Implementation of Genomic Evaluation for Digital Dermatitis in Canada

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Abstract

Digital dermatitis represents the most prevalent hoof lesion in Canada, with almost 20% of cows affected. A data collection system of hoof lesions, which uses standardized and reliable scores, was developed in Canada within a four-year project started in 2014. Hoof trimmers willing to share data and to develop a standard protocol were identified across Canada. Consecutively, a pipeline for a routine flow of hoof lesion records from hoof trimmers to Canadian DHI and to Canadian Dairy Network (CDN) was developed. The data collected through this pipeline were then used to develop a herd management report provided by DHI, and a national genomic evaluation for digital dermatitis offered by CDN. The genomic evaluation was introduced in December 2017, using hoof lesions recorded by hoof trimmers between 2006 and 2017. Heritability and repeatability estimates for digital dermatitis were 0.08 and 0.20, respectively. Breeding values were estimated for Holstein cattle with a univariate linear animal model. Other possible indicator traits for digital dermatitis, such as selected conformation traits, were not included due to low genetic correlations, and low contribution to increase in prediction reliability. Single-step genomic evaluation was implemented using a reference population of 19,459 animals (5,268 sires and 14,191 cows, respectively). The average reliability for bulls in the reference population was 77%. Correlations between GEBV for resistance to digital dermatitis and traits currently under selection were all favorable.

Key words: Digital dermatitis, Single-step genomic evaluation, hoof trimmer

Introduction

Digital dermatitis represents the most prevalent hoof lesion in Canada, with 20% of cows affected (Chapinal *et al.*, 2013; Malchiodi *et al.*, 2017). In Ontario, Cramer *et al*. (2008) reported prevalence of 46.4% and 25.7% of cows with at least one hoof lesion in free-stall housing systems and tie-stall barns, respectively. Digital dermatitis was the most common lesion in both tie-stall and free-stall barns, with 69.7% and 96.7% of herds with affected cows, respectively. The presence of digital dermatitis poses a financial loss for the farmers, due to the costs associated with treating the lesion, as well as to decreased cow performance, as digital dermatitis has been reported to affect milk production (Ettema *et al.*, 2007; Amory *et al.*, 2008). Therefore, a key goal of Canadian dairy herds is to reduce the incidence of hoof lesions, particularly digital dermatitis, which can be achieved both by improving management practices, and through genetic selection. A system to collect hoof lesion data, which uses standardized and reliable scores, was developed in Canada within a four-year project started in 2014. The project aimed to use standardized claw lesion data collected by hoof trimmers, and to initiate a routine data flow to end users for improving hoof health, both at the management and genetic level.

Materials and Methods

Standardize Hoof Lesions Data Collection

The trimmers involved in the project were trained to use a rugged touch-screen computerized lesion recording system (Hoof Supervisor, Dresser, WI). To increase the participation in the project, a French version of the program was also developed and it is now available to Canadian hoof trimmers. The recording system is based on lesion descriptions proposed by the International Lameness Committee, a global collaboration of researchers, veterinarians, academics, and hoof trimming professionals (Egger-Danner *et al.*, 2015). In order to facilitate the correct identification of the lesion and to more consistently score lesion severity, the hoof trimmers were asked to participate in training sessions and they were provided with a lesion severity scoring guide containing example photos of each lesion created by Alberta hoof trimmers (Alberta dairy hoof health project, 2014).

Data Pipeline

Develop a data pipeline was critical to assure the success of the program. An interface for the download and upload of DHI herd information and hoof health data from the Hoof Supervisor system was developed. Using the interface drastically decreased the amount of time needed for the trimmer to upload the data. Canadian

DHI transferred the data received from the trimmers to Canadian Dairy Network (CDN), which in turn provided weekly genomic evaluation for resistance to hoof lesions (Figure 1).

Figure 1. Data Pipeline

Canadian DHI will provide a management report for hoof health using the same data.

Hoof Health Management Report

A working group with hoof trimmers, dairy advisors, veterinarians, and researchers was created with the aim of developing a new DHI management report on hoof health. The report will include the prevalence of lesions on farm, their trends over time, and benchmarks with province and national averages. These values will be available for the most prevalent lesions, such as digital dermatitis, sole ulcer, sole hemorrhage, white line disease, and heel erosion. This report will be provided in addition to the report for lameness, already available through Canadian DHI, and based on data collected directly by the producer. Prevalence of the lesions has been reported to be very different among housing system (Cramer *et al.*, 2008). Therefore, different benchmarks will be calculated and reported on three different housing types: free-stall with robot, free-stall with milking parlor, and tie-stall.

Genomic Evaluation for Digital Dermatitis

Data were recorded by 54 trimmers servicing 1,080 Canadian herds between 2009 and 2017. In order to be included in the analyses, the trimming sessions needed to be recorded in the first 500 d postpartum and a minimum of 10 records per hoof trimming session per herd was required. Based on the low repeatability of the lesions, all available hoof-trimming sessions were included in the analysis to maximize the accuracy of the evaluation.

As data are collected directly by the hoof trimmers, not all of the cows that are in the herds during the trimming period are normally presented to the hoof trimmer and the pre-selection is rarely random, leading to potential bias and, consequently, inaccuracies in the genetic evaluation. The effect of the pre-selection of cows to be presented to the hoof trimmer was largely investigated and it did not appear to have a sizeable impact on the genetic evaluation (Malchiodi *et al.*, 2017). Based on these results, only cows with trimming data were considered in the analyses. Digital dermatitis was treated as a binary variable (0; 1), where 1 was assigned to the presence of a lesion. Digital dermatitis recorded in first and later lactations were considered as the same trait.

Digital dermatitis was analyzed using a linear animal model, considering the fixed effects of herd-date of hoof-trimming, hoof trimmer, parity at trimming, and stage of lactation at trimming, the random additive genetic animal effect, and the random permanent environmental effect. A multiple-trait approach using other traits, such as feet and legs conformation traits, was not implemented due to low genetic correlations of these traits with digital dermatitis, and to the low contribution to the increase in prediction reliability. Variance components were estimated using AIREMLF90 (Misztal *et al.*, 2014).

A single-step genomic evaluation was implemented at CDN using the MIX99 and related software (MiX99 Development Team, 2017). The reference population included 19,459 animals (5,268 sires, 7,178 cows, and 7,013 cows with data, respectively). Animals were genotyped either with 50K SNP panel or a low-density panel and imputed to 50K using F-Impute (Sargolzaei *et al.*, 2014).

Results and Discussion

Heritability of Digital Dermatitis

The prevalence of digital dermatitis in Holsteins was 17.1%. This is similar to what has previously been reported in other Canadian studies in Alberta (Solano *et al.*, 2016), and for free-stall herds in Ontario (Cramer *et al.*, 2008), which reported prevalence of digital dermatitis of 21.8% and 22,7% respectively.

Digital dermatitis had a heritability of 0.08 (0.001). These results are in line with what was previously reported for this lesion (König *et al.*, 2008; Swalve *et al.*, 2008; Gernand *et al.*, 2012).

Genomic Evaluation of Digital Dermatitis

Genomic evaluation for resistance to digital dermatitis was released by CDN only for Holstein bulls. In order to have an official evaluation, a sire is required to have daughters in a minimum of 5 herds and reliability higher than 70%. Despite a low heritability, the distribution of the sire EBV shows exploitable variation (Table 1). As for all functional traits evaluated by CDN, the sire proofs are expressed as Relative Breeding Values (RBV), with a mean of 100 and a standard deviation of 5 for the base sires. RBV are reversed in sign, thus, higher RBV indicate better resistance to digital dermatitis. The top 10% of sires had an average RBV of 114 (from 112 to 117) and presented, on average, 93% of healthy records. The bottom 10% of sire showed an average RBV of 82 (from 11 to 84) and had, on average, only 62% of healthy records. The average reliability for bulls in the reference population was 77%.

Table 1. Percentage of healthy records from the best and the worst 10 sires according to their estimated breeding values for resistance to digital dermatitis.

Bulls	Percentage of Healthy Records			
	Mean	SD	Min	Max
Bottom 10	61	14.1	33	86
Top 10	93	7.3	80	100

Finally, correlations between RBV for resistance to digital dermatitis and other traits currently under selection in Canada were all favorable (from -0.01 to 0.40). Therefore, selecting for digital dermatitis should not negatively affect the selection of other economical important traits.

Future Implications

Since 2017, hoof trimmers who use the latest available version of the Hoof Supervisor system, started to collect data for digital dermatitis using the alternative proposed M-scoring system (Döpfer *et al.*, 1997). This definition of digital dermatitis has been reported to have higher heritability and to increase the accuracy of the estimated breeding values, as it better represents this hoof lesion (Schöpke *et al.*, 2015). As the data collected with the new system will be accumulating, the effect of the M-score on the genetic evaluation of digital dermatitis will be investigated.

A sub-index for hoof health, which includes all hoof lesions weighted by their estimated economic weights, is under development. In addition to digital dermatitis, the multiple trait single-step genomic evaluations will include 7 other hoof lesions: interdigital dermatitis, interdigital hyperplasia, heel erosion, sole hemorrhage, sole ulcer, toe ulcer, and white line diseases.

Conclusions

A centralized data collection system that routinely transfers data recorded by hoof trimmers into a coherent and sustainable national database was developed in Canada. Data recoded by hoof trimmers represent valuable information and were used to create a genetic evaluation system for resistance to digital dermatitis. Despite a low heritability, an exploitable genetic variation for digital dermatitis was found in Canadian Holstein population.

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