

Genetic Analyses of Hoof Lesions in Canadian Holsteins Using an Alternative Contemporary Group

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Abstract

A key goal of dairy herds is to reduce the incidence of hoof lesions, which can be achieved both by improving management practices, and through genetic selection. Previous research has shown that data collected by hoof trimmers can be used for genetic evaluation of hoof health. Generally, not all cows in the herd are trimmed during the lactation and the pre-selection process for which cows are presented or not to the hoof trimmer needs to be considered. The objective of this study was to estimate genetic parameters for individual hoof lesions in Canadian Holsteins using an alternative contemporary group, in order to consider all cows in the herd during the period of the hoof trimming sessions, also those that were not examined by the trimmer over the entire lactation. Data were recorded by 26 hoof trimmers serving 365 herds located in Alberta, British Columbia and Ontario, and trained to use a rugged touch-screen computerized lesion recording system. A total of 108,032 hoof trimming sessions from 53,654 cows were collected between 2009 and 2012. Hoof lesions included in the analysis were digital dermatitis, interdigital dermatitis, interdigital hyperplasia, sole hemorrhage, sole ulcer, toe ulcer, and white line lesion. All variables were analyzed as binary traits, as the presence or the absence of the lesions. At first, only cows that were examined by the hoof trimmers were analyzed. Heritabilities (SE) for digital dermatitis, interdigital dermatitis, interdigital hyperplasia, sole hemorrhage, sole ulcer, toe ulcer, and white line lesion were 0.067 (0.007), 0.015 (0.003), 0.036 (0.005), 0.017 (0.003), 0.038 (0.006), 0.006 (0.002), and 0.017 (0.002), respectively. In a second step, cows without a record but present in the herd during the period of the hoof trimming sessions were included in the analyses, and a “no-lesions” label was assigned to all hoof traits for that trimming session. Heritabilities (SE) for digital dermatitis, interdigital dermatitis, interdigital hyperplasia, sole hemorrhage, sole ulcer, toe ulcer, and white line lesion were 0.053 (0.005), 0.011 (0.002), 0.025 (0.004), 0.012 (0.002), 0.031 (0.004), 0.004 (0.001), and 0.012 (0.002), respectively. Despite the low heritability, differences between daughter groups were observed based on the best and worst breeding values of the sires in both the groups. The pre-selection process, which leads cows to be trimmed or not during the lactation, did not affect the heritability and the breeding values estimation.

Key words: hoof lesions, dairy

Introduction

Hoof lesions represent a welfare issue and an economical loss for the farmers, due to the costs associated with treating the lesion, as well as to decreased cow performance. The presence of hoof lesions has been reported to affect milk production (Amory *et al.*, 2004) and to be associated with lower reproductive performance of the cows. Data recorded in Europe and North America shows that 40 to 70% of cows in dairy herds have at least one type of hoof lesion (Chapinal *et al.*, 2013;

Manske *et al.*, 2002). Therefore, a key goal of dairy herds is to reduce the incidence of hoof lesions, which can be achieved both by improving management practices, and through genetic selection. Previous research has shown that data collected by hoof trimmers can be used for genetic evaluation of hoof health (Chapinal *et al.*, 2013). However, not all the cows that are in the herds during the trimming period are examined. The percentage of not-examined cows varies among herds, and including only herds with high percentage of trimmed cows may lead to bias due to

selecting herd with a specific management (van der Spek et al., 2013). Van der Spek *et al.* (2013) reported that the selection of cows for trimming does not affect the heritability. However, the result may change with the prevalence of not trimmed cows in the dataset. The objective of this study was to estimate genetic parameters for individual hoof lesions in Canadian Holsteins using an alternative contemporary group, in order to consider the effect of the pre-selection of cows for trimming.

Materials and Methods

Data were recorded by 26 trimmers serving in 365 herds in Alberta, British Columbia and Ontario between 2009 and 2012. The trimmers involved in the project were trained to use a rugged touch-screen computerized lesion recording system (Hoof Supervisor, Dresser, WI). In order to be included in the analyses, the trimming sessions needed to be recorded in the first 500 d postpartum and a minimum of 10 records per hoof trimming session per herd was required. Because the majority of the cows only had one visit during the lactation (65%), only the first hoof-trimming session was included in the analyses. In order to evaluate the effect of the pre-selection of cows to be presented to the hoof trimmer, two different contemporary groups were created. The first group of cows (Group 1) included only data from cows presented at least one time to the trimmer during the course of lactation for a given herd. The second group (Group 2) included all cows in a given herd that were presented or not to the hoof trimmer during the lactation. When the cows did not have hoof trimming session in a given lactation, the trimming session date was replaced with the first trimming session available in that herd during the lactation, and the value 0 was assigned to all hoof traits for that trimming session. The final data set consisted of 75,559 hoof-trimming records from 53,654 cows, for Group 1, and 104,446 hoof-trimming records from 70,394 cows, for Group 2. The final pedigree files for the first and the second dataset contained 196,879 and 230,267 animals, respectively, and included 7 generations.

Statistical Analysis

Data were analyzed with a linear animal model, using the average information-restricted maximum likelihood (AI-REML) procedure, in the derivative-free approach to multivariate analysis (DMU) package (Madsen and Jensen, 2008). The following linear animal model was applied to all lesion traits:

$$Y_{ijklmn} = \mu + HD_i + TRIMMER_j + PARITY_k + STAGE_l + a_m + pe_n + e_{ijklmn};$$

where Y_{ijklmn} is the observation for one of the lesion traits, μ is the overall mean, HD_i is the fixed effect of herd-date of hoof trimming ($i = 1$ to 3,086), $TRIMMER_j$ is the fixed effect of hoof trimmer ($j = 1$ to 26), $PARITY_k$ is the fixed effect of parity at trimming ($k = 1$ to 7 and more), $STAGE_l$ is the fixed effect of stage of lactation at trimming ($l = 1$ to 16; class1: 0 - 30 d, class2 = 31 - 60 d, ..., class15: 421 - 450 d, and class16: 451 - 500 d after calving), a_m is the random additive genetic animal effect ($m = 1$ to 196,879, for Group 1; or 1 to 230,367, for Group 2), pe_n is the random permanent environmental effect ($n = 1$ to 53,654, for Group 1; or 1 to 70,394, for Group 2), and e_{ijklmn} is the random error term.

Table 1. Percentage of hoof trimming records with hoof lesions including only the first trimming session of the lactation from cows that have been visited at list one time by the trimmer during the lactation (Group 1), and from all the cows that were in the herds during the trimming period (Group 2).

Trait ¹	Group 1	Group 2
Records, n	73,559	104,446
DD, %	20.0	14.1
ID, %	1.9	1.3
IH, %	2.1	1.4
SH, %	4.8	3.4
SU, %	7.0	4.9
TU, %	1.6	1.1
WL, %	5.4	3.8
ANY, %	37.8	26.6

¹DD = Digital Dermatitis; ID = Interdigital Dermatitis; IH = Interdigital Hyperplasia; SH = Sole hemorrhage; SU = Sole ulcer; TU = Toe ulcer; WL = White line lesion; ANY = At least one lesion.

Results and Discussion

The prevalence of hoof lesions is reported in Table 1. On average, 37.8% of cows presented to hoof trimmers were affected by at least one hoof lesion. The more common lesion was digital dermatitis (20% of cows presented to the hoof trimmers affected), followed by sole ulcer and white line lesions (7 and 5.4% of cows presented to the hoof trimmers affected). As expected, the prevalence of hoof lesions decreased when the second contemporary group was considered. The prevalence of cows with at least one lesion drops to around 27%. This prevalence may be underestimated, because some of the cows that have been considered healthy are perhaps cows with not detected lesions. The prevalence of each lesion was 29 to 31% lower when all cows present in a given herd during the trimming period were considered and it was assumed that not trimmed cows were cows without any lesions. This value represents the proportion of not trimmed cows in Group 2 (30% of cows).

Heritabilities of Hoof Lesions

When only hoof-trimmed cows were included in the analysis, estimated heritability of foot lesions ranged from 0.006 to 0.067 (Table 2). Similar heritabilities for hoof lesions have been previously reported (van der Linde *et al.*, 2010; Chapinal *et al.*, 2013). Chapinal *et al.* (2013) reported a heritability of 0.076 for infectious lesions. In the current study, digital dermatitis and interdigital dermatitis were considered as separate traits, and their heritabilities were 0.067 and 0.015, respectively. This result was probably affected by the large difference in prevalence between these two infectious lesions, as heritability estimated with linear model is frequency dependent when binary traits are analyzed.

Similarly, horn lesions were previously reported to have an estimated heritability of 0.028 (Chapinal *et al.*, 2013), ranging in the current study from 0.006 to 0.038 for different horn lesions. Koenig *et al.* (2005) obtained similar results for digital dermatitis, using a logistic approach, and estimated a heritability of 0.073. In the same study, slightly higher heritabilities were shown for sole ulcer and

interdigital hyperplasia (0.086 and 0.104, respectively).

Table 2. Heritability (SE) from univariate linear animal model when only hoof trimmed cows were considered (Group 1), and from all the cows that were in the herds during the trimming period (Group 2).

Trait ¹	h ²	
	Group 1	Group 2
DD	0.067 (0.007)	0.053 (0.005)
ID	0.015 (0.003)	0.011 (0.002)
IH	0.036 (0.005)	0.025 (0.004)
SH	0.017 (0.003)	0.012 (0.002)
SU	0.038 (0.006)	0.031 (0.004)
TU	0.006 (0.002)	0.004 (0.001)
WL	0.017 (0.004)	0.012 (0.002)
ANY	0.065 (0.007)	0.048 (0.005)

¹DD = Digital Dermatitis; ID = Interdigital Dermatitis; IH = Interdigital Hyperplasia; SH = Sole hemorrhage; SU = Sole ulcer; TU = Toe ulcer; WL = White line lesion; ANY = At least one lesion.

The estimated heritability was slightly lower when contemporary group was included (Table 2). However, when heritability on the underlying scale was considered, this difference was reduced (data not shown), indicating that the aforementioned differences were probably mostly related to a lower frequency of hoof lesions in Group 2. In agreement with findings reported by van der Spek *et al.* (2013), these results suggest that the pre-selection process of cows for trimming does not have an effect on the estimated heritabilities.

Estimated Breeding Values

Despite a low heritability of hoof lesions, the distribution of the sire EBV shows exploitable variation among sires. EBVs were reversed in sign. Thus, higher EBV corresponds to sires with higher number of healthy daughters (Table 3). The large variation among sires was similar for the two contemporary groups. For digital dermatitis, the most prevalent lesion, only 10% of daughters of the top 10% sires were affected, while 35.2% of daughters of the bottom 10% of sire were affected for Group 1. For Group 2, only 6.8% of daughters of the top 10% sires were affected, while 27.3% of daughters of the bottom 10% of sire were

affected by digital dermatitis. A large variability has been already reported in a study on Canadian Holstein involving a smaller dataset (Chapinal *et al.*, 2013). The 10 sires with the higher EBV were reported to have 15% of daughters with infection lesions, while 53% of the daughter of the 10 sires with the worst EBV presented infection lesions. The corresponding values for resistance to horn lesions were 7 and 24 % for the 10 sires with the best and worst EBV, respectively. In the current study, for sole ulcer, the more prevalent horn lesion, 3.8 and 2.8% of daughters of the top 10% of sires were affected for Group 1 and Group 2, respectively, while 12.4 and 9.6% of daughters of the worst 10% of sires were affected for Group 1 and Group 2, respectively.

Table 3. Percentage of daughters with hoof lesions from all (average), the top 10% and bottom 10% sires according to their EBV for resistance to digital dermatitis (DD), sole ulcer (SU) and interdigital hyperplasia (IH), when only hoof trimmed cows were considered (Group 1), and when all cows present in the herd at time of hoof trimmer visit were included (Group 2).

Trait ¹	Percentage of daughters with a hoof lesion		
	Average ²	Top 10%	Bottom 10%
Group 1			
DD	20.7	10.0	35.2
IH	2.1	0.6	5.4
SU	6.7	3.8	12.4
Group 2			
DD	14.6	6.8	27.3
IH	1.5	0.6	4.1
SU	4.7	2.8	9.6

¹DD = Digital Dermatitis; IH = Interdigital Hyperplasia; SU = Sole ulcer;

²Only sires with at least 30 daughters in Group 1 were considered (N = 233)

Conclusions

In spite of a low estimated heritability, an exploitable genetic variation for hoof lesions in Canadian Holstein population was found, and therefore, there is a possibility for improvement through direct selection in the

long term. The standardization of hoof lesion data collection is key to study this type of trait. The inclusion of non trimmed cows in the data set did not influence the estimation of heritability for hoof lesions. Further studies using other approaches, such as the use of a threshold model, could be performed in order to better compare the use of different contemporary groups and confirm these results.

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