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Genotype by environment interactions on culling rates and 305-day milk yield of Holstein cows in 3 US regions

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ABSTRACT

The objective of this study was to investigate genotype by environment interactions for culling rates and milk production in large and small dairy herds in 3 US regions, using genotypes, pedigree, and phenotypes. Single nucleotide polymorphism (SNP) marker variances were also estimated in these different environments. Culling rates including cow mortality were based on 6 Dairy Herd Improvement termination codes reported by dairy producers. Separate data sets for culling rates and 305-d milk yield were created for large and small dairy herds in the US regions of the Southeast (SE), Southwest (SW), and Northeast (NE) for the first 3 lactation cows that calved between 1999 and 2008. Genomic information from 42,503 SNP markers on 34,506 bulls was included in the analysis to predict genomic estimated breeding value (GEBV) of culling rates and 305-d milk yield with a single-step genomic BLUP using a bivariate threshold-linear model. Cow replacement rates in large SE and NE herds were higher. Heritability estimates of culling rates ranged from 0.03 to 0.11, but the differences were small between large and small herds and among the 3 US regions. Genetic correlations between culling rates and 305-d milk yield were medium to high for cows sold for poor production and reproduction problems. Correlations of GEBV for culling rates among the 3 US regions ranged from 0.34 to 0.92 and were lower between the SW and the other regions, especially in small herds. Correlations of GEBV between large and small herds ranged from 0.44 to 0.90 and were lower in the SW. These results indicate genotype by environment interactions of cow culling rate between the US regions and between large and small herds. Correlations of top 30 SNP marker effects for culling rates between 2 US regions ranged from 0.64 to 0.98 and were higher than those of more SNP marker effects except for a culling reason "sold for dairy purpose." Those correlations between large and small herds ranged from 0.67 to 0.98. High correlations of top SNP marker effects on culling reasons between the US regions and between large and small herds suggest that major markers can be useful for selection in different environments. The SNP variance shown in a marker gene segment on chromosome 14 was strongly associated with milk production in large and small herds in the NE but not in the SE and SW. Marker genes on chromosome 14 also showed a strong association with cow culling rates due to poor production and mortality in large herds in the NE.

Key words: genotype by environment interaction, culling rate, milk production, US Holstein

INTRODUCTION

A single-step genomic BLUP (**ssGBLUP**) can predict not only genomic EBV (**GEBV**) for economically important traits in livestock using pedigree, genotypes, and phenotypes but also SNP marker effects or direct genomic values (**DGV**; Aguilar et al., 2010; Wang et al., 2012). To investigate the existence of genotype by environment interaction, correlation of DGV or SNP marker effects in different environments, as well as GEBV, can be used. These interactions may be identified more accurately using DGV or SNP effects because genotypes can contain more genetic information than pedigree by including Mendelian sampling.

Gene expression for performance in dairy cattle can differ depending on environmental conditions such as season or climate, age, feed or nutrient, and management (Kolmodin et al., 2002; Windig et al., 2005). Usually, performance in dairy cattle is a composite trait (e.g., milk yield is composed of water, fat, protein, lactose, and minerals). Gene expressions for these components are partly controlled by environment and may interact with each other. Survival traits such as productive life and stayability are also a composite trait. By analyzing culling reasons such as sold for dairy purposes, poor production, reproductive problems, or mastitis or dead, using DHI termination codes and genotypes, we may be able to separate the composite survival trait into several traits (culling reasons) because the high lon-

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gevity of dairy cows can be influenced by producer's culling decision based on milk production levels, cow health, milk market prices in the region, and genes, which can interact with environments. In addition, genotype by environment interactions for cow longevity may be strongly or weakly revealed using genomic information than using only pedigree information. It may result in improving productive life and longevity for cows more efficiently. Tsuruta et al. (2014) reported that heritability estimates for cow mortality and 305-d milk yield in Holsteins and genetic correlations between those 2 traits were different in 3 US regions (Southeast, Southwest, and Northeast). If correlations of GEBV for traits among the 3 US regions are not high (e.g., <0.9), it indicates that the genotype by environment interaction should exist and different breeding programs may be required in the 3 regions. Nowadays, culling rates including cow mortality reported in DHI can be likewise analyzed using genotypes although results from those traits may be difficult to interpret because the trait definition may differ across farms and regions. And main culling reasons such as "sold for dairy purpose" or "poor milk production" can be different in each farm, based on management and selection strategies.

The objectives of this research were to investigate genotype by environment interactions by comparing differences of GEBV and SNP marker variances of cow culling rates and milk production for US Holsteins in large and small herds across US regions, using the ssGBLUP with genotypes, pedigree, and phenotypes.

MATERIALS AND METHODS

Termination codes and 305-d milk yields recorded in the DHI Program were obtained from USDA-Agricultural Research Service (Beltsville, MD). The following 12 termination codes were recorded in DHI farms: 1: sold for locomotion problems (**LOCO**), 2: sold for dairy purposes (**DAIRYP**), 3: sold for poor production (**POORP**), 4: sold for reproductive problems (**REPRO**), 5: sold for other reasons (**OTH**), 6: died (**DD**), 7: sold for mastitis or high SCC (**MAST**), 8: lactation ended with abortion (**ABORT**), 9: sold for udder problems, 0: still in herd (**SIH**), **A**: sold for undesirable conformation, **B**: sold for aggressiveness. The DHI farm can chose one of the termination codes for a cow when she is culled. Nine out of 12 termination codes were reported in the Southeast (**SE**: North Carolina, South Carolina, Georgia, Florida, Tennessee, Alabama, Mississippi, Arkansas, and Louisiana), Southwest (**SW**: Oklahoma, Texas, New Mexico, and Arizona), and Northeast (**NE**: Maine, New Hampshire, Vermont, Massachusetts, Rhode Island, Connecticut, and New York) regions of the United States (Table 1). We chose these 3 regions because we expect different climates (SE: hot and wet, SW: hot and dry in summer, NE: warm in summer cold and wet in winter), different managements including herd sizes, and different milk markets (SE: fluid, SW: cheese, NE: fluid and cheese; USDA-AMS, 2014). No termination codes 9, A, or B were reported in these regions. Termination codes 1, 5, and 8 were excluded from this study because events of codes 1 and 8 were too few (1% or less) and code 5 contains multiple unknown reasons for culling. Thus, 6 termination codes including 5 culling reasons and SIH were analyzed. In these 5 culling reasons, DAIRYP and POORP can be classified as voluntary culling, whereas REPRO, DD, and MAST can be classified as involuntary culling. Cows that calved from 1999 to 2008 and had at least one test-day record for the first 3 lactations in each of the 3 regions were extracted from the DHI file. Although the cause of death was unknown, the code DD was included to define cow mortality in this analysis. In each region, the data set was split into 2 groups based on the number of cows per herd-year: large herds with ≥100 cows and small herds with <100 cows. The number 100 is arbitrary, creating almost equal-size data sets for small and large herds in NE, but larger-size data sets for large herds in SW because the average herd size is large in SW, compared with the herd size in SW and NE. Selection decision may be made by different reasons in small and large herds in the 3 regions.

A bivariate threshold-linear animal model was used to estimate genetic parameters and to predict genomic EBV (GEBV) for termination codes and 305-d milk yields as repeated records in the first 3 parities. Thus, the binary traits were defined as the probability (culling rate) a cow will be culled within the first 3 parities (DAIRYP, POORP, REPRO, and MAST), as the probability (mortality) a cow will be dead within the first 3 parities (DD), and as the probability (stayability) a cow will remain in the herd within the first 3 parities (SIH). The analysis was conducted separately for large and small herds in the 3 US regions. Table 2 presents the binary trait definition for termination codes. Cows with codes DAIRYP, POORP, REPRO, and MAST, which were culled for a reason, those with DD, which had died, and those with SIH, which stayed in the herd, were categorized as 1 (yes), otherwise 0 (no). The code for SIH in this bivariate model may be confusing. Each termination code was assumed exclusive and independent events. For instance, if a cow stayed in the herd, the code is 1 (yes) for the trait SIH, otherwise (a cow was culled for some reason or died), it is 0 (no). If a cow was culled for poor production, the code is 1 (yes) for the trait POORP, otherwise (a cow stayed in the herd or was culled for other reasons), it is 0 (no). When a