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Short communication: Genetic characterization of digital cushion thickness

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ABSTRACT

Dairy cow lameness is a serious animal welfare issue. It is also a significant cause of economic losses, reducing reproductive efficiency and milk production and increasing culling rates. The digital cushion is a complex structure composed mostly of adipose tissue located underneath the distal phalanx and has recently been phenotypically associated with incidence of claw horn disruption lesions (CHDL); namely, sole ulcers and white line disease. The objective of this study was to characterize digital cushion thickness genetically and to investigate its association with body condition score (BCS), locomotion score (LOCO), CHDL, and milk production. Data were collected from 1 large closely monitored commercial dairy farm located in upstate New York; 923 dairy cows were used. Before trimming, the following data were collected by a member of the research team: BCS, cow height measurement, and LOCO. Presence or not of CHDL (sole ulcer or white line disease, or both) was recorded at trimming. Immediately after the cows were hoof trimmed, they underwent digital sonographic B-mode examination for the measurement of digital cushion thickness. Factors such as parity number, stage of lactation, calving date, mature-equivalent 305-d milk yield (ME305MY), and pedigree information were obtained from the farm's dairy management software (DairyCOMP 305; Valley Agricultural Software, Tulare, CA). Univariate animal models were used to obtain variance component estimations for each studied trait (CHDL, BCS, digital cushion thickness average, LOCO, height, and ME305MY) and a 6-variate analysis was conducted to estimate the genetic, residual, and phenotypic correlations between the studied traits. The heritability estimate of DCTA was 0.33 ± 0.09, whereas a statistically significant genetic correlation was estimated between DCTA and CHDL (−0.60 ± 0.29). Of the other genetic correlations, significant estimates were derived for BCS with LOCO (−0.49 ± 0.19) and ME305MY (−0.48 ± 0.20). Digital cushion thickness is moderately heritable and genetically strongly correlated with CHDL.

Key words: digital cushion, genetics, lameness, claw horn disruption lesion

Short Communication

Lameness is a significant financial and welfare issue because of its high prevalence in herds throughout the world and its debilitating effects (Cook, 2003; Espejo and Endres, 2007; Bicalho and Oikonomou, 2013). Sole ulcers and white line disease, often described together as claw horn disruption lesions (**CHDL**) are the most prevalent claw diseases associated with lameness and pain (Murray et al., 1996), comprising 65% of all lesions diagnosed in visibly lame cows (Bicalho et al., 2007). The digital cushion is a complex structure composed mostly of adipose tissue located underneath the distal phalanx; it plays an important function in dampening compression of the corium tissue beneath the cushion (Logue et al., 2004; Räber et al., 2004, 2006). Our research group conducted an observational cross-sectional study to investigate the association between claw horn lesions and the thickness of the digital cushion and reported that digital cushion thickness was a strong predictor of lameness (Bicalho et al., 2009). Digital cushion thickness was also associated with BCS, increasing gradually as BCS increased.

Low to moderate heritability estimates, ranging from 0.01 to 0.22, have been reported for lameness (Boettcher et al., 1998; Zwald et al., 2004), specific foot lesions (van der Waaij et al., 2005; Laursen et al., 2009; van der Linde et al., 2010), and locomotion scores (Onyiro and Brotherstone, 2008), suggesting that, although these are traits largely influenced by environmental factors, alleviation of their impact could partially be achieved through genetic selection. Body condition score has already been shown to be moderately heritable in several studies (Berry et al., 2003; Banos et al., 2005) and low BCS is phenotypically (Bicalho et al., 2009; Schöpke et al., 2013) and genetically (Van Dorp et al., 1998; Kougioumtzis et al., 2013) associated with increased susceptibility to lameness. However, to the best of our knowledge, digital cushion thickness and its

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relationships with BCS, lameness, or CHDL have not yet been studied genetically. Therefore, the objective of this study was to characterize digital cushion thickness genetically and to investigate its association with BCS, locomotion score (**LOCO**), CHDL, and milk production.

Data were collected from a large commercial dairy farm located in Cayuga County, New York. Lactating cows were housed in 6-row freestall barns with concrete stalls covered with rubber mattresses and bedded with recycled composted manure solids. All lactating cows were scheduled to receive routine hoof trimming twice yearly. A protocol created in DairyCOMP 305 (Valley Agricultural Software, Tulare, CA) prompted trimming for lactating cows. Furthermore, all cows received routine hoof trimming at dry off. Trained farm employees observed cows walking into the milking parlor and recorded the identification number of visually lame cows daily. Visually lame cows were then directed to the in-house hoof trimmers for therapeutic hoof trimming. Farm employees trimming the cows were all trained by members of the Ambulatory and Production Medicine Clinic at Cornell University (Ithaca, NY). Recordings from 2 previous observational studies conducted by our research group were used (Bicalho et al., 2009; Machado et al., 2011). Briefly, data were collected from July 2008 to January 2009 using lactating cows that were scheduled for routine hoof trimming. The cows were restrained for hoof trimming with a standing chute H-Series (Comfort Hoof Care Inc., Baraboo, WI). Before cows entered the trimming chute, the following data were collected by a member of the research team: BCS, which ranged from 1 to 5, with a quarter point system as described by Edmonson et al. (1989); cow height measurement, assessed as the distance in centimeters from the floor to the dorsal aspect of the caudal sacral joint; and locomotion score on a scale from 1 to 5, with 1 being the most desirable score (Bicalho et al., 2007). Presence or not of CHDL was recorded at trimming. Immediately after the cows were hoof trimmed, they underwent digital sonographic B-mode examination with an Aquila Vet ultrasound machine (Esaote Europe BV, Maastricht, the Netherlands) equipped with a curved array dual-frequency probe set at 7.5 MHz. The examination was always completed at the typical sole ulcer site, assessing the distance from the inner margin of the sole to the distal edge of the tuberculum flexorum of the third phalanx. The anatomical area of the digital cushion targeted for ultrasonography was the middle pad (Räber et al., 2006). Ultrasonography of all 8 digits or at least the 4 hind digits was performed. The ultrasound machine settings (i.e., depth, echo-amplification, persistence, preprocessing, and postprocessing) were kept unchanged throughout the study. All data obtained from each cow's digital cushion thickness values were used for the calculation of a digital cushion thickness average (**DCTA**) and this value was used for all analyses in the present study. Factors such as parity number, calving date, and mature-equivalent 305-d milk yield (**ME305MY**) were obtained from the farm's dairy management software (DairyCOMP 305; Valley Agricultural Software). Additionally, DairyCOMP 305 was used to obtain information regarding the studied cows' sires, dams, and maternal grandsires. This information was used for the creation of a pedigree file. Only cows with available pedigree information were used in this study. Eventually, 923 cows that were daughters of 128 sires were included. The total number of animals included in the pedigree file was 1,837. Of the 972 recordings on these cows, 440 were on first-lactation animals, 282 on second-lactation, 133 on third-lactation, and 117 on fourth-or-greater-lactation animals.

Univariate animal models were used to obtain variance components estimations for each studied trait (CHDL, BCS, DCTA, LOCO, height, and ME305MY) separately. Claw horn disruption lesions were modeled with a logistic regression function to account for the binary nature of the trait. All models included the fixed effects of parity, year/month of calving (class variables), and age at calving (continuous variable). Models for all traits except ME305MY also included the linear and quadratic effect of DIM representing the stage of lactation when recordings were taken. The cow was fitted in the model as a random effect including the pedigree relationship matrix. Variance components derived from the univariate analysis were used as starting values in a 6-variate animal model that aimed to decompose covariances and estimate the genetic, residual, and phenotypic correlations between the studied traits. Estimates of variance components obtained were used to calculate heritabilities for each trait. The same models as in the univariate analysis were used for each trait. All analyses were performed with the use of the ASReml software package (Gilmour et al., 2006).

Descriptive statistics of all traits considered in this study are shown in Table 1. Heritability estimates and genetic and residual (nonadditive genetic) correlations of DCTA, BCS, LOCO, CHDL, height, and ME305MY derived from the 6-variate analysis are presented in Table 2. The heritability estimate for DCTA was 0.33 ± 0.09 ($P < 0.001$), whereas a statistically significant genetic correlation was estimated between DCTA and CHDL (−0.60 ± 0.29; $P < 0.05$). Heritability estimates were 0.09 ± 0.06 ($P = 0.13$) for CHDL, 0.24 ± 0.08 ($P < 0.001$) for BCS, 0.30 ± 0.08 ($P < 0.001$) for LOCO, 0.66 ± 0.07 ($P < 0.001$) for height, and 0.40 ± 0.16 ($P < 0.05$) for ME305MY. Statistically significant genetic correlations were estimated between BCS