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Modelling heat-stress genotype-by-environment interactions for milk yield in Texas and Wisconsin Holsteins

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Introduction

Heat Stress contributes to annual losses of 1.5 billion dollars in the U.S dairy industry (St-Pierre *et al*., 2003). By 2030, annual temperature is expected to rise 1.45-2.37°F, with US milk production decreasing by 0.6 to 1.35% (USDA-ERS, 2014). Genetic selection for improved heat tolerance has been studied as an effective permanent strategy (Aguilar *et al*., 2009; Dikmen *et al*., 2013, Tiezzi *et al* ., 2017). Genotype-by-environment (G×E) interactions associated with heat stress contribute to production losses, impaired fertility, welfare concerns, and increased complexity in genetic evaluations. Milk Test-day records collected at different environments provide an opportunity to model heat-stress effects and characterize how genetics respond to environmental variation through reaction norm models. The objective of this study was to evaluate the extent of heat stress using test-day milk yields of US Holstein cows in the states of Texas (TX) and Wisconsin (WI), as the initial step towards developing genomic predictions for heat tolerance.

Materials & Methods

Data- Data for this study were obtained from the National Cooperator Database which is managed by Council on Dairy Cattle Breeding, USA. It consisted of 854,650 milk test day records from 95,730 Holstein cows in Texas across 13 herds and 784,748 milk test day records from 87,275 Holstein cows in Wisconsin across 31 herds. To ensure representativeness, animals in their first lactation from larger management groups were selected. Herds with the highest number of animals were subsequently included until approximately 100,000 unique animal IDs were represented. Records with test days in milk exceeding 305 days were excluded from the dataset; 5-305 days. Records for animals with fewer than five test day observations were excluded to enhance data reliability. The filtered phenotypic data were categorized for a two-trait analysis into two seasonal groups: summer and non-summer. For the summer category, two definitions were used: (1) May to September and (2) June to August, referred to as the restrictive model.

Single-Trait Model- A repeatability test-day model was used to estimate the additive genetic component of general milk production. The analysis was conducted using the Average Information Restricted Maximum Likelihood algorithm implemented in blupf90+ family of programs (Misztal 2014).
The model used for these analyses was represented as:

$$y_{ijklm} = HTD_i + (DIM \times s)_j + Age_k + a_l + pe_l + \epsilon_{ijklm,}$$

where y_{ijklm} denotes the test-day milk yield, while HTD_i was the fixed effect of herd-test-day, defined by adding each test-day to the calving date. The stage of lactation $(DIM \times s)_j$ was categorized into 10 classes for days in milk specified by 30-d increments (5–34, 35–64, 65–94, 95–124, 125–154, 155–184, 185–214, 215–244, 245–274, and 275–305 d) and estimated as a fixed effect nested within 4 calving seasons (December to February, March to May, June to August, and September to November). Age (Age_k) was also added as a fixed effect to account for variations due to the age of cow. The random effects modelled included the additive genetic effect of the animal (a_l), permanent environmental effect (pe_l), and residual effect (e_{ijklm}).

Scenarios for Analysis- The single-trait analysis was conducted using five distinct scenarios to evaluate variations in test-day milk yield under differing environmental conditions. In the first scenario (*Combined),* we used the full dataset containing all test-day records. In the second scenario (*Summer)*, we focused on the summer months from May to September, while the third scenario (*Non-Summer)* analyzed test-day milk yields from the non-summer months, where all months excluding May to September were included. The fourth scenario (*Summer _Restricted*) restricted the dataset to a narrower summer period, specifically June to August, and the fifth cenario (*Non-Summer_Restricted*) evaluated a restricted non-summer period, excluding the months of June to August.

Two-Trait Model- A two-trait model was evaluated to estimate genetic correlations ($\mathbf{r_{g12}}$) between summer and non-summer test-day milk yields. We analysed same two scenarios; broad seasonal distinctions (*Summer*) and restricted peak-stress months of summer (*Summer_restricted*). Same fixed and random effects were used as the single-trait analysis to isolate genetic and environmental effects under varying heat loads.

Results & Discussion

Single-trait variance components and heritability- Variance component estimates for test day milk yield from single trait analyses are summarised in Table 1 for Texas and Wisconsin across five scenarios (combined, summer, non-summer and their restricted conditions). Across all scenarios, additive genetic variance accounted for a moderate proportion of the total phenotypic variance, resulting in consistent heritability estimates between locations.

Using the complete dataset (combined), estimated heritability (±SE) for milk yield was 0.23 ± 0.007 in TX and 0.22 ± 0.006 in WI. Additive genetic variance was lower in TX (40.7) than in WI (56.1), while residual variance was also lower in TX (83.3 vs. 103.7). The permanent environmental component explained a substantial proportion of phenotypic variance in both states, indicating the importance of long-lasting, non-genetic influences acting consistently across test days within cows.

During summer, heritability estimates were 0.24 ± 0.009 in TX and 0.23 ± 0.007 in WI, with slightly reduced genetic variance relative to non-summer months. Non-summer heritabilities were 0.22 ± 0.008 (TX) and 0.21 ± 0.007 (WI). In both locations, summer months were characterized by reduced residual variance, particularly under the restricted summer definition, suggesting lower short-term environmental heterogeneity during this period.

Restricted summer analyses yielded heritability estimates similar to those obtained using the broader summer definition. In TX, heritability remained stable at 0.23 ± 0.010, while in WI it was 0.22 ± 0.009. Across all scenarios, heritability estimates were similar between Texas and Wisconsin, indicating comparable proportions of additive genetic variance relative to total phenotypic variance, even though the absolute values of genetic, permanent environmental, and residual variances differed between states.

Table1. Variance components estimate and standard error for single-trait test-day milk yields for Texas and Wisconsin using 5 scenarios

Scenarios	Location	Genetic Variance	PE Variance	Residual Variance	Heritability (h^2)
Combined	Texas	40.69 ± 1.41	48.03 ± 1.14	83.29 ± 0.17	0.23 ± 0.007
	Wisconsin	56.13 ± 1.57	69.96 ± 1.14	103.65 ±0.19	0.22 ± 0.006
Summer	Texas	35.57 ± 1.56	51.12 ± 1.32	71.92 ± 0.26	0.24 ± 0.009
	Wisconsin	47.71 ± 1.71	85.12 ± 1.35	85.12 ± 0.27	0.23 ± 0.007
Non-Summer	Texas	42.47 ± 1.65	53.55 ± 1.36	79.07 ± 0.24	0.22 ± 0.008
	Wisconsin	54.41 ± 1.88	72.53 ± 1.42	103.93 ±0.26	0.21 ± 0.007
Summer_Restricted	Texas	34.40 ± 1.90	52.27 ± 1.63	65.50 ± 0.34	0.23 ± 0.010
	Wisconsin	45.56 ± 2.06	96.73 ± 1.70	65.85 ± 0.31	0.22 ± 0.009
Non-Summer_Restricted	Texas	40.29 ± 1.76	49.34 ± 1.46	84.29 ± 0.25	0.22 ± 0.009
	Wisconsin	54.41 ± 1.88	72.53 ± 1.42	103.93 ±0.26	0.21 ± 0.007

Two-trait analyses- Results from two-trait analyses treating summer and non-summer milk yield as distinct but correlated traits are presented in Table 2. In TX, estimated heritabilities were 0.24 ± 0.008 for summer and 0.22 ± 0.008 for non-summer, with a high genetic correlation of 0.91 ± 0.008. In WI, heritabilities were slightly higher, at 0.23 ± 0.006 (summer) and 0.25 ± 0.006 (non-summer), with an even stronger genetic correlation of 0.95 ± 0.005.

Restricted summer analyses produced results consistent with those obtained using the broader summer definition. In TX, heritabilities were 0.23 ± 0.008 (Summer) and 0.22 ± 0.008 (Non-summer), with a genetic correlation of 0.91 ± 0.008. In WI, heritabilities were 0.22 ± 0.008 and 0.21 ± 0.007, and the genetic correlation increased to 0.97 ± 0.004, indicating minimal genotype re-ranking between summer and non-summer milk production under restricted summer conditions.

Overall, the high genetic correlations observed in both states indicate that, under the seasonal definitions of heat stress used in this study, milk yield expressed under heat-stress and non-heat-stress conditions is largely controlled by the same genetic determinants. Nevertheless, moderate reductions in genetic variance during summer, particularly in Texas, suggest some sensitivity of milk yield expression to heat load, motivating further investigation using reaction-norm models.

Table2. Heritabilities and genetic correlations estimate for two-trait test-day milk yields for Texas and Wisconsin

Scenarios	Location	h^2 (Summer)	h^2 (Non-summer)	Genetic correlation (r_{g12})
Summer	Texas	0.24 ± 0.008	0.22 ± 0.008	0.91 ± 0.008
	Wisconsin	0.23 ± 0.006	0.22 ± 0.006	0.95 ± 0.005
Summer_Restricted)	Texas	0.23 ± 0.008	0.22 ± 0.008	0.91 ± 0.008
	Wisconsin	0.22 ± 0.008	0.21 ± 0.007	0.97 ± 0.004

Future studies include to calculate a heat load function using weather station data to split the data into records collected into hot or thermoneutral conditions. Then expand the model to evaluate the impact of heat stress on protein, fat, and somatic cell count and further states. A genome-wide association study will be implemented to search for genomic regions associated with heat tolerance.

Conclusions

The results suggest that a two-trait model is effective in capturing seasonal effects related to heat stress definition explained in the study. Heat stress in TX was expected to be higher than WI. Preliminary results suggest a potential reranking in TX but genomic predictions with environmental data may make it clear. Genetics of heat stress in WI did not suggest a significant re-ranking of animals.

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