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Investigating the genetic background of bovine digital dermatitis using improved definitions of clinical status

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ABSTRACT

Bovine digital dermatitis (DD) is an increasing claw health problem in all cattle production systems worldwide. The objective of this study was to evaluate the use of an improved scoring of the clinical status for DD via M-scores accounting for the dynamics of the disease; that is, the transitions from one stage to another. The newly defined traits were then subjected to a genetic analysis to determine the genetic background for susceptibility to DD. Data consisted of 6,444 clinical observations from 729 Holstein heifers in a commercial dairy herd, collected applying the M-score system. The M-score system is a classification scheme for stages of DD that allows a macroscopic scoring based on clinical inspections of the bovine foot, thus it describes the stages of lesion development. The M-scores were used to define new DD trait definitions with different complexities. Linear mixed models and logistic models were used to identify fixed environmental effects and to estimate variance components. In total, 68% of all observations showed no DD status, whereas 11% were scored as infectious for and affected by DD, and 21% of all observations exhibited an affected but noninfectious status. For all traits, the probability of occurrence and clinical status were associated with age at observation and period of observation. Risk of becoming infected increased with age, and month of observation significantly affected all traits. Identification of the optimal month concerning DD herd status was consistent for all trait definitions; the last month of the trial was identified. In contrast, months exhibiting the highest least squares means of transformed scores differed depending on trait definition. In this respect, traits that can distinguish between healthy, infectious, and noninfectious stages of DD can account for the infectious potential of the herd and can serve as an alert tool. Estimates of heritabilities of traits studied ranged between 0.19 (±0.11) and 0.52 (±0.17), revealing a tendency for higher values for more complex trait definitions. In terms of genetic selection, all trait definitions identified the best (i.e., most resistant) animals, but only the new trait definitions were able to distinguish between animals with average and high predispositions for DD. Considering repeated measurements resulted in heritability estimates ranging between 0.13 (±0.05) and 0.29 (±0.10).

Key words: hoof disorder, digital dermatitis, M-score, genetic parameter

INTRODUCTION

Bovine digital dermatitis (**DD**) is an infectious claw disease (Cheli and Mortellaro, 1974) affecting cattle in all production systems (Rodriguez-Lainz et al., 1999; Wells et al., 1999; Cramer et al., 2009). Herd prevalence levels of DD are wide ranging and associated with multiple risk factors affecting DD incidence (Holzhauer et al., 2006; Cramer et al., 2009; Schöpke et al., 2013). For instance, breed, parity, stage of lactation (Holzhauer et al., 2006), and BCS (Schöpke et al., 2013) influence herd prevalences.

Among all disorders of the bovine hoof, DD is known to generate high costs (Bruijnis et al., 2010; Gomez et al., 2015) and it impairs animal welfare by causing painful lesions along the coronary band. Key parameters limiting the severity of DD infections are early identification and the efficiency of topical treatment (Döpfer et al., 2012), making both detection and treatment important to achieve a "manageable endemic state of disease" (Döpfer and Bonino Morlán, 2008). Different clinical stages and the transitions between these stages characterize the dynamics of DD in groups of cattle. Döpfer et al. (1997) established a classification system for stages of DD that allows a macroscopic scoring based on clinical inspections of the bovine foot. This so-called M-scale system describes the stages of lesion development. The 5 M-stages for clinical stages of DD are as follows: **M0** = normal skin appearance; **M1** = small focal circumscribed damage of the epithelium at the skin horn border (<2.0 cm in diameter); **M2** = circumscribed ulcerative skin defect with a red or

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greyish surface that can have a white epithelial margin and overlong hair (>2.0 cm in diameter); **M3** = the healing stage of DD, after the M2 lesion has covered itself with a scab; **M4** = chronic stage of DD that is characterized by a thickened epithelium or proliferative growth of the epithelium (heel warts); and **M4.1** = the chronic stage as described under M4, but with an M1 lesion within its perimeter (Döpfer et al., 1997; Berry et al., 2012). Berry et al. (2012), Holzhauer et al. (2008), and Gomez et al. (2014) describe the scoring system for DD in detail and present successful applications of the scoring method. The scoring system also allows the categorization of "DD cow types" with regard to the number of acute clinical DD events (Döpfer et al., 2004; Holzhauer et al., 2008). These DD cow types are precisely defined in Döpfer et al. (2004), Holzhauer et al. (2006), and Gomez et al. (2014). Based on the recurrence of M2 lesions, cows are classified into type I: cows that never develop M2 stages; type II: cows that develop M2 stages once and never again for prolonged period, and type III: cows that develop M2 stages repeatedly; for example, every 14 d. These DD cow types have been shown to differ in their immune response against *Treponema* spp. (Gomez et al., 2014), which are considered to be the most important bacterial agents during the pathogenesis of DD (e.g., Evans et al., 2008; Klitgaard et al., 2008; Yano et al., 2010; Gomez et al., 2012; Zinicola et al., 2015).

Despite knowledge regarding the different stages of DD, estimations of co-variance components have neglected the dynamics of DD and the approaches are predominantly based on simple trait definitions of classifying cows, such as affected or unaffected by DD. The resulting dichotomous response variables have been analyzed using linear, threshold, and recursive models (König et al., 2008; Swalve et al., 2011; Häggman and Juga, 2013). Resulting estimates for the heritability of DD vary between 0.05 and 0.14. This range reflects the variety in the types of models used for analysis, including linear as well as threshold models. The lower estimates (0.05) arise from analyses using recursive models (König et al., 2008). Schöpke et al. (2013) estimated a comparatively high heritability for DD (0.14), possibly attributable to the study design, in which the same person evaluated all animals for the presence of DD. The application of threshold random regression models revealed a varying genetic background during the course of lactation with higher heritabilities for DD directly after calving; for example, 0.28 at DIM 6 and 0.23 at DIM 20 (Gernand and König, 2014). Grouping different diseases into "dermatitis" resulted in slightly varying estimates (Buch et al., 2011; Ødegård et al., 2013; van der Spek et al., 2013). Stoop et al. (2010) and van der Linde et al. (2010) used a categorical trait definition (4 classes of severity) and obtained heritability estimates for DD of 0.09 applying linear models. Genetic-statistical analyses based on data from the macroscopic scoring system of different clinical stages using the M-scale (Döpfer et al., 1997; Berry et al., 2012) have not been reported in the literature and observations regarding transitions between stages of DD have not been used for genetic-statistical analyses.

The hypothesis of the present study was that application of the more detailed scoring system for DD stages, in addition to records about transitions between clinical stages of DD, would improve the phenotype definition of DD, and consequently allow for better assessment of the genetic background for this infectious disease. The purpose of this study was to define new traits based on clinical inspections of cows' feet using the M-scale, to identify factors associated with these traits, and to estimate genetic parameters for the DD traits defined during the study.

MATERIALS AND METHODS

Data were collected in a commercial Holstein dairy herd (in Wisconsin, United States) that was endemically affected by DD. The number of pregnant heifers initially included in the study was 729. The total duration of the study was 15 mo, from July 2011 to September 2012, with a mean (SD) individual cow observation time of 175.6 d (20.1), a minimum of 2.6 mo, and a maximum of 7.4 mo. The heifers' back feet were inspected in a stand-up chute (M-Series; Comfort Hoof Care Inc., Baraboo, WI) on a regular basis starting when the heifer moved into a pregnant-heifer pen. Feet evaluations occurred at least 3 times per heifer during the study. Additional observations between regular evaluations were available for 61.3% of the heifers. Additional observations were usually, but not always, associated with topical treatments and follow-up evaluations to check clinical cure posttreatment. Treatment was the application of 15 mL of dry tetracycline-HCl powder (Tet-Sol 324; Alpharma Inc., Fort Lee, NJ) directly on the cleaned surface of an active DD lesion matching the inclusion criterion of larger than 2 cm in diameter under a light wrap that was removed after 24 and 48 h. Maximum number of observations per cow was 14. A group of 38 heifers had only 2 observations during the observation time. In total, there were 6,444 clinical observations using the 5-point scale as defined by Döpfer et al. (1997) and Gomez et al. (2014). Briefly, lesions were classified as follows: M0 for unaffected animals with no clinical lesions; M1 for infected heifers with early lesions <2 cm in diameter (nonactive); and M2 for infected heifers with a classic active lesion of >2 cm of diameter considered infectious. An M4 stage denotes late and chronic