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Genomic selection for producer-recorded health event data in US dairy cattle

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ABSTRACT

Emphasizing increased profit through increased dairy cow production has revealed a negative relationship of production with fitness and health traits. Decreased cow health can affect herd profitability through increased rates of involuntary culling and decreased or lost milk sales. The development of genomic selection methodologies, with accompanying substantial gains in reliability for low-heritability traits, may dramatically improve the feasibility of genetic improvement of dairy cow health. Producer-recorded health information may provide a wealth of information for improvement of dairy cow health, thus improving profitability. The principal objective of this study was to use health data collected from on-farm computer systems in the United States to estimate variance components and heritability for health traits commonly experienced by dairy cows. A single-step analysis was conducted to estimate genomic variance components and heritabilities for health events, including cystic ovaries, displaced abomasum, ketosis, lameness, mastitis, metritis, and retained placenta. A blended **H** matrix was constructed for a threshold model with fixed effects of parity and year-season and random effects of herd-year and sire. The single-step genomic analysis produced heritability estimates that ranged from 0.02 (standard deviation = 0.005) for lameness to 0.36 (standard deviation = 0.08) for retained placenta. Significant genetic correlations were found between lameness and cystic ovaries, displaced abomasum and ketosis, displaced abomasum and metritis, and retained placenta and metritis. Sire reliabilities increased, on average, approximately 30% with the incorporation of genomic data. From the results of these analyses, it was concluded that genetic selection for health traits using producer-recorded data are feasible in the United States, and that the inclusion of genomic data substantially improves reliabilities for these traits.

Key words: dairy cattle, health, genomic selection

INTRODUCTION

Previous emphasis on increased profit through increasing dairy cow production has made a negative relationship of production with fitness traits become apparent (Rauw et al., 1998). An alternative to increasing net profit is to decrease management costs by improving the overall health of the cows (Zwald et al., 2004a). Declining health of cows can affect the profitability of a herd by affecting several aspects, such as additional culling, decreased and lost milk sales, veterinary expenses, and additional labor (Hansen, 2000; Harder et al., 2006). Kelton et al. (1998) estimated the cost of several common health events ranging from $39 per lactation with an event of cystic ovaries up to $340 per case of left-displaced abomasum. Over the past 15 yr, however, these economic costs may have drastically changed. More recent studies have looked at the average cost per case of specific hoof and leg disorders such as sole ulcers, digital dermatitis, and foot rot. The average cost per case of these events was estimated to be $216.07, $132.96, and $120.70, respectively (Cha et al., 2010). These estimates accounted for factors such as milk loss, treatment cost, and decreased fertility. Other recent research estimated the factors that contribute to the cost of an incidence of mastitis. The average cost of clinical mastitis per case was approximately $179, with $115 of that the result of lost milk, $14 from increased mortality, and $50 from treatment costs (Bar et al., 2008).

Genetic selection is an appealing tool for improvement of health traits. Difficulty is encountered, however, as no mandated or consistent recording system of health traits exists in the United States. In some European countries, recording of health events is mandatory. Genetic selection for increased disease resistance has been performed for more than 30 yr and the potential for genetic improvement in health-related traits has been demonstrated in Scandinavian cattle breeds (Philipsson and Lindhé, 2003; Abdel-Azim et al., 2005). Genetic improvement of clinical mastitis incidence has also been demonstrated in Nordic cattle (Heringstad et al., 2003; Philipsson and Lindhé, 2003). The lack of health-related phenotypes in the United States creates

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an obstacle to genetic improvement. Several previous studies have confirmed the possibility of using on-farm recorded health information for genetic improvement. Zwald et al. (2004a) used on-farm recorded health data from 2001 through 2003 and concluded that this data would allow genetic selection to be possible. Prior research was completed to analyze if producer-recorded data from a similar data set to the current study accurately reflected the true incidences of health events after several editing constraints were put in place. Phenotypic relationships were also examined between common health events and compared with results from epidemiological studies to further validate the data (Parker Gaddis et al., 2012).

Although genetic improvement in some health traits has been demonstrated, progress is slow, especially when compared with the improvements achieved in production traits. Health traits are typically categorized as being lowly heritable. Low sire reliabilities are also common for health traits due to a combination of low heritability and limited availability of phenotypes. Dense marker data have been shown in many studies to improve reliability of prediction (Harris and Johnson, 2008; Hayes et al., 2009; VanRaden et al., 2009). Increased availability of dense molecular marker data may allow progress to be achieved at a quicker rate, especially for lowly heritable traits. Marker information is attainable at birth, which could decrease the generation interval required to achieve an acceptable reliability. Genomic selection methodologies are currently being widely investigated and implemented in dairy cattle breeding (VanRaden et al., 2009; Veerkamp et al., 2011), as well as in other species (Ostersen et al., 2011; Simeone et al., 2012); however, most of this research has involved traditional traits, such as those related to production (VanRaden et al., 2009; Olson et al., 2011).

One method of including SNP marker data into genetic analyses is the single-step method. Misztal et al. (2009) and Legarra et al. (2009) proposed the single-step method, as an alternative to multi-stage approaches. The single-step procedure replaces the pedigree (**A**) and genomic (**G**) relationship matrices with a blended **H** matrix (Aguilar et al., 2010; Christensen and Lund, 2010) that combines the information from **A** and **G**. The **H** matrix can be implemented similarly to the **A** relationship matrix in BLUP analyses (Legarra et al., 2009). This allows a straight-forward application of genomic data to complicated models and complex data structures (Aguilar et al., 2010).

Several studies have incorporated functional traits along with production traits using genomic data (Brøndum et al., 2011; Koivula et al., 2012), although the vast majority of these were conducted outside the United States. The objective of the current study was to perform pedigree- and genomic-based analyses on producer-recorded health data to estimate variance components and heritabilities for health traits commonly encountered by dairy cows in the United States, thereby confirming a genetic component of major health events. A multiple-trait genetic analysis using pedigree data was completed to identify genetic relationships among common health events, including cystic ovaries (**CYST**), displaced abomasum (**DSAB**), ketosis (**KETO**), lameness (**LAME**), mastitis (**MAST**), metritis (**METR**), and retained placenta (**RETP**). Single-step methodology was used to incorporate genomic information into a multiple-trait analysis of common health events, using the estimates from pedigree-based analyses as starting values. Reliabilities were compared between the pedigree-based analyses and genomic-based analyses. Genetic correlations with more commonly reported fitness traits, including daughter pregnancy rate (VanRaden et al., 2004), productive life (VanRaden and Wiggans, 1995), SCS, net merit (Cole et al., 2010), and milk yield, were also approximated.

MATERIALS AND METHODS

Voluntary producer-recorded health event data were available from Dairy Records Management Systems (Raleigh, NC) from US farms from 1996 through 2012. The health events included in the analyses were MAST, METR, CYST, DSAB, KETO, LAME, and RETP from cows of parities 1 through 5. Cows with records in later parities were required to have records for all prior parities. Data quality edits were applied as described in Parker Gaddis et al. (2012). Minimum and maximum constraints were imposed on the data by herd-year to avoid using records from herd-years that over- or underreported an event. Extended lactations lasting up to 400 d postpartum were included in the analyses under the assumptions that cows with extended lactations were likely to be those that had not become pregnant. This decreased fertility could potentially be attributable to poor health, which could be reflected in the data. Production data included a variable indicating if a cow was removed from the herd during the lactation. Records being coded as anything other than a normal lactation were originally removed from the data set. These records included cows removed from the herd during lactation, potentially for health-related reasons. Analyses were later completed including these terminated records, as no significant difference was found when terminated records were included. After editing, there were 134,226 total first-parity records from 12,893 sires and 13,534 maternal grandsires. There were 174,069 total records from parities 2 through 5