Development of genetic and genomic evaluation for wellness traits in US Holstein cows

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ABSTRACT

In March 2016, Zoetis Genetics offered the first commercially available evaluation for wellness traits of Holstein dairy cattle. Phenotypic data on health events, pedigree, and genotypes were collected directly from producers upon obtaining their permission. Among all recorded health events, 6 traits were chosen to be included in the evaluation: mastitis, metritis, retained placenta, displaced abomasum, ketosis, and lameness. Each trait was defined as a binary event, having a value of 1 if a cow has been recorded with a disorder at any point during the lactation and zero otherwise. The number of phenotypic records ranged from 1.8 million for ketosis to 4.1 million for mastitis. Over 14 million pedigree records and 114,216 genotypes were included in the evaluation. All traits were analyzed using univariate threshold animal model with repeated observations, including fixed effect of parity and random effects of herd by year by season of calving, animal, and permanent environment. A total of 45,425 single nucleotide polymorphisms were used in the genomic analyses. Animals genotyped with low-density chips were imputed to the required number of single nucleotide polymorphisms. All analyses were based on the single-step genomic BLUP, a method that combines phenotype, pedigree, and genotype information. Predicted transmitting abilities were expressed in percentage points as a difference from the average estimated probability of a disorder in the base population. Reliabilities of breeding values were obtained by approximation based on partitioning of a function of reliability into contributions from records, pedigree, and genotypes. Reliabilities of genomic predicted transmitting abilities for young genotyped and pedigreed females without recorded health events had average values between 50.2% (displaced abomasum) and 51.9% (mastitis). Genomic predictions for wellness traits can provide new information about an animal's genetic potential for health and new selection tools for dairy wellness improvement.
Key words: wellness traits, dairy cattle, single-step genomic BLUP, reliability

INTRODUCTION

Interest is growing in the use of genetic improvement strategies as a component to the management of health in dairy cattle. Breeding strategies that incorporate information on health traits have the potential to improve animal well-being and overall effectiveness of dairy operations. Dairy animals that experience health events have a negative effect on herd profitability through increased culling, veterinary expenses, and labor, as well as monetary losses through reduced milk sales (Parker Gaddis et al., 2014). Guard (2009) estimated the expenses related to the common dairy cow diseases to range from $181 per case of ketosis to $391 per case of displaced abomasum. Dairy researchers and producers have focused on providing the best environment to reduce health events through nutrition, management, and housing. However, improving functional traits genetically presents a challenge, because health traits have low heritability and may be difficult and expensive to measure and record.

Genetic evaluation of health traits has a long tradition in countries with routine health data recording. In Scandinavian countries, health traits have been included in breeding programs since the mid-1970s (Heringstad and Østerås, 2013); currently, over 97% of Norwegian dairy cows are included in the recording system (Heringstad, 2010; Haugaard et al., 2012). In other countries, the use of direct health data in genetic evaluation is progressing rapidly. Routine data collection and genetic evaluation for health traits in Germany and Austria started in 2006 (Fuerst et al., 2011). In France, clinical mastitis has been included in

routine genetic evaluation since 2010 (Govignon-Gion et al., 2012). In 2014, genetic evaluation for mastitis resistance was introduced for Canadian dairy cows; the evaluation is based on clinical mastitis incidence recorded in the first and second lactation and SCS (Koeck et al., 2012; Miglior et al., 2014). In Canada, research is currently underway to implement genetic evaluation for ketosis and displaced abomasum in December 2016, followed by metritis and retained placenta, hoof health and lameness, and other functional traits in the following years (Beaver and VanDoormal, 2016).

Currently, genetic evaluation and selection for dairy health traits in the United States is based on indicator traits. Somatic cell score, certain feet and leg traits, and productive life are included in the national genetic evaluation and have shown desirable genetic trends in recent years. However, the availability of predictions for these traits has not resulted in the expected reduction in the incidence of mastitis, lameness, or metabolic diseases in dairy herds (NAHMS, 2007), possibly because of low heritabilities of the indicator traits and the incomplete correlations with the target traits. The most frequently cited reason for not using direct health data in genetic evaluation of dairy cattle is the absence of a national system to collect health record data. Although most dairy producers record health information of their animals, the user-defined nature of health records makes it more difficult to use health data in a genetic evaluation due to insufficient accuracy and inconsistency of recording (Wenz and Giebel, 2012). On the other hand, studies based on large amounts of producer-recorded health events have shown that genetic selection for wellness traits should result in favorable genetic trends for health in dairy cattle as long as the health recording protocol within a herd can be assumed fairly consistent (Zwald et al., 2004; Parker Gaddis et al., 2012, 2014).

Advances in methodology used in genomic evaluation have resulted in improved accuracy of selection for traits with low heritabilities and incomplete information. The single-step genomic BLUP (**ssGBLUP**) method (Misztal et al., 2009; Aguilar et al., 2010) is being widely adopted as the method of choice in genomic evaluation. The method uses joint information on pedigree, phenotype, and genomic data in a single analysis. The ssGBLUP works in the same way as traditional BLUP, except that it modifies the additive relationship matrix by incorporating relationships estimated from genotyped animals. The ssGBLUP method is rapidly gaining popularity in both research and commercial communities due to its simplicity and applicability to most evaluation models and data structures. The method is considered free of double counting and preselection bias (Misztal et al., 2013a). Parker Gaddis et al. (2014) applied ssGBLUP methodology to approximately 300,000 records of health events and concluded that the inclusion of genomic data would substantially improve accuracy of selection for health traits.

Although several research projects have shown the value and feasibility of selection for wellness traits, national evaluation based on direct health records in the United States seems unlikely in the near term (Chesnais et al., 2016). In response to market needs for genetic improvement of dairy wellness traits, and in collaboration with the Holstein Association USA (Brattleboro, VT), University of Georgia in Athens, and customers, Zoetis Genetics launched a project to develop genetic and genomic evaluation for wellness traits in dairy cattle. In particular, this project focuses on creating genomic tools that would allow commercial dairy farmers to make management and selection decisions based on genetic predisposition of their heifer calves for wellness traits that will be expressed later in life. The objective of our study was to develop foundations for commercially viable genetic and genomic evaluation for wellness traits in Holstein dairy cattle based on producer-recorded data and ssGBLUP methodology.

MATERIALS AND METHODS

Data Sources

Phenotypic data were obtained directly from producers upon obtaining their signed permissions. Data were obtained from approximately 240 herds located in 29 different states in all regions of the United States. Each herd provided information on 13,720 animals, on average. As of January 2016, over 3 million health events from approximately 14.5 million lactation records have been collected for the analysis. For some herds, the records dated back to the 1990s.

Data from on-farm software was extracted and processed using internally written scripts. Pedigree information, lactation data, and health events were extracted from the backup files and converted into standard USDA-defined data-exchange formats (https://www.cdcb.us/formats/formats.html). Phenotypic records on about 25,000 animals collected from past research projects conducted by Zoetis (Vukasinovic et al., 2013) or obtained from collaborators were also added to the data set.

Pedigree information was supplied by Holstein Association USA for all registered bulls born between 1950 and 2014 and cows born between 2005 and 2014. Pedigree information for nonregistered animals was obtained from farm software backup files. For animals with owner permissions and genomically tested at Zoetis, pedigree information was initially supplied by the customer on the order form and later updated based