J. Dairy Sci. 96:6070–6078
http://dx.doi.org/10.3168/jds.2013-6833

Genetic parameters for claw disorders and the effect of preselecting cows for trimming

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ABSTRACT

Claw disorders are important traits relevant to dairy cattle breeding from an economical and welfare point of view. Selection for reduced claw disorders can be based on hoof trimmer records. Typically, not all cows in a herd are trimmed. Our objectives were to estimate heritabilities and genetic correlations for claw disorders and investigate the effect of selecting cows for trimming. The data set contained 50,238 cows, of which 20,474 cows had at least one claw trimming record, with a total of 29,994 records. Six claw trimmers scored 14 different claw disorders: abscess (AB), corkscrew claw (CC), (inter-)digital dermatitis or heel erosion (DER), double sole (DS), hardship groove (HG), interdigital hyperplasia (IH), interdigital phlegmon (IP), sand crack (SC), super-foul (SF), sole hemorrhage (SH), sole injury (SI), sole ulcer (SU), white line separation (WLS), yellow discoloration of the sole (YD), and a combined claw disorder trait. Frequencies of the claw disorders for trimmed cows ranged from 0.1% (CC, YD, HG) to 23.8% (DER). More than half of the cows scored had at least one claw disorder. Heritability on the observed scale ranged from 0.02 (DS, SH) to 0.14 (IH) and on the underlying scale from 0.05 to 0.43 in trimmed cows. Genetic correlations between laminitis-related claw disorders were moderate to high, and the same was found for hygiene-related claw disorders. The effect of selecting cows for trimming was first investigated by including untrimmed cows in the analyses and assuming they were not affected by claw disorders. Heritabilities on the underlying scale showed only minor changes. Second, different subsets of the data were created based on the percentage of trimmed cows in the herd. Heritabilities for IH, DER, and SU tended to decrease when a higher percentage of cows in the herd were trimmed. Finally, a bivariate model with a claw disorder and the trait "trimming status" was used, but heritabilities were similar. Heritability for trimming status was relatively high (0.09). Genetic correlations of trimming status with claw disorders were generally moderate to high. To conclude, the effect of selecting cows for trimming on the heritability for claw disorders is negligible. Selecting herds with a high fraction of cows being trimmed tended to decrease heritability. Trimming status, as such, is a heritable trait and correlated with claw disorders and is therefore an interesting trait to include in the genetic evaluation.
Key words: foot health, dairy cattle, heritability, trimming status

INTRODUCTION

Claw disorders are among the most important health traits in dairy cattle breeding, with prevalences >70% (Manske et al., 2002; Somers et al., 2003; van der Waaij et al., 2005; Capion et al., 2009). Claw disorders are usually painful and therefore affect cow welfare (Enting et al., 1997; Bruijnis et al., 2012a,b). In addition, clinical and subclinical claw disorders cause considerable economic losses (Enting et al., 1997; Bruijnis et al., 2010, 2012a,b); claw and leg disorders are the third most economically important trait in dairy cattle after mastitis and fertility problems (Enting et al., 1997). The economic loss due to claw disorders is estimated to be $75 per cow per year (Bruijnis et al., 2010).

Claw disorders can be divided into different categories according to their etiology: hygiene-related claw disorders [e.g., (inter-)digital dermatitis, interdigital phlegmon, heel horn erosion, and interdigital hyperplasia], nutrition- or laminitis-related claw disorders (e.g., sole hemorrhage, sole ulcer, double sole, and white line problems), and traumatic disorders (e.g., excessive abrasion of the sole and injuries).

Several risk factors for claw disorders have been reported; for example, hygiene, grazing time, herd size, nutrition, parity, and stage of lactation (Toussaint-Raven et al., 1985; Faye and Lescourret, 1989; Enevoldsen et al., 1991a,b; Philipot et al., 1994; Koenig et al., 2005; Sogstad et al., 2005, 2007; Somers et al., 2005a,b; Barker et al., 2009; Chapinal et al., 2010; Kujala et al., 2010). Holstein cows were at higher risk of develop-

Received March 20, 2013.
Accepted June 5, 2013.
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ing claw disorders compared with Meuse Rhine IJssel (Holzhauer et al., 2006), Norwegian cattle (Baird et al., 2009), and Ayrshire cows (Kujala et al., 2009). These breed differences indicate a genetic background for claw health. Genetic selection provides a means to improve claw health but requires genetic variation. Heritabilities of multiple claw disorders scored by claw trimmers have been estimated previously and range from 0.01 to 0.14 (Huang and Shanks, 1995; van der Waaij et al., 2005; van der Linde et al., 2010).

In general, data on claw disorders are collected by hoof trimmers during regular farm visits. Typically, the farmer selects the cows to be trimmed. Having observations on a selected sample might affect the estimated heritabilities. By selecting herds with a high percentage of cows trimmed, the preselection of cows to be trimmed can be reduced because most cows are trimmed; for example, van der Waaij et al. (2005) only included herds with at least 70% of the cows trimmed, and van der Linde et al. (2010) only included herds with at least 50% of the cows trimmed. However, selection of specific herds might also have consequences for the estimated genetic parameters. The objective of this research is to estimate the heritability for different claw disorders of Holstein dairy cows and to investigate the effect of untrimmed cows on the heritability estimates. In addition, genetic and phenotypic correlations among claw disorders will be estimated.

MATERIALS AND METHODS

Data

The initial data set contained 56,612 Holstein-Friesian cows. Cows with both parents unknown or with 2 different trimming records on the same date were removed. The final data set contained 50,238 cows, of which 20,474 cows had a claw trimming record with a total of 29,994 claw trimming records. The total number of animals in the pedigree was 212,536. The 50,238 cows descended from 3,603 sires with an average of 13 daughters per sire. The trimmed cows descended from 1,746 sires with an average of 17 daughters per sire, and 333 sires had at least 10 daughters with trimming records. Data were collected by 6 professional claw trimmers, from January 2007 through February 2012 during routine visits to 574 dairy farms in France. Repeated trimming occurred both within and across lactations; 69% of the cows had 1 trimming record, 20% had 2 trimming records, and 11% had 3 or more trimming records. Claw disorders were recorded for the hind legs and scored as a binary trait: 0 = no claw disorder, 1 = claw disorder in at least one hind leg. Table 1 gives an overview of the claw disorders that were scored and their abbreviations and definitions. Recorded claw disorders were abscess (**AB**), corkscrew claw (**CC**), digital dermatitis (**DD**), double sole (**DS**), heel horn erosion (**HE**), hardship groove (**HG**), interdigital dermatitis (**ID**), interdigital hyperplasia (**IH**), interdigital phlegmon (**IP**), sand crack (**SC**), super-foul (**SF**), sole hemorrhage (**SH**), sole injury (**SI**), sole ulcer (**SU**), white line separation (**WLS**), and yellow discoloration of the sole (**YD**). We combined DD, ID and HE into one disorder, called dermatitis-erosion (**DER**), because of inconsistency in recording individual lesions between trimmers. A combined claw disorder trait that included all disorders was created indicating the absence (score 0) or presence (score 1) of at least one claw disorder.

The farmer decided which cows were to be trimmed. As a result, not all cows present in a herd were trimmed during a routine visit of the claw trimmers. In addition, information was available on cows present in a herd at the moment of trimming (e.g., parity, stage of lactation, and pedigree).

Statistical Analyses

The following linear animal model was used:

$$\begin{aligned} Y_{ijklmn} = \; & \mu + H_i + YS_j + P_k + L_l \\ & + Animal_m + PE_n + e_{ijklmn}, \end{aligned}$$

where Y_{ijklmn} is a claw disorder; μ is the overall mean; H_i is the fixed effect of herd i; YS_j is the fixed effect of year-season of trimming j (season was defined as spring: March–May, summer: June–August, autumn: September–November, winter: December–February); P_k is the fixed effect of the kth parity ($k = 1$, 2, 3, and ≥ 4); L_l is the fixed effect of the lth lactation stage at trimming ($l = 1$ to 10, group 1–9 are 50 d each, with the first group from 1 to 50 d, the second group from 50 to 100 d, and so on; cows with lactation stage $\geq$450 d were combined in group 10); $Animal_m$ is the random additive genetic effect of the mth cow $N \sim \left(0, \mathbf{A}\sigma_a^2\right)$, where $\mathbf{A}$ is the additive genetic relationships matrix among cows; PE_n is the random permanent environment effect $N \sim \left(0, \mathbf{I}\sigma_{pe}^2\right)$; and e_{ijklmn} is the random residual effect $N \sim \left(0, \mathbf{I}\sigma_e^2\right)$, where $\mathbf{I}$ is the identity matrix. Heritabilities and repeatabilities were estimated based on univariate analyses. Heritability (h^2) was calculated as

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_{pe}^2 + \sigma_e^2},$$

and repeatability (r) as