J. Dairy Sci. 100:1–9
https://doi.org/10.3168/jds.2016-11558

Genetic parameters for hoof health traits estimated with linear and threshold models using alternative cohorts

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ABSTRACT

A national genetic evaluation program for hoof health could be achieved by using hoof lesion data collected directly by hoof trimmers. However, not all cows in the herds during the trimming period are always presented to the hoof trimmer. This preselection process may not be completely random, leading to erroneous estimations of the prevalence of hoof lesions in the herd and inaccuracies in the genetic evaluation. The main objective of this study was to estimate genetic parameters for individual hoof lesions in Canadian Holsteins by using an alternative cohort to consider all cows in the herd during the period of the hoof trimming sessions, including those that were not examined by the trimmer over the entire lactation. A second objective was to compare the estimated heritabilities and breeding values for resistance to hoof lesions obtained with threshold and linear models. Data were recorded by 23 hoof trimmers serving 521 herds located in Alberta, British Columbia, and Ontario. A total of 73,559 hoof-trimming records 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 disease. All variables were analyzed as binary traits, as the presence or the absence of the lesions, using a threshold and a linear animal model. Two different cohorts were created: Cohort 1, which included only cows presented to hoof trimmers, and Cohort 2, which included all cows present in the herd at the time of hoof trimmer visit. Using a threshold model, heritabilities on the observed scale ranged from 0.01 to 0.08 for Cohort 1 and from 0.01 to 0.06 for Cohort 2. Heritabilities estimated with the linear model ranged from 0.01 to 0.07 for Cohort 1 and from 0.01 to 0.05 for Cohort 2. Despite a low heritability, the distribution of the sire breeding values showed large and exploitable variation among sires. Higher breeding values for hoof lesion resistance corresponded to sires with a higher prevalence of healthy daughters. The rank correlations between estimated breeding values ranged from 0.96 to 0.99 when predicted using either one of the 2 cohorts and from 0.94 to 0.99 when predicted using either a threshold or a linear model.

Key words: hoof lesion, threshold model, genetic parameter

INTRODUCTION

Several studies in Europe and North America have reported a high prevalence of hoof lesions in dairy herds, with 40 to 70% of cows having at least 1 type of hoof lesion (Manske et al., 2002; Buch et al., 2011; Chapinal et al., 2013). The large prevalence of hoof lesions represents a significant welfare problem, but it also poses an economic loss for farmers because of the costs associated with treating the lesion and with decreased cow performance. The presence of hoof lesions has been reported to reduce milk production (Ettema et al., 2007; Amory et al., 2008) and to be associated with a lower reproductive performance of cows (Hultgren et al., 2004). Therefore, reducing the incidence of hoof lesions is important. This reduction can be achieved through improvement in management practices and possibly through genetic selection. Previous studies of Canadian Holsteins showed that hoof lesion data collected by hoof trimmers can be used for genetic evaluation of hoof health (Chapinal et al., 2013). However, not all cows in the herds are usually presented to the hoof trimmer during the trimming period, and the reasons for selection are usually not reported. Whether a cow is presented to the hoof trimmer is unlikely to be random because cows showing hoof problems may be selected for examination over cows that appear to be healthy.

Received June 3, 2016.
Accepted December 5, 2016.
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This selection could result in erroneous estimations of the prevalence of hoof lesions on the farm and may also affect the genetic evaluation of those traits. Considering only herds with a high percentage of trimmed cows may lead to bias through selecting herds with a specific management strategy or herds with more lame cows (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 nontrimmed cows in the population.

Threshold models are theoretically better for use when binary traits, such as the presence or absence of a hoof lesion, are considered. Moreover, they offer a better comparison between traits that have different incidences because linear models are known to be frequency dependent when applied to binary traits (Gianola, 1982). However, linear models are computationally more practical for the scale and scope of routine genetic evaluations. Furthermore, previous work did not show relevant differences between sire rankings for the 2 models (Weller et al., 1988; Hagger and Hofer, 1990).

The objectives of this study were (1) to estimate genetic parameters for individual hoof lesions in Canadian Holsteins using an alternative cohort to consider all cows in the herd during the period of the hoof trimming sessions, including those that were not examined by the hoof trimmer over the entire lactation; and (2) to compare the estimated heritabilities and breeding values for resistance to hoof lesions obtained with threshold and linear models.

MATERIALS AND METHODS

Data

Hoof lesions were recorded in 521 herds located in Alberta (from June 2009 to November 2012), British Columbia (from October 2010 to March 2012), and Ontario (from August 2011 to July 2012). Data were recorded by 23 trimmers trained to use a rugged touchscreen computerized lesion recording system (Hoof Supervisor, Dresser, WI) based on lesion descriptions proposed by the International Lameness Committee, a global collaboration of researchers, veterinarians, academics, and hoof trimming professionals. Hoof trimmers were also provided with a lesion severity scoring guide containing example photos of each lesion created by Alberta hoof trimmers to facilitate the correct denomination of the lesion and to more consistently score lesion severity (Alberta Dairy Hoof Health Project, 2014). Hoof lesions included in the analysis were digital dermatitis (**DD**), interdigital dermatitis (**ID**), interdigital hyperplasia (**IH**), sole hemorrhage (**SH**), sole ulcer (**SU**), toe ulcer (**TU**), and white line diseases (**WL**). Due to very low frequency, corkscrew claw, heel horn erosion, foot rot, axial fissure, vertical fissure, horizontal fissure, thin sole, and unidentified lesions were combined into a single group denominated "other lesions" and were considered only for descriptive purpose. Finally, a variable was created that included the absence or the presence of any of the hoof lesions previously described. All traits were coded as binary variables (0; 1), where 1 was assigned to the presence of a lesion. The initial data set included 126,621 hoof-trimming records. Trimming sessions with missing calving date (9.2%) and trimming data recorded after 500 d postpartum (2.6%) were deleted. If the trimming date did not correspond to the period in which the cow was in the herd (1.3%), the trimming session was deleted. A minimum of 10 records per hoof trimming session per herd were required to include data for any particular day in the analysis (1.3% of the records were deleted). The majority of the cows (65%) were trimmed only once during the lactation; therefore, only the first hoof trimming session was included in the analyses, as previously described by Chapinal et al. (2013). Finally, 2 different cohorts were created. The first cohort (Cohort 1) included only data from cows that had been visited at least once by the trimmer during the course of lactation. In the second cohort (Cohort 2), all cows that were in a given herd during the trimming period were included in the analyses, including cows that did not have any hoof data during the lactation. In such cases, the trimming session date was replaced with the first trimming session available in that herd during the lactation, and a value of 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 when only trimmed cows were considered (Cohort 1) and 104,446 records from 70,394 cows in Cohort 2. The final pedigree files for the first and the second data set contained 196,879 animals and 230,267 animals, respectively, and included 7 previous generations.

Models

When linear models are applied to binary traits, the heritability estimates are frequency dependent (Gianola, 1982). Including the nontrimmed cows in the data set (Cohort 2) changed the incidence of each trait, decreasing the prevalence of each lesion. To account for this decrease and to better compare the 2 cohorts, a threshold approach was applied. Although threshold models are more appropriate to analyze binary traits, linear models are easier to implement for the scale and scope of a routine genetic evaluation. Therefore,