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Validation of genomic predictions for wellness traits in US Holstein cows

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ABSTRACT

The objective of this study was to evaluate the efficacy of wellness trait genetic predictions in commercial herds of US Holstein cows from herds that do not contribute phenotypic information to the evaluation. Tissue samples for DNA extraction were collected from more than 3,400 randomly selected pregnant Holstein females in 11 herds and 2 age groups (69% nulliparous, 31% primiparous) approximately 30 to 60 d before their expected calving date. Lactation records from cows that calved between September 1, 2015, and December 31, 2015, were included in the analysis. Genomically enhanced predicted transmitting abilities for the wellness traits of retained placenta, metritis, ketosis, displaced abomasum, mastitis, and lameness were estimated by the Zoetis genetic evaluation and converted into standardized transmitting abilities. Mean reliabilities of the animals in the study ranged between 45 and 47% for each of the 6 traits. Animals were ranked by their standardized transmitting abilities within herd and age group then assigned to 1 of 4 groups of percentile-based genetic groups of equal size. Adverse health events, including retained placenta, metritis, ketosis, displaced abomasum, mastitis, and lameness, were collected from on-farm herd management software, and animal phenotype was coded as either healthy (0), diseased (1), or excluded for each of the 6 outcomes of interest. Statistical analysis was performed using a generalized linear mixed model with genetic group, age group, and lactation as fixed effects, whereas herd and animal nested within herd were set as random effects. Results of the analysis indicated that the wellness trait predictions were associated with differences in phenotypic disease incidence between the worst and best genetic groups. The difference between the worst and best genetic groups in recorded disease incidence was 2.9% for retained placenta, 10.8% for metritis, 1.1% for displaced abomasum, 1.7% for ketosis, 7.4% for mastitis, and 3.9% for lameness. Odds ratio estimates between the highest and lowest genetic groups ranged from 1.6 (lameness) to 17.1 (displaced abomasum) for the 6 traits analyzed. These results indicate that wellness trait information of young calves and heifers can be used to effectively predict meaningful differences in future health performance. Improving wellness traits through direct genetic selection presents a compelling opportunity for dairy producers to help reduce disease incidence and improve profitability when coupled with sound management practices.

Key words: Holstein, health, mastitis, genomics

INTRODUCTION

Genetic evaluation and selection in dairy cattle has primarily focused on yield traits such as milk, fat, and protein production. Over the course of the last 30 yr, researchers at the USDA Animal Genome Improvement Laboratory (Beltsville, MD) have added to the production traits by developing national genetic evaluations for indirect health predictions including linear SCC (Schutz, 1994), productive life (VanRaden and Klaaskate, 1993), livability (Miller et al., 2008), and daughter pregnancy rate (Kuhn et al., 2004). These indirect health predictions are currently available from the Council on Dairy Cattle Breeding (**CDCB**), and evidence exists that these traits elicit some genetic improvement for resistance to adverse health events (e.g., metritis, displaced abomasum) via correlated response (Vukasinovic et al., 2017). However, presumably as a result of current management practices and the genetic antagonisms between adverse health events and production traits, the incidence of many common diseases in contemporary dairy production systems within the United States continued to increase (Jones et al., 1994; Lucy, 2001; APHIS, 2009). As a result, dairy cows today are generally considered to be less robust than previous generations.

The decline in the health and wellness of dairy animals led to a growing interest in the use of genetic improvement as part of a comprehensive health management strategy for dairy cows (Weigel et al., 1998; Heriazon et al., 2013; Thompson-Crispi et al., 2014). Producer-recorded health events have been successfully used by researchers to identify genetic differences between dairy sires in daughter susceptibility to common

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health disorders, including, but not limited to, metritis, displaced abomasum, and mastitis (Zwald et al., 2004, 2006; Neuenschwander et al., 2012; Parker Gaddis et al., 2014). When coupled with sound management practices, genetic improvement programs that incorporate direct assessment of genetic risk for adverse health events have the potential to improve animal well-being and the financial viability of the dairy by reducing culling rates, veterinary expenses, labor requirements, and discarded milk (Parker Gaddis et al., 2014). Reducing the incidence of these adverse health events can help to improve profitability, as the economic impact of these adverse health events is estimated to range between $203 for a case of ketosis to $438 per case of displaced abomasum (Gaurd, 2009).

In response to industry needs for genetic improvement of dairy wellness traits, and in collaboration with the US Holstein Association (Brattleboro, VT), researchers at the University of Georgia-Athens, and commercial dairy producers; Zoetis Genetics developed a dairy cattle genetic and genomic evaluation to estimate genetic risk for 6 health events in US Holstein dairy cattle (Vukasinovic et al., 2017). Conveyed as a standardized transmitting ability (**STA**), the wellness trait predictions include genomically enhanced genetic predictions for retained placenta, metritis, ketosis, displaced abomasum, mastitis, and lameness. The development of this genetic evaluation, including a description of the phenotypes, statistical model, generation of the genomically enhanced predicted transmitting abilities (**gPTA**), and reliabilities have been reported previously (Vukasinovic et al., 2017). This wellness trait genetic evaluation system uses single-step best linear unbiased prediction (BLUPF90) to estimate an animal's genetic risk to experience these 6 health events. Single-step BLUPF90 simultaneously incorporates multiple sources of data (phenotypes, pedigree, and genotypes) to minimize bias, improve the computational efficiency of the genetic evaluation, and increase the timeliness of the genetic predictions for experiencing the health events (Misztal et al., 2009, 2013, 2014).

An accepted best practice in any genetic evaluation or predictive algorithm is to evaluate the association of the genetic predictions with the observed performance of the evaluated animals in an external population. For that reason, a multiyear validation study was conducted to evaluate the efficacy of the genomically enhanced genetic predictions for wellness traits in US Holstein cows. This study was conducted using US Holstein cows managed in herds that do not contribute phenotypes to the genetic evaluation. The objective of our study was to demonstrate the ability of wellness trait predictions to accurately predict disease incidence using herds that do not contribute phenotypes to the genetic evaluation. In the current study, we hypothesized that animals with the highest genetic risk for the wellness traits would have a higher phenotypic incidence than animals with the lowest genetic risk through 305 DIM.

MATERIALS AND METHODS

Experimental Design

A power calculation was conducted to determine the size of the population necessary to detect a statistically significant difference in the disease incidence between 2 genetic groups where the difference in incidence is 20% of the mean of the population. The maximum number of animals per herd was limited to 350 with an α of 0.05 and a β of 0.8, according to the methodology described previously (Dohoo et al., 2009). This study was powered to have an 80% (β) probability of detecting a significant difference at the 0.05 (α) level if the true differences were at least 20% between the contrasted genetic groups. Power calculations were conducted for all 6 health events, and the health event requiring the largest population was used as the target sample size. The power calculations estimated that a population of 3,000 animals would be sufficient to detect statistically significant differences in phenotypic incidence of 20% between 2 genetic groups for all 6 health events.

Phenotypic Data

Herds, Animals, and Study Duration. Eleven large herds (average 4,180 lactating cows) distributed across the major dairy-producing regions of the United States were enrolled in this study based on 4 criteria: (1) did not contribute phenotypic data to the Zoetis genetic evaluation for wellness traits, (2) recorded health events at an incidence similar to the national incidence in the wellness trait genetic evaluation for at least 5 of the 6 health events (Vukasinovic et al., 2017), (3) were not applying selection pressure (e.g., heifer culling) based on genomically enhanced genetic predictions, and (4) were of sufficient size to have at least 200 first parity and 100 second parity projected calving events between September 1 and December 31, 2015. Animals in first parity in 2015 (age group A) and second parity in 2015 (age group B) were selected for our study, as these age groups represent the majority of lactating animals on US dairies. Enrolling multiple age groups in the study afford the opportunity to quantify the potential effects of selection bias in the first lactation on the genetic predictions and phenotypic incidence.