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Genetic evaluation of claw health traits accounting for potential preselection of cows to be trimmed

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ABSTRACT

Claw lesions are one of the most important health issues in dairy cattle. Although the frequency of claw lesions depends greatly on herd management, the frequency can be lowered through genetic selection. A genetic evaluation could be developed based on trimming records collected by claw trimmers; however, not all cows present in a herd are usually selected by the breeder to be trimmed. The objectives of this study were to investigate the importance of the preselection of cows for trimming, to account for this preselection, and to estimate genetic parameters of claw health traits. The final data set contained 25,511 trimming records of French Holstein cows. Analyzed claw lesion traits were digital dermatitis, heel horn erosion, interdigital hyperplasia, sole hemorrhage circumscribed, sole hemorrhage diffused, sole ulcer, and white line fissure. All traits were analyzed as binary traits in a multitrait linear animal model. Three scenarios were considered: including only trimmed cows in a 7-trait model (scenario 1); or trimmed cows and contemporary cows not trimmed but present at the time of a visit (considering that nontrimmed cows were healthy) in a 7-trait model (scenario 2); or trimmed cows and contemporary cows not trimmed but present at the time of a visit (considering lesion records for trimmed cows only), in an 8-trait model, including a 0/1 trimming status trait (scenario 3). For scenario 3, heritability estimates ranged from 0.02 to 0.09 on the observed scale. Genetic correlations clearly revealed 2 groups of traits (digital dermatitis, heel horn erosion, and interdigital hyperplasia on the one hand, and sole hemorrhage circumscribed, sole hemorrhage diffused, sole ulcer, and white line fissure on the other hand). Heritabilities on

the underlying scale did not vary much depending on the scenario: the effect of the preselection of cows for trimming on the estimation of heritabilities appeared to be negligible. However, including untrimmed cows as healthy caused bias in the estimation of genetic correlations. The use of a trimming status trait to account for preselection appears promising, as it allows consideration of the exhaustive population of cows present at a time a trimmer visited a farm without causing bias in genetic parameters.

Key words: claw lesion, genetic parameter, dairy cattle

INTRODUCTION

Claw lesions are one of the most important health issues in dairy cattle. They are quite frequent: in some studies more than 50% of cows show at least one lesion (e.g., Manske et al., 2002; Van der Linde et al., 2010; Van der Spek et al., 2013). Claw lesions have important consequences, both in terms of animal welfare and profitability of herds (Enting et al., 1997; Van der Waaij et al., 2005; Charfeddine and P rez-Cabal, 2017). Reducing the prevalence of claw lesions is therefore of major interest in dairy farms. Claw health traits have a low but nonzero heritability, indicating a possibility of improvement through genetic selection, but also that the frequencies of claw disorders can mainly be reduced through proper herd management. Only a few countries have developed a national genetic evaluation for claw health traits (the Netherlands, Stoop et al., 2010; Denmark, Finland, and Sweden, Johansson et al., 2011; with a first evaluation in Sweden in 2006, Eriksson, 2006), and among these countries claw health phenotypes are often available only on a subset of cows: those scored by trimmers when they visit herds. As a consequence, a possible preselection effect of cows for trimming may affect genetic evaluations, particularly when the recording of claw health information is only

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recent and hence when the subset of phenotyped cows is small. However, the percentage of trimmed cows usually varies from one herd to another. Selecting only herds with high trimming proportions to ensure that almost all cows have been scored by a trimmer may allow for a reduction of the preselection but might also cause biases (van der Spek et al., 2013) because only herds with a specific herd management would be selected.

The objectives of the present study were to investigate the importance of the preselection of cows for trimming in Holstein herds in France, to compare the ways of accounting for this preselection and to assess their effect on the estimation of genetic parameters of claw health traits.

MATERIALS AND METHODS

Data

The phenotypes used were trimming information recorded from April 2014 to August 2016 on French Holstein cows by professional trimmers who followed the same training. The trimmers visited farms when called by farmers to trim their cows; the data recording itself was free of charge for the farmers. Trimming records from a cow were eliminated if the cow was not of the Holstein breed, was in lactation 4 or higher, had one or both parents unknown, was over 550 DIM at trimming, or was not registered for official milk recording. Only hind claw information was kept because front hooves were not often trimmed and showed fewer lesions than hind hooves. If for a given cow one of the hind claws was not scored, the cow record was eliminated. As most of the cows (84%) had only one trimming information, only the first trimming record of each cow was kept. Records were also eliminated if the trimmer recorded information for less than 5 cows during a given visit.

In some parts of the study nontrimmed cows were also included; these were cows present in the herd when the trimmer came but not scored by the trimmer; the nontrimmed cows were edited using the same rules as the trimmed cows (lactation stage, parity...). As for the trimmed cows, only the first information was kept for nontrimmed cows (i.e., only one observation for the whole productive life, not per lactation), mainly because the number of repeated records was too low for a proper estimation of repeatability. The trimming date associated with nontrimmed cows was the date of the first trimming in the herd on which they were present.

The final data sets contained 25,511 cows when considering trimmed cows only and 57,399 cows when including also nontrimmed cows. The pedigree of the cows was traced back for 4 generations, leading to pedigree files of 85,040 animals when including only trimmed

cows as phenotyped animals and 164,836 animals when including trimmed and nontrimmed cows.

Traits

The lesion traits considered were those defined according to the International Committee for Animal Recording (ICAR) claw health atlas (ICAR, 2015), with minor differences: sole hemorrhage circumscribed (SHC) was only recorded by the trimmers if it was present on the specific spot of the sole where a sole ulcer (SU) usually appears; SU was only recorded by the trimmers if it was present at its usual spot on the sole, whereas it can be recorded on any spot of the sole according to the ICAR atlas; and white line fissure (WLF) was recorded jointly with white line abscess (see Institut de l'Élevage, 2015 for details), whereas WLF are recorded as 2 different lesions in the ICAR atlas. Only traits with a prevalence of at least 5% in the data set were kept in this study: digital dermatitis (DD), heel horn erosion (HHE), interdigital hyperplasia (IH), SHC, sole hemorrhage diffused (SHD), SU, WLF, in which double sole was also included. The traits DD, HHE, and IH can be classified as infectious traits and SHC, SHD, SU, and WLF as noninfectious traits. A cow was given a score of 1 for a lesion if the lesion was observed by the trimmer, 0 if it was not. When nontrimmed cows were considered as healthy for all lesion traits, they were assigned a score of 0 for all lesions.

To assess the effect of the preselection of cows for trimming, a trimming status trait was created (see below). A cow's value for trimming status was 1 if she was trimmed and 0 otherwise.

Statistical Analysis

Genetic parameters for claw health traits were estimated fitting a multitrait linear animal model, using the restricted maximum likelihood methodology with the WOMBAT software (Meyer, 2007). The linear model was

$$y_{ijkl} = \mu + hv_i + p_j + s_k + a_l + \varepsilon_{ijkl},$$

where y_{ijkl} is the observed performance for DD, HHE, IH, SHC, SHD, SU, or WLF; μ is the general mean; hv_i is the herd-date of visit contemporary group; p_j is the parity of the cow; s_k is the lactation stage of the cow (1–50 d, 51–100 d, 101–150 d, 151–200 d, 201–250 d, 251–300 d, 301–350 d, 351–400 d, and 401–550 d); a_l is the animal's additive genetic value treated as a random effect with a variance-covariance matrix proportional

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