

Genome Wide Association Study on Cow Mortality in Three US Regions

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ABSTRACT: Our objective was to conduct a genome-wide association study on cow mortality and 305-d milk yield for three lactations and determine if there were differences in the genetic architecture in three US regions. Genomic EBV of mortality and milk yield were estimated with a single-step genomic BLUP using a threshold-linear model. Genomic information was included on 34,506 bulls. Data consisted of the entire US data and three regions SE: southeast, SW: southwest, and NE: northeast for first three lactation cows calving from 1999 to 2008. As expected, a segment on chromosome 14 was significantly associated with milk production in all regions. Chromosome 14 showed a strong association with the first parity mortality for the entire US, with NE showing a strong association for all three parities. Within SE and SW regions, no single region stood out for mortality on chromosomes for three parities.

Keywords: Genome wide association study; Cow mortality; Region

Introduction

The cow mortality rate increased from 3.8% in 1996 to 5.7% in 2007 (USDA-AIPL, 2007). McConnel et al. (2008) reported that cow mortality was associated with lameness, respiratory disease and mastitis and was dependent on management decisions in each region of the US. Cow mortality, from Dairy Herd Improvement reports, is farmer provided information. The termination code = “dead” is the primary reason given for a cow leaving a herd, particularly late in lactation. This trait can be difficult to interpret because its definition and recording method may differ across farms and regions. Our objective was to conduct a genome-wide association study (GWAS) on cow mortality and 305-d milk yield for three lactations and determine if there were differences in the genetic architecture associated with these traits in three different regions of the US.

Materials and Methods

Data. Genomic EBV of cow mortality and 305-d milk yield were estimated with a single-step GBLUP using a threshold-linear model. Specifics of termination codes are described in Tokuhisa et al. (2014). The single nucleotide polymorphism (SNP) file contained 42,503 usable SNP markers for 34,506 bulls obtained from USDA-AIPL. Data consisted of the entire US DHI data for three lactations for cows calving from 1999 to 2008 (Table 1). Three US re-

gions SE: southeast, SW: southwest, and NE: northeast were selected for regional comparison.

Table 1. Number of records in three regions and US.

Parity	SE [§]	SW	NE	US
1	293,494	272,934	883,887	6,233,306
2	255,821	227,413	733,904	5,179,887
3	182,694	156,421	516,256	3,542,544

[§]SE: southeast, SW: southwest, NE: northeast

Model. A bivariate threshold-linear animal model was used to estimate genetic parameters and genomic EBV (GEBV) for cow mortality and 305-d milk yield. The analysis was conducted separately for three parities and for three US regions and the entire US. The number of records and animals are presented in Table 1. The model for 305-d milk yield included: fixed effects of herd year, age at calving, month of calving and days in milk class and random additive genetic and residual effects, and the model for cow mortality included fixed effects of age at calving, month of termination and days in milk class and random herd year, additive genetic and residual effects.

Software. The Gibbs sampling program THRGIBBS1F90 (Tsuruta and Misztal (2006)) for threshold-linear models was used to estimate genetic parameters and predict GEBV. The POSTGIBBSF90 program was used to determine the convergence and calculate posterior means of genetic parameters and GEBV. For GWAS, PREGSF90 and POSTGSF90 by I. Aguilar were used to estimate SNP marker effects and those variances. The GWAS followed the methodology of Wang et al. (2012).

Results and Discussion

Cow mortality increased by year and parity (Table 2). The highest mortality was found in SE. Table 3 showed that heritability estimates for cow mortality in all regions were higher than 1.3% reported by Miller et al. (2008). Those estimates in the first parity were 4%, 6%, 6%, and 4% for SE, SW, NE, and US, respectively and were within ±0.01 for each region in later parities. Genetic correlations between cow mortality and 305-d milk yield in the first parity were 0.14, -0.01, 0.28, and 0.25 for SE, SW, NE, and US, respectively.

Table 2. Cow mortality (%) in three regions and US.

Parity	Year	SE [§]	SW	NE	US
1	98	2.2	1.5	1.2	1.1

	99	3.3	2.1	1.8	1.8
	00	3.2	2.2	1.8	1.8
	01	2.4	2.1	1.8	1.9
	02	2.4	2.1	1.9	1.9
	03	2.4	1.6	1.9	1.9
	04	4.1	2.5	2.5	2.4
	05	3.9	2.3	2.6	2.5
	06	4.6	3.2	2.7	3.0
	07	5.3	4.8	3.3	4.0
	All	3.3	2.4	2.2	2.2
2	98	3.0	1.9	1.7	1.4
	99	4.2	2.8	2.6	2.3
	00	4.1	3.3	2.6	2.4
	01	4.0	3.0	2.6	2.5
	02	3.5	2.5	2.7	2.4
	03	3.1	2.2	3.1	2.6
	04	5.5	3.0	4.2	3.4
	05	5.0	2.9	4.2	3.5
	06	6.4	4.3	4.9	4.4
	07	8.1	5.6	6.4	6.1
	All	4.8	3.3	3.7	3.2
3	98	4.3	2.8	2.1	1.8
	99	5.9	4.1	3.4	3.0
	00	5.8	4.2	3.4	3.3
	01	5.2	3.8	3.5	3.4
	02	5.1	3.3	3.6	3.4
	03	4.6	3.4	4.3	3.6
	04	8.4	4.9	6.2	5.0
	05	7.3	4.7	6.5	5.3
	06	9.6	6.0	7.3	6.5
	07	12.	9.2	10.3	9.4
	4				
	All	7.2	5.0	5.4	4.9

[§]SE: southeast, SW: southwest, NE: northeast

Table 3. Estimates of genetic parameters[&] for cow mortality and 305-d milk yield in three regions and US.

	SE [§]	SW	NE	US
Parity 1				
h ² _v : milk	0.28	0.32	0.35	0.29
h ² : mortality	0.04	0.06	0.06	0.04
Genetic correlation	0.14	-0.01	0.28	0.25
Parity 2				
h ² : milk	0.22	0.29	0.16	0.16
h ² : mortality	0.05	0.07	0.05	0.04
Genetic correlation	0.20	0.01	0.33	0.25
Parity 3				
h ² : milk	0.13	0.15	0.19	0.13
h ² : mortality	0.04	0.06	0.06	0.03
Genetic correlation	0.29	0.31	0.19	0.13

[§]SE: Southeast, SW: Southwest, NE: Northeast

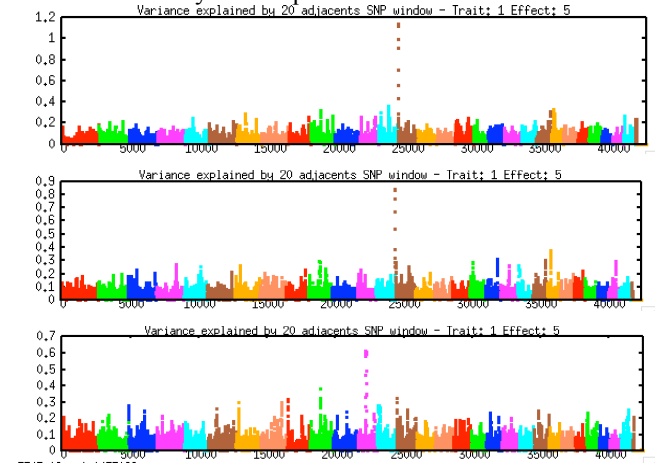
[¶]h²: Heritability

The genome was divided into equal segments of 20 sequential SNPs. As expected, a segment on chromosome 14 was significantly associated with milk production in all regions (Figure 1). The proportion of the total genetic variance for 305-d milk yield, explained by this segment, was 1%, 1%, 3% and 4% for SE, SW, NE region, and total US, respectively. Chromosome 14 showed a strong association with first parity mortality for the entire US, with the NE showing a strong association for all three parities (Fig-

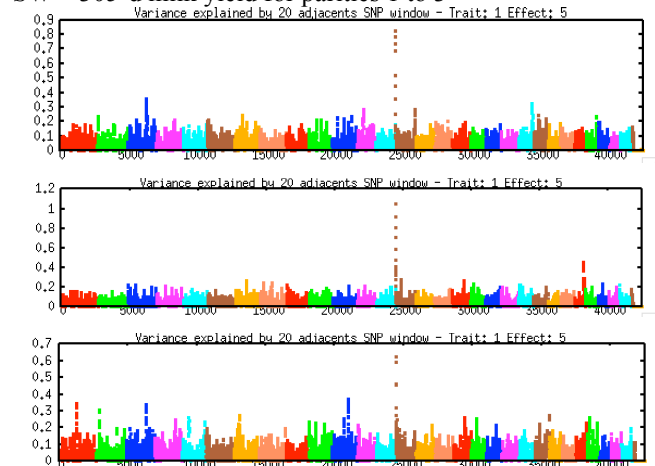
ure 2). Milk components (higher or lower %fat) could be a possible explanation. Within the SE and SW regions, chromosome 14 did not show a significant association for any of the three parities.

Figure 1: Manhattan plots for 305-d milk yield in three regions (SE: southeast, SW: southwest, NE: northeast) and US

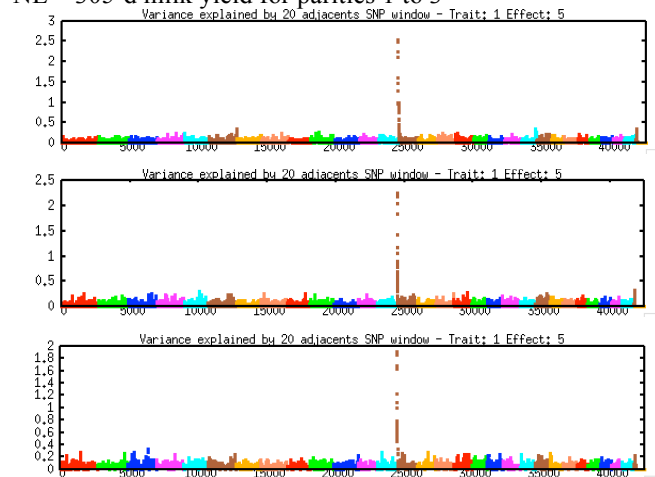
SE – 305-d milk yield for parities 1 to 3



SW – 305-d milk yield for parities 1 to 3



NE – 305-d milk yield for parities 1 to 3



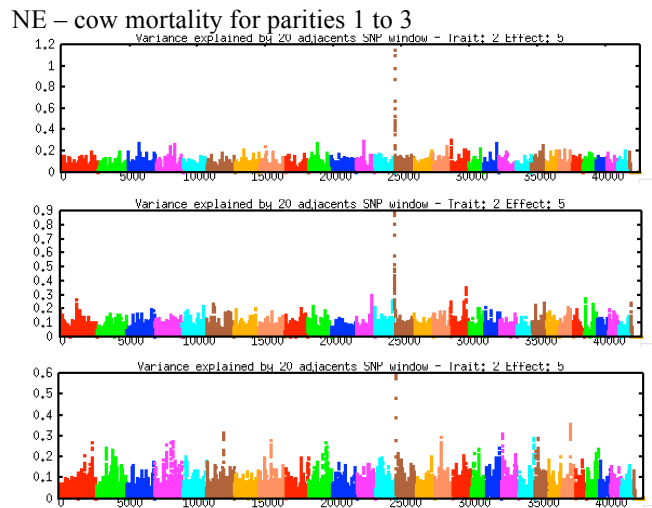
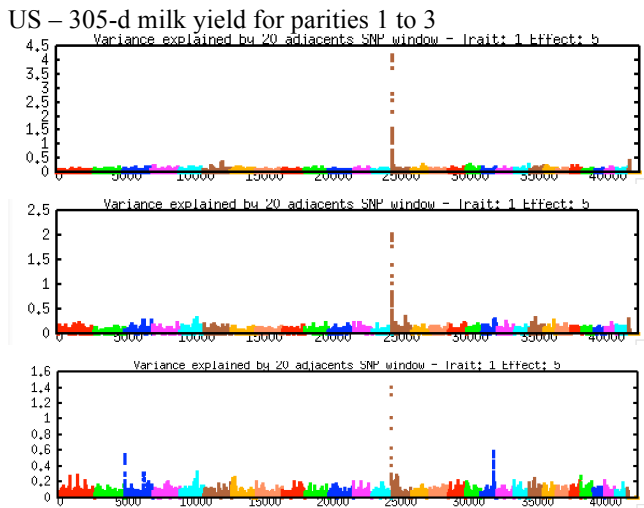
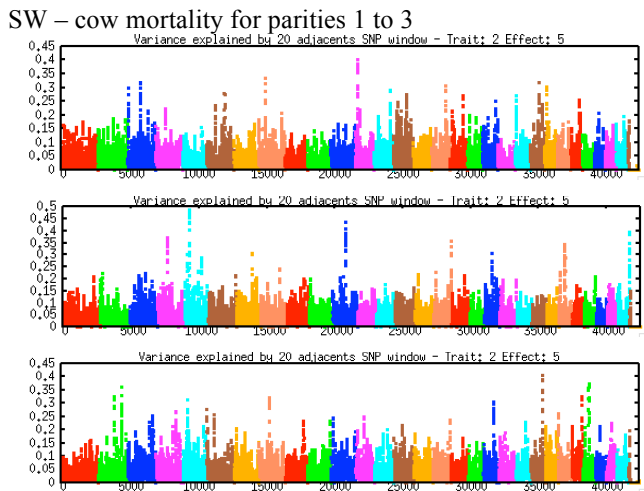
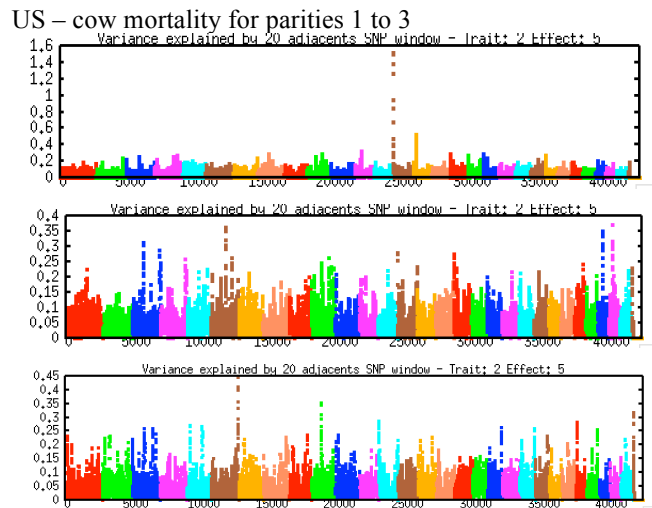
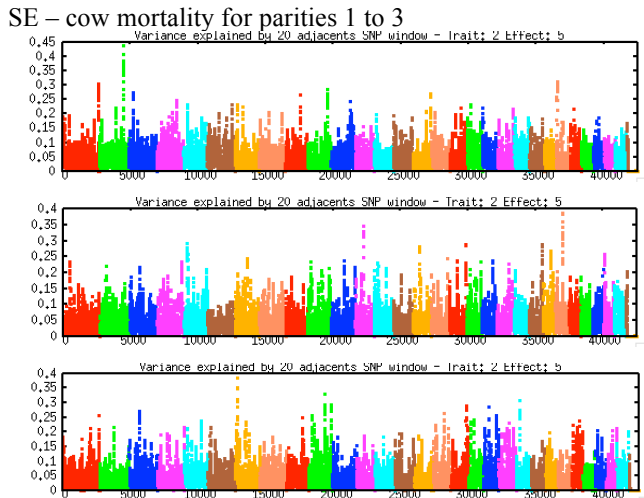


Figure 2: Manhattan plots for cow mortality in three regions (SE: southeast, SW: southwest, NE: northeast) and US



Conclusion

This farmer-recorded trait on cow mortality could be being interpreted differently and/or there could be different traits (genomic segments) responsible for cow mortality in different regions of the country.

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