

Genetic associations between lameness and feet and leg conformation traits in Holsteins

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INTRODUCTION

Lameness is among the 3 most costly diseases in dairy cattle together with mastitis and fertility problems (Kossaibati and Esslemont, 1997). Losses are mainly caused by reduced milk yield, increased premature culling, prolonged calving interval, veterinary costs and additional labor and treatments by the dairy producer (Enting et al., 1997).

As disease recording programs are not widely implemented, feet and leg conformation traits are most commonly used as indicator traits. However, selection for these traits alone has not reduced lameness problems.

In Canada a disease recording system was implemented in 2007. Eight diseases, including lameness, are recorded by producers. The objectives of the current study were to estimate the heritability of lameness in Holsteins using data recorded by dairy producers in Canada, and to investigate genetic correlations between lameness and feet and legs conformation traits (including locomotion score) recorded by breed classifiers.

MATERIAL AND METHODS

Data

Data for lameness and conformation traits from April 2007 to December 2011 were obtained from the Canadian Dairy Network (Guelph, Ontario). Lameness cases were recorded by producers according to the disease definition described by Kelton et al. (1998), where lameness is defined as an episode of abnormal gait attributable to either the foot or leg, regardless of etiology or duration. As recording of lameness cases is voluntary, only herds with a minimum disease frequency (reported cases per herd and year) of 1% were considered to ensure reliable and continuous data recording. For all analyses, lameness was defined as a binary trait (0 = healthy, 1 = lame) based on whether or not the cow had at least 1 lameness case recorded within the first 305 d after calving.

Conformation traits were routinely recorded by professional type classifiers. 6 traits related to feet and legs were included in the analyses: feet and legs, foot angle, heel depth, bone quality, rear leg side view and rear leg rear view. In addition, locomotion score recorded during conformation evaluation in free-stall barns was available since 2005. Feet and legs were scored on a scale from 40 to 89. The remaining conformation traits and locomotion were scored on a

linear 1 to 9 scale. The optimum score for each trait is shown in Table 1. Only first classifications within 365 DIM were analyzed, reclassification records were not considered.

Only first lactation Holstein cows with an age between 19 and 43 months were considered. In total, 50,315 first lactation cows had records on lameness and of those 44,476 cows had records on conformation traits, and 19,417 cows had a locomotion score.

The animal pedigree file was generated by tracing the pedigrees of cows 7 generations back. The resulting pedigree file contained the relationship of 228,023 animals.

Models

Linear animal models were fitted using the average information-restricted maximum likelihood (AI-REML) procedure in the derivative-free approach to multivariate analysis (DMU) package (Madsen and Jensen, 2008).

Phenotypic association of conformation traits with lameness. In order to assess the effect of each feet and leg conformation trait on lameness, the following model was used:

$$Y_{ijklmn} = \mu + AGE_i + YS_j + FLT_k + hy_l + a_m + e_{ijklmn}$$

where Y_{ijklmn} is the observation for lameness, μ is the overall mean, AGE_i is the fixed effect of age at calving ($i = 1$ to 16 ; $1 = <22$ mo, $2 = 22$, ..., $15 = 35$ mo, $16 = >35$ mo), YS_j is the fixed effect of year-season of calving ($j = 1$ to 15 ; seasons: January-March, April-June, July-September, October-December), FLT_k is the fixed effect of each feet and leg conformation trait and locomotion ($k = 1$ to 10 for feet and legs and 1 to 9 for the remaining conformation traits), hy_l is the random herd-year of calving effect ($l = 1$ to $2,864$), a_m is the random additive genetic animal effect ($m = 1$ to $228,023$), and e_{ijklmn} is the random error term. The overall score for feet and legs was coded in 5 points intervals ($1 = 40-44$, ..., $10 = 85-89$).

Genetic association between lameness and conformation traits. Bivariate analyses were run between lameness and feet and legs, foot angle, heel depth, bone quality, rear leg side view, rear leg rear view and locomotion. The following model was used for lameness:

$$Y_{ijklm} = \mu + AGE_i + YS_j + hy_k + a_l + e_{ijklm}$$

where Y_{ijklm} is the observation for lameness, μ is the overall mean, AGE_i is the fixed effect of age at calving ($i = 1$ to 16 ; $1 = <22$ mo, $2 = 22$, ..., $15 = 35$ mo, $16 = >35$ mo), YS_j is the fixed effect of year-season of calving ($j = 1$ to 15 ; seasons: January-March, April-June, July-September, October-December), hy_k is the random herd-year of calving effect ($k = 1$ to $2,864$), a_l is the random additive genetic animal effect ($l = 1$ to $228,023$), and e_{ijklm} is the random error term.

The model for conformation traits and locomotion was:

$$Y_{ijklm} = \mu + AGE_i + LC_j + HRC_k + a_l + e_{ijklm}$$

where Y_{ijklm} is the observation for one of the conformation traits, μ is the overall mean, AGE_i is the fixed effect of age at calving ($i = 1$ to 16 ; $1 = <22$ mo, $2 = 22$, ..., $15 = 35$ mo, $16 = >35$ mo), LC_j is the fixed effect of stage of lactation at classification ($j = 1$ to 11 ; $1 = 0$ to 30 d, $2 = 31$ to 60

d, ..., 10 = 271 to 300 d, and 11 = 301 to 365 d after calving), HRC_k is the fixed effect of herd-round-classifier ($k = 1$ to 4,862), a_l is the random additive genetic animal effect ($l = 1$ to 228,023), and e_{ijklm} is the random error term.

RESULTS AND DISCUSSION

Lameness frequency was 9.0% in first lactation Holstein cows. The frequency of lameness varies greatly among studies, from 1.3% reported in Norwegian Red cattle (Guttormsen (2011) to 48% found in two dairy herds in New York State (Booth et al., 2004). Similar to our study, Zwald et al. (2004) reported a lameness frequency of 10% based on producer recorded data in US Holstein cows. Also, Bielfeldt et al. (2005) found a lameness frequency of 10% in dairy cattle in Switzerland.

The effect of each conformation trait on lameness is plotted in Figures 1A to 1G. Generally, the optimum score for all conformation traits and locomotion was associated with the lowest lameness frequency. Specifically, a higher feet and leg score was associated with a lower frequency of lameness. Very low (score = 1 and 2) or very steep foot angle (score = 8 and 9) was associated with a higher lameness frequency (Figure 1B) than average. Additionally, extremely shallow heel depth (score = 1 and 2) was associated with a much higher percentage of lame cows than average (Figure 1C). Regarding rear leg side view, curved legs were associated with a higher lameness frequency (Figure 1E). A higher frequency of lameness was also associated with low scores for rear leg rear view (hocked-in legs; Figure 1F) and for locomotion (Figures 1G).

Heritabilities and genetic correlations for lameness and conformation traits are given in Table 2. The heritability estimate for lameness was 0.01. Boettcher et al. (1998) analyzed data of clinical lameness recorded on a scale from 0 to 4 from about 1,300 US Holstein cows and found a much higher heritability of 0.10 based on a linear model. Similar to our result, Kadarmideen et al. (2000) obtained a heritability of 0.02 for lameness in UK Holstein cows.

Heritabilities of the conformation traits ranged from 0.04 for heel depth to 0.24 for bone quality. For locomotion a heritability of 0.02 was obtained. Compared to the heritability estimates used in the routine genetic evaluation in Canada (Huapaya and Kistemaker, 2011; Interbull, 2013), estimates in this study were similar or slightly lower.

Lameness had the strongest genetic relationship with locomotion (-0.70). In a previous study by Onyiro et al. (2008), a strong favorable genetic association of -0.67 was found between digital dermatitis and locomotion. Also, van der Linde et al. (2010) found that locomotion was significantly genetically correlated with digital dermatitis, interdigital dermatitis, sole ulcer and interdigital hyperplasia, with estimates ranging from -0.24 to -0.58.

Genetic correlations between lameness and conformation traits were lower and ranged from -0.46 (lameness and feet and legs) to 0.17 (lameness and rear leg side view). Boettcher et al. (1998) reported higher genetic correlations of -0.76 and -0.68 between clinical lameness and foot angle and clinical lameness and rear leg rear view, respectively, whereas the genetic correlation between clinical lameness and rear leg side view (0.13) was comparable to our estimate. Investigating the genetic relationships between specific claw disorders and conformation traits,

Koenig et al. (2005), Uggla et al. (2008) and van der Linde et al. (2010) found similar estimates to our study. In Swedish Holsteins, Uggla et al. (2008) found that most of the genetic correlations between claw disorders and conformation traits were low or not significant, with estimates ranging from -0.04 to 0.15. Slightly higher genetic correlations in the range of -0.51 to 0.41 were obtained by van der Linde et al. (2010) in Dutch Holstein cows. Also, in a recent study in Canadian Holstein cows, genetic correlations between hoof lesions and conformation traits were found to be low to moderate (Chapinal et al., 2013).

Overall, genetic correlations between lameness and feet and leg conformation traits were low to moderate, whereas locomotion was highly correlated with lameness. Our results indicate that locomotion is a promising indicator trait to reduce lameness frequency in dairy cattle.

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Table 1. Description of feet and leg conformation traits and locomotion

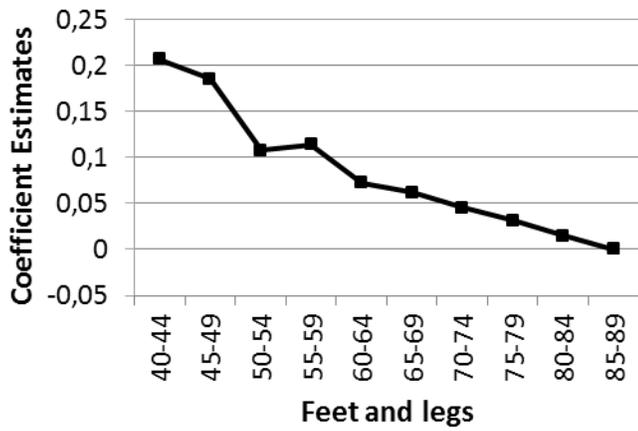
Trait	Description of trait	Optimum	Records, n	Mean
Feet and legs	Overall feet and leg score (40 = poor, 89 = very good)		44,476	78.3
Foot angle	Angle of toe (1 = extremely low, 9 = extremely steep)	7	44,476	5.5
Heel depth	Depth of heel on outside claw (1 = extremely shallow, 9 = extremely deep)	7/8	44,476	5.4
Bone quality	Flatness of bone (1 = extremely coarse, 9 = extremely flat)	8	44,476	5.9
Rear leg side view	Degree of curvature viewed from side (1 = extremely straight, 9 = extremely curved)	5	44,476	5.2
Rear leg rear view	Turn of hock when viewed from rear (1 = extremely hocked- in, 9 = extremely straight)	9	44,476	5.1
Locomotion	1 = lame, 9 = even gait, long strides	9	19,417	5.1

Table 2. Heritabilities and genetic correlations with standard errors (SE) for lameness, feet and leg conformation traits and locomotion

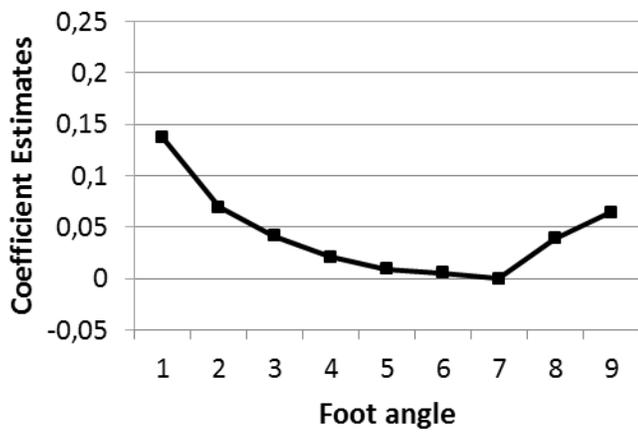
Trait	Heritability		Genetic correlation with lameness	
	Estimate	SE	Estimate	SE
Lameness	0.01	0.004		
Feet and legs	0.05	0.008	-0.46	0.14
Foot angle	0.07	0.010	-0.07	0.14
Heel depth	0.04	0.008	-0.27	0.15
Bone quality	0.24	0.015	-0.02	0.12
Rear leg side view	0.14	0.014	0.17	0.13
Rear leg rear view	0.06	0.009	-0.31	0.15
Locomotion	0.02	0.008	-0.70	0.17

Figure 1. Effect of feet and leg conformation traits and locomotion on lameness by score (SD of lameness = 0.28)

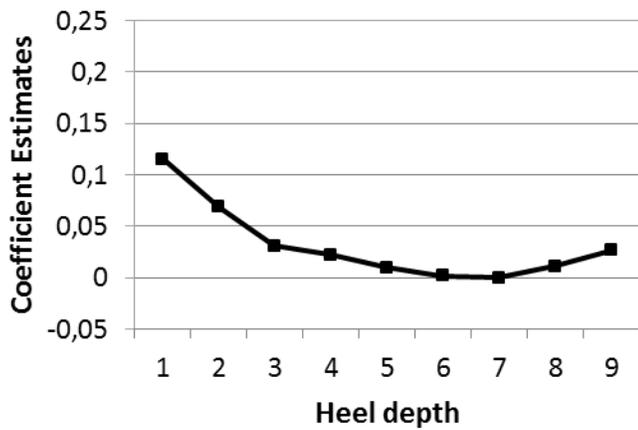
A)



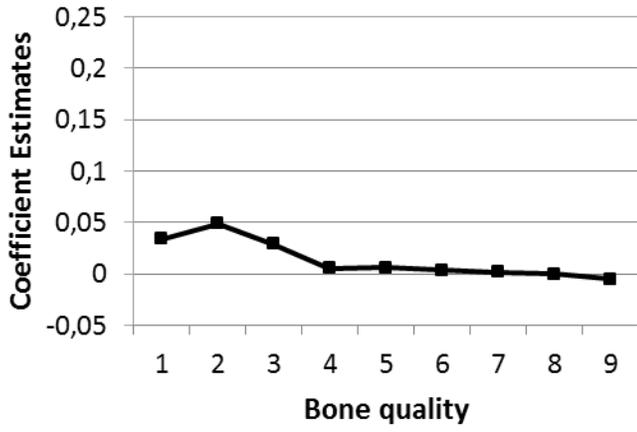
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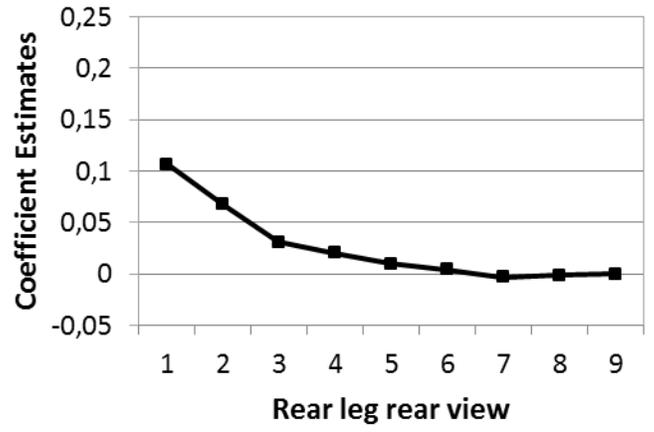
C)



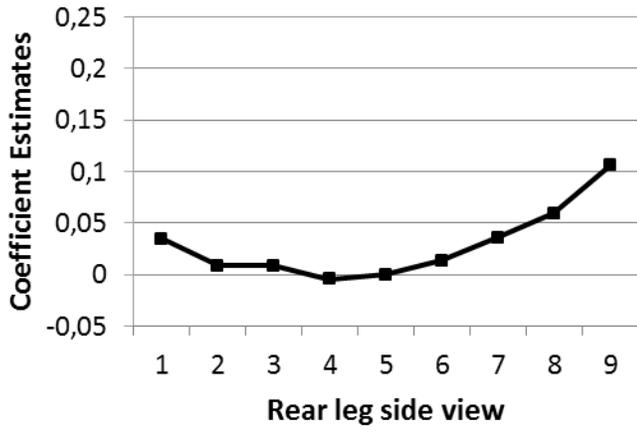
D)



F)



E)



G)

