+ program implementing the Gibbs sampling method (Lourenco *et al*., 2022). The number of iterations and burn-in were set to 200,000 and 50,000 for the estimation of genetic parameters of hoof and leg disorders, and to 150,000 and 50,000 for the estimation of genetic correlations between hoof and leg disorders, STY, and feet and leg conformation traits. The convergence was assessed by visual inspection of variance components. Posterior means and standard deviations of the variance components were calculated using every 10th sample after convergence.

Results

The incidence rates of individual hoof and leg disorders by lactation are presented in Table 1. The rates ranged from 0.5 to 1.5% in the first lactation, from 1.0 to 1.7% in the second lactation, and from 1.3 to 2.6% in the third lactation, indicating an increasing trend in disease incidence with parity.

Table 1. Incidence rates (%) of individual hoof and leg disorders for the first third lactations.

Disorder	Lactation		
	1	2	3
AR[1]	1.3	1.6	2.1
ID	1.2	1.4	1.5
IP	1.5	1.7	1.8
DD	0.7	1.3	1.3
PP	0.5	1.0	1.6
WL	0.9	1.6	2.6
SU	0.6	1.2	2.0

[1]AR = Arthritis, ID = Interdigital dermatitis, IP = Interdigital phlegmon, DD = Digital dermatitis, PP = Purulent pododermatitis, WL = White line lesion, SU = Sole ulcer

The estimates of heritability for hoof and leg disorders and genetic correlations among the disorders are presented in Table 2. Heritability estimates ranged from 0.30% to 1.80% and were low across all disorders. Their genetic correlations ranged from 0.001 to 0.903, indicating variation in the strength of genetic relationships among the disorders.

Table 2. Posterior means (SDs) of heritability (diagonal) and genetic correlations (below the diagonal) for hoof and leg disorders.

Trait	AR[1]	ID	IP	DD	PP	WL	SU
AR	0.004(0.00)						
ID	0.359(0.06)	0.003(0.00)					
IP	0.262(0.07)	0.896(0.02)	0.006(0.00)				
DD	0.245(0.05)	0.772(0.03)	0.722(0.03)	0.010(0.00)			
PP	0.356(0.07)	0.169(0.04)	0.197(0.05)	0.001(0.04)	0.004(0.00)		
WL	0.365(0.06)	0.253(0.04)	0.333(0.03)	0.067(0.03)	0.903(0.01)	0.009(0.00)	
SU	0.291(0.06)	0.137(0.04)	0.178(0.03)	0.203(0.03)	0.282(0.04)	0.409(0.03)	0.018(0.00)

[1]AR = Arthritis, ID = Interdigital dermatitis, IP = Interdigital phlegmon, DD = Digital dermatitis, PP = Purulent pododermatitis, WL = White line lesion, SU = Sole ulcer

Table 3 shows genetic correlations between hoof and leg disorders and STY, feet and leg conformation traits. Hoof and leg disorders, STY, and LOC were defined such that higher values are more favorable. Positive genetic correlations were estimated between STY and most disorders, with values of 0.63 for AR, 0.27 for ID, 0.42 for PP, and 0.36 for SU ($P < 0.001$). Furthermore, ID, DD, and SU showed positive genetic correlations greater than 0.6 with LOC; however, only the correlation for ID was statistically significant ($P < 0.001$).

Table 3. Posterior means (SDs) of genetic correlations between hoof and leg disorders and STY, feet and leg conformation traits.

Trait	STY[1]	SV	RV	FA	BQ	HD	LOC
AR	0.63*(0.07)	–0.21 (0.10)	–0.22 (0.13)	–0.31*(0.11)	–0.08 (0.10)	–0.31 (0.09)	–0.51 (0.20)
ID	0.27*(0.08)	0.13 (0.10)	0.01 (0.14)	–0.27 (0.13)	0.33*(0.08)	–0.27 (0.16)	0.69*(0.13)
IP	–0.01 (0.07)	–0.06 (0.10)	–0.23 (0.11)	0.03 (0.13)	0.14 (0.11)	0.20 (0.15)	0.21 (0.15)
DD	–0.06 (0.11)	–0.08 (0.14)	0.17 (0.14)	0.25 (0.15)	0.08 (0.12)	0.23 (0.15)	0.73 (0.07)
PP	0.42*(0.15)	–0.08 (0.21)	–0.19 (0.25)	0.29 (0.31)	0.06 (0.22)	–0.10 (0.21)	0.36 (0.23)
WL	0.36*(0.09)	–0.35 (0.14)	–0.07 (0.15)	0.07 (0.18)	0.09 (0.17)	0.34*(0.15)	0.54 (0.23)
SU	0.12 (0.12)	–0.03 (0.13)	0.40 (0.15)	0.15 (0.22)	0.21 (0.12)	0.06 (0.23)	0.70 (0.13)

[1]STY = Stayability, SV = Rear legs side view, RV = Rear legs rear view, FA = Foot angle, BQ = Bone quality, HD = Heel depth, LOC = Locomotion.
*: The estimate was significantly different from zero ($P < 0.001$).

Discussion

A previous study reported that the incidence of digital dermatitis decreased with parity, whereas the incidence of white line disease and sole ulcer increased (Malchiodi *et al*., 2017). However, the incidence patterns of infectious hoof and leg disorders do not necessarily agree with this study. One possible explanation for this discrepancy is the differences in the data sources. While previous studies used data collected from hoof trimmers, the present analysis used diagnostic records from veterinarians, which likely included mild or chronic cases. Consequently, the accumulation of disease history may have resulted in the observed increase in incidence as parity progressed.

In previous studies, heritability estimates for DD ranged from 0.01 to 0.14 (van der Waaij *et al*., 2005; Onyiro *et al*., 2008; Häggman *et al*., 2013; Malchiodi *et al*., 2017), ID were reported as 0.03 and 0.12 (Häggman *et al*., 2013; Malchiodi *et al*., 2017), WL ranged from 0.02 to 0.04 (van der Waaij *et al*., 2005; Häggman *et al*., 2013; Malchiodi *et al*., 2017), and SU ranged from 0.01 to 0.08 (van der Waaij *et al*., 2005; Häggman *et al*., 2013; Malchiodi *et al*., 2017), all of which were low. The heritability estimated in this study were even lower than those previously reported. The incidences of hoof and leg disorders in this study was low (≤2% across all parities), and the application of a linear model to low incidence binary traits may have resulted in low heritability estimates.
Additionally, genetic correlations among hoof and leg disorders varied depending on the specific combination of disorders; however, all estimates were positive. These results suggest that the magnitude of genetic correlations differs among disorder combinations, but that shared genetic factors such as metabolic status, immune function, and hoof conformation may be involved. Therefore, improvement in any one of these diseases is expected to lead to genetic improvement in the same direction for the other diseases.
Furthermore, positive genetic correlations were observed between hoof and leg disorders and STY. Onyiro *et al*. (2008) reported a favorable genetic correlation between DD and longevity, which is consistent with the tendency observed in this study. In addition, strong positive genetic correlations were estimated between hoof and leg disorders and LOC, consistent with the findings of van der Waaij *et al*. (2005). In Japan, genetic improvement for hoof and leg disorders has not yet been implemented; however, improvement in longevity and locomotion may contribute to a reduction in these disorders.

Conclusions

In this study, heritability estimates for hoof and leg disorders were low; however, moderate to high genetic correlations were estimated between hoof and leg disorders and both STY and LOC. These results indicate that genetic improvement of hoof health can be achieved more effectively through selection incorporating correlated traits, rather than focusing solely on hoof disorders. In particular, the strong genetic correlation between hoof and leg disorders and LOC suggests that deterioration in locomotion (lameness) caused by hoof and leg disorders is closely related to specific disorders. Therefore, hoof health should be regarded not only as a management issue but also as a potential objective for genetic improvement by leveraging its genetic correlations with STY and LOC. This study is, to the best of our knowledge, the first report in Japan to estimate genetic parameters for hoof and leg disorders using veterinary clinical records.

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