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Estimation of regional genetic parameters for mortality and 305-d milk yield of US Holsteins in the first 3 parities

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ABSTRACT

Several research reports have indicated increasing dairy cow mortality in recent years. The objectives of this research were to characterize the phenotypic differences in mortality in the first 3 parities across 3 regions of the United States to estimate the heritability of mortality of Holstein cows across regions and parities, and to estimate genetic and environmental correlations between milk yield and mortality across parities and regions. Dairy Herd Information (DHI) milk yield and mortality data were obtained from 3 different US regions: the Southeast (SE), Southwest (SW), and Northeast (NE). A total of 3,522,824 records for the first 3 parities were used: 732,009 (SE), 656,768 (SW), and 2,134,047 (NE) from 1999 to 2008. Cows that received a termination code of 6—“Cow died on the dairy; downer cows that were euthanized should be included here”—were given a mortality score of 2 (dead), whereas all other codes were assigned a mortality score of 1 (alive). Average annual mortalities in the first 3 parities across regions ranged from 2.2 to 7.2%, with mortality frequency increasing with increasing parity across all regions and with the SE having the highest mortality frequency. For genetic analysis, a 2-trait (305-d milk yield and mortality) linear-threshold animal model that fitted fixed effects of herd-year (for 305-d milk yield), cow age, days in milk (in month classes), month-of-termination, and random effects of herd-year (for mortality), animal, and residual was implemented. The model was used to estimate variance components separately for each region and parity. Heritability estimates for mortality were similar for all regions and parities, ranging from 0.04 to 0.07. Genetic correlations between mortality and 305-d milk yield across the first 3 parities were 0.14, 0.20, and 0.29 in SE; −0.01, 0.01, and 0.31 in SW; and 0.28, 0.33, and 0.19 in NE. We detected an adverse genetic relationship between milk production and mortality; however, the moderate magnitudes of the genetic corre-

lations suggest that indices that include both milk yield and mortality could be effective in identifying sires that would provide opportunities for minimizing death loss even when selecting for increased milk yield.

Key words: mortality, parity, region, US Holstein

INTRODUCTION

In the dairy industry, production traits such as milk, protein, and fat yields have been recognized as the most economically important traits, and therefore animals have been selected mainly for these traits (Miglior et al., 2005). As a result, a 16% increase in milk yield was obtained from 2003 to 2012 in the US milk cow population (USDA-NASS, 2013).

However, recent increases in mortality are a concern to dairy producers (Pinedo et al., 2010). Miller et al. (2008) analyzed a sample of herds from a national data set that was edited to exclude any records of mortality before the first test day and reported that dairy cow death frequency increased from 1.96% in 1996 to 4.63% in 2005. In 2007, annual cow mortality of 1.5% was estimated in the beef industry, whereas an annual cow mortality of 5.7% was reported in the dairy industry (USDA-APHIS, 2007, 2010).

Herd or regional differences that influence mortality include climate, nutrition, prevalence of diseases, and management. Because many of these factors are confounded and may differ across region, proper management is required to lower mortality within each herd or region. McConnel et al. (2008) has examined many herd management factors associated with dairy cow mortality. Several states within the United States have combinations of high heat and humidity during certain times of the year that can lead to heat stress conditions in high-producing dairy cows. Bohmanova et al. (2008) reported that states within the southeastern United States had a much higher frequency of test days where there was moderate to severe heat stress compared with those in the northeastern United States. West (2003) has reported that heat stress can cause body temperature to increase, leading to health problems, including death. Vitali et al. (2009) reported that high humidity

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Table 1. Distribution of 305-d milk yield and mortality records across parity and regions

Region	First parity		Second parity		Third parity	
	Milk	Mortality	Milk	Mortality	Milk	Mortality
Southeast	278,526	293,494	241,878	255,821	170,664	182,694
Southwest	259,922	272,934	217,352	227,413	147,924	156,421
Northeast	866,700	883,887	711,211	733,904	492,026	516,256

and temperature caused higher cow mortality due to heat stress. Currently, indirect selection to lower the risk of cow mortality is provided by selection on productive life (Cole et al., 2010). Productive life is included in the net merit formula, which is used for ranking dairy bulls and semen purchases by dairy farmers.

The objectives of this research were to characterize the phenotypic differences in mortality across regions and parity, to estimate heritability of mortality of Holstein cows in the first 3 parities in 3 US regions using DHI termination codes, and to estimate the genetic and environmental correlations between milk yield and mortality across parities and regions.

MATERIALS AND METHODS

Data

No animal care and use protocol was necessary for this research project because all the records used were field data. Dairy Herd Information data that contained records from 1999 to 2008 were obtained from the USDA Animal Improvement Programs Laboratory (Beltsville, MD). Lactation records of cows that had at least one test-day record, that were from parity ≤ 3 , and that had a termination or culling code were retained for analysis. Termination or culling codes included death (including downer cows that were euthanized), locomotion problems, poor production, reproduction problems, mastitis or high SCC, udder problems, other or not specified reasons, lactation with or without abortion, and selling for dairy purposes. For mortality analysis, cows with the termination code 6—“Cow died on the dairy; downer cows that were euthanized should be included here”—were assigned a code of 2, and cows that had other termination codes were assigned a code of 1. A total of 3,522,824 mortality and 305-d milk yield records in the first 3 parities in 3 regions were available for analysis. Table 1 presents the distribution of records across parities and regions. The 305-d milk yield records were standardized to 305-d and for age of cow (mature equivalent) using DHI adjustment procedures. Southeast (SE) data consisted of 732,009 records and included the following states: North Carolina, South Carolina, Georgia, Florida, Tennessee, Alabama, Mississippi, Arkansas, and Louisiana. Southwest (SW) data

consisted of 656,768 records and included the states of Oklahoma, Texas, New Mexico, and Arizona. Finally, the Northeast (NE) data consisted of 2,134,047 records from Maine, New Hampshire, Vermont, Massachusetts, Rhode Island, Connecticut, and New York.

Calculations for Phenotypic Trends

To describe the seasonal pattern of mortality, monthly mortality frequencies were calculated within region and parity with SAS software (SAS Institute, 2008). The mortality frequency for any month within a region and parity was the number of animals that received a termination code of death or euthanasia due to downer cow syndrome within that month expressed as a percentage of all cows present within each parity and region. The annual mortality within a parity and region can then be obtained by summation of the monthly mortality frequencies.

Models for Genetic Analysis

To estimate genetic parameters, the following 2-trait linear-threshold animal model was used for 305-d milk yield and mortality:

$$y_{ijklm} = HY_i + MOT_j + AGE_k + DIM_l + ANI_m + e_{ijklm}$$

where y_{ijklm} = observations of 305-d milk yield and mortality (binary; alive = 1 or dead = 2); HY_i = fixed (random) effect of herd year for 305-d in milk yield (mortality); MOT_j = fixed effect of month of termination; AGE_k = fixed effect of age of a cow; DIM_l = fixed effect of DIM (in month classes); ANI_m = random animal genetic effect; and e_{ijklm} = random error.

Covariances of genetic (G), herd-year (HY), and residual (R) effects are given below:

$$V(\mathbf{G}) = \begin{bmatrix} \sigma_{305}^2 & \sigma_{305,m} \\ \sigma_{m,305} & \sigma_m^2 \end{bmatrix},$$

$$V(\mathbf{HY}) = \begin{bmatrix} 0 & 0 \\ 0 & \sigma_{HY}^2 \end{bmatrix},$$

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