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Genetic parameters for hoof lesions and their relationship with feet and leg traits in Canadian Holstein cows

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ABSTRACT

The objectives were (1) to estimate the genetic parameters and breeding values of hoof lesions, (2) to estimate the phenotypic effect of each feet and legs conformation traits on hoof lesions, and (3) to estimate genetic correlations between hoof lesions with feet and legs conformation traits. The presence or absence of specific hoof lesions was recorded for each hoof. Lesions were classified into infectious (digital and interdigital dermatitis, foot rot, and heel erosion), horn (sole and toe ulcer, sole hemorrhage, and white line disease), and other lesions (interdigital hyperplasia, fissures, thin soles, and corkscrew claw). A total of 34,905 hoof health records from 27,179 cows and 365 herds, collected by 18 different hoof-trimmers in Ontario, Alberta, and British Columbia, were analyzed using linear animal models. In addition, 5 feet and leg conformation traits (foot angle, heel depth, bone quality, rear leg side view, and rear leg rear view) and locomotion from primiparous cows were considered (n = 11,419 and 6,966 cows, for conformation traits and locomotion, respectively). At least one lesion was found in nearly 40% of the hoof trimming records. The heritability estimates for hoof lesions ranged from 0.01 for front horn lesions to 0.09 for rear infectious lesions. Despite the low heritability estimates, we observed large variability in sire estimated breeding value (EBV) for resistance to hoof lesions. Positive genetic correlations were found between the occurrence of front and rear infectious lesions (0.77) and between front and rear horn lesions (0.61), but not between infectious and horn lesions (0.08). For most of the conformation traits, low scores were phenotypically associated with higher incidence of horn lesions, whereas we found no evidence of a phenotypic effect of feet and leg traits on infectious lesions. The heritability of the conformation traits ranged from 0.04 for rear leg rear view to 0.22 for bone quality, whereas that for locomotion was 0.03. The genetic correlations between hoof lesions and conformation traits were low to moderate, yet most of the estimates were associated with high standard errors. In conclusion, although hoof lesions are lowly heritable traits, sufficient genetic variation exists (as evidenced by large variability in sire EBV) for genetic improvement through direct selection in the long term. Standardization of hoof health data collection is encouraged.

Key words: infectious lesion, horn lesion, locomotion, genetic parameter

INTRODUCTION

Maintaining hoof health is a challenge in modern dairy herds. Recent studies in North America and Europe have reported prevalences of 40 to 70% of the cows with at least one hoof lesion (Manske et al., 2002; Sogstad et al., 2005; Buch et al., 2011). Hoof lesions compromise the welfare of animals (Whay et al., 2003) and can result in reduced milk yield (Warnick et al., 2001; Amory et al., 2008), reduced fertility (Hernández et al., 2001; Meléndez et al., 2003), and increased risk of premature culling (Rajala-Schultz and Gröhn, 1999; Booth et al., 2004). Many factors affect the risk of hoof lesions, including environmental factors, such as the design of the facilities and management practices (Barker et al., 2009; Cook and Nordlund, 2009; Cramer et al., 2009), and genetics (van der Waaij et al., 2005; van der Linde et al., 2010; Buch et al., 2011). Therefore, the incidence of hoof lesions can be reduced by improved management practices and genetic selection.

Hoof lesions are heritable and, although estimated heritability estimates are low (ranging from 0.01 to 0.20; Koenig et al., 2005; van der Waaij et al., 2005; van der Linde et al., 2010), long-term improvement of hoof health can be achieved by direct genetic selection

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for hoof lesion resistance. Several studies showed only low to moderate correlations between hoof lesions and feet and leg conformation traits (Onyiro et al., 2008; Laursen et al., 2009; van der Linde et al., 2010). As a result, indirect genetic selection for hoof lesion resistance has not been very effective. However, genetic correlations differ depending on the definition of the conformation traits and the population studied. Most of the studies on genetic parameters for hoof lesions have been conducted in Europe (Laursen et al., 2009; van der Linde et al., 2010; Buch et al., 2011). Thus, the potential of hoof lesion data for direct genetic selection for hoof health and of conformation data to predict and indirectly select for hoof health in North America has to be investigated.

Hoof lesions have traditionally been classified according to their etiology and pathogenesis (Greenough, 2007) into infectious or partly infectious lesions (e.g., digital and interdigital dermatitis, foot rot, and heel erosion), mostly related to environmental hygiene, and horn lesions (e.g., sole and toe ulcer, sole hemorrhage, and white line disease), mostly caused by metabolic or mechanical factors. Previous studies reported strong genetic correlations between specific lesions within each category (van der Waaij et al., 2005; van der Linde et al., 2010; Buch et al., 2011) but, to our best knowledge, genetic parameters for these 2 categories have not been estimated. Thus, the objectives of the current study were (1) to estimate the genetic parameters and breeding values of hoof infectious and horn lesions, (2) to estimate the phenotypic effect of each feet and legs conformation trait on hoof lesions, and (3) to estimate genetic correlations between hoof lesions with feet and legs conformation traits.

MATERIALS AND METHODS

Data Description

Hoof lesions were recorded by hoof trimmers from March 2004 to July 2005 in Ontario, from June 2009 to October 2011 in Alberta, and from October 2010 to October 2011 in British Columbia, Canada. Hoof trimmers visited farms according to the herd standard hoof-trimming protocol. Commonly, cows were routinely hoof trimmed once or twice per lactation, or if clinical signs were detected at the time of the hoof trimmer's visit. However, the reason for hoof trimming was not recorded for logistic reasons (i.e., farmers would likely have to prepare 2 separate lists of cows for the hoof trimmer, and the hoof trimmer would have to make a distinction when entering the data). The data recorded in Ontario were part of an observational study (Cramer et al., 2008), whereas the data recorded in Alberta and British Columbia were part of the ongoing Alberta Dairy Hoof Health Project (details on which can be found at www.hoofhealth.ca). In brief, 7 hoof trimmers in Alberta and 6 hoof trimmers in British Columbia were trained to use a rugged touch-screen computerized lesion recording system (Hoof Supervisor, Dresser, WI). This system facilitates the routine and consistent collection of hoof lesion data, based on lesion descriptions proposed by the International Lameness Committee, a global collaboration of researchers, veterinarians, academics, and hoof-trimming professionals.

As the majority of the cows (68%) were only hoof trimmed once during the same lactation, only the first hoof-trimming session was included in the analyses, similar to the methods of Buch et al. (2011). Furthermore, a preliminary analysis showed similar results when genetic parameters were estimated using the last hoof-trimming session of the lactation. Records taken more than 500 d after calving were discarded. Four seasons of hoof trimming were defined: January to March, April to June, July to September, and October to December, and the variable herd-year-season was created. The herd-year-season categories with fewer than 5 hoof-trimming records were discarded. The final data set consisted of 34,905 hoof-trimming records from 27,179 cows from 365 herds, collected by 18 different hoof trimmers.

Hoof lesions were recorded as presence or absence of specific hoof lesions in each hoof: sole and toe ulcer, sole hemorrhage, white line disease (separation and abscesses), digital and interdigital dermatitis, foot rot, heel erosion, interdigital hyperplasia, fissures, thin soles, and corkscrew claw. For the analyses, lesions were classified according to their etiology and pathogenesis (Greenough, 2007) into (1) infectious or partly infectious lesions (digital and interdigital dermatitis, foot rot, and heel erosion), (2) horn lesions, caused by metabolic or mechanical factors (sole and toe ulcer, sole hemorrhage, and white line disease), and (3) other lesions (interdigital hyperplasia, fissures, thin soles, and corkscrew claw). This classification was chosen to (a) give the study a practical approach, because there is no intention, in the near future, to develop a genetic evaluation system for each individual lesion trait, (b) prevent the misclassification of diseases that have similar etiology and pathogenesis and that can be hard to distinguish in routinely collected data sets, and (c) avoid the analysis of traits that are highly correlated as if they were independent traits. Nine hoof lesion binary traits (0 = no lesion, 1 = at least 1 lesion) were created at the cow level: (a) having at least one lesion in any hoof, (b) having at least one lesion in a front hoof, (c) having at least one lesion in a rear hoof, (d) having at least one infectious lesion in any hoof, (e) having at least one horn