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Incorporating multiple meteorological variables into genetic evaluation models for growth traits in American Angus cattle

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Introduction

The performance of beef cattle raised under extensive conditions is directly influenced by the environmental conditions in which they are exposed. The cow calf sector in the USA beef cattle production is primarily pasture-based, with herds experiencing varying levels of climate variability across locations. Several studies defined discrete USA ecoregions by clustering normalized historical series of climate variables to study population structure and diversity and estimate genotype-by-environment (GxE) interactions (Blackburn *et al.,* 2017; Braz *et al.,* 2021). Advances in geographic information systems (GIS), together with the availability of historical weather time series at finer spatial and temporal resolution allow a more detailed characterization of the environmental conditions experienced by animals from a contemporary group in a given location. In previous studies, we classified herds according to their climate variability, and observed greater variability in genetic and phenotypic trends in herds exposed to more fluctuating environments (Rovere *et al.,* 2022). Incorporating climate variables into genetic prediction models may help better characterize environmental conditions affecting traits of interest and estimate GxE interactions along gradients of local climate variables. In this context, the objective of this study was to evaluate the effects of different farming environments on growth traits in American Angus cattle.

Materials & Methods

Phenotypic and pedigree data for weaning weight adjusted to 205 days (WW205) were provided by the American Angus Association (Saint Joseph, MO, USA). The dataset included animals born between 1990 and 2019, comprising 574,550 phenotypic records and a pedigree file with 725,311 animals. The data comprised 35 herds located in areas with different climate conditions over the period studied, described in previous studies (Rovere *et al.,* 2023). Herd locations were classified into five groups based on the frequency of higher-than-usual temperature-humidity index (THI) events during the period considered. Specifically, five herds were selected from each of groups 1 to 4 (lower extreme THI frequency) and 15 herds from group 5 (highest extreme THI frequency), to balance the amount of information across climate groups. Two birth seasons were defined: season 1 (S1), from October to March, and season 2 (S2) from April to September. Herd-year-season groups with fewer than five records were excluded from the analyses. The historical time series used to characterize the farming environment consisted of daily meteorological data collected from NASA Power (Sparks, 2018), and corresponding to the GPS coordinates of each herd.

Statistical models. A principal component analysis (PCA) was performed on birth herd-year-season combinations using the mean of daily records of the season of eight meteorological variables[1]. We used the squared cosine of the first principal component (54.7% of the total variance) to quantify the distance of the environment at each herd location from the center of the climatic space considered. We used this measure to characterize the climate of herd locations, and it was scaled (cos_s^2) for inclusion in the statistical analyses. The first model was used to estimate the environmental effect on WW205:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{e}, \quad (1)$$

where **y** is a vector of WW205 records; **b** is a vector of fixed effects including age of the dam (5 levels); calf sex (2 levels); the combined effect of herd-birth year (967 levels), which is the effect of interest; and the combined effect of cos_s^2 and season. Season had two levels (S1, S2) and cos_s^2 was categorized in 7 levels defined as: [0,0.1], (0.1,0.2], (0.2,0.3], (0.3,0.4], (0.4,0.5], (0.5,0.6], and (0.6,1.0]; $\mathbf{a} \sim N(0, \mathbf{A}\sigma_a^2)$ represents the random additive genetic effects, where **A** is the pedigree-relationship matrix and σ_a^2 is the total additive genetic variance; **X** and **Z** are the corresponding incidence matrices of the described effects; and $\mathbf{e} \sim N(0, \mathbf{I}\sigma_e^2)$ is the vector of residuals, such that σ_e^2 is the residual variance. A second model, a reaction norm model, aimed to estimate GxE interactions, was defined as:

$$\mathbf{y} = \mathbf{X_r b_r} + \mathbf{Z_r a_r} + \mathbf{e}, \quad (2)$$

where $\mathbf{b_r}$ is a vector of the fixed effects in Model (1), excluding the combined effect of cos_s^2 and season, and $\mathbf{X_r}$ is the corresponding incidence matrix; $\mathbf{Z_r}$ is a matrix of four covariates associated to a third-order Legendre orthogonal polynomial on cos_s^2: (1) a constant term, and (2-4) the first, second, and third-order polynomials; $\mathbf{a_r} \sim N(\mathbf{0}, \mathbf{G} \otimes \mathbf{A})$ is the vector of additive genetic effects associated to the Legendre orthogonal polynomials of cos_s^2, such that **G** is a 4x4 matrix of total additive genetic (co)variances associated to random regression coefficients in $\mathbf{a_r}$; and $\mathbf{e} \sim N(0, \mathbf{I}\sigma_e^2)$ as in Model (1). The genetic (co)variances at a given cos_s^2 were obtained as $\mathbf{Var\Sigma = zGz'}$, where **z** is the vector of Legendre orthogonal polynomials covariates evaluated at that cos_s^2 value. The heritability was calculated as $Var\Sigma_i / (Var\Sigma_i + \sigma_e^2)$. The analyses were implemented using the BLUPF90 family of programs (Lourenco *et al.,* 2022).

Results & Discussion

The geographical distribution of the herds analyzed is presented in Figure 1.A, identified by their climate group and the number of records representing each climate group previously defined. Figure 1.B shows the relative contribution of the eight climate variables to the first two principal components. Temperature and snow related variables contributed most to the first principal component, whereas wind and humidity related variables contributed most to the second principal component. Precipitation contributed similarly to both principal components (~9-10%). Fifty percent of the data had cos_s^2 below 0.24, and only 25% were above 0.43, which occurred in 12 herds (34% of the herds). The distribution of records by season was S1~79% and S2~21%, although every herd had records in both seasons. The range of cos_s^2 in S1 (0-1) was broader than that in S2 (0.00-0.46), indicating more variation in the farming environments during S1. The results of Model (1) showed that the average WW205 decreased from the lowest to the highest values of cos_s^2 in both seasons, with larger differences in S1 (~43.5 kg between the extremes, Figure 2.C). Farms with records in more extreme environments (high cos_s^2) varied with the season. Figures 2.A and 2.B show the geographical distribution of herds

[1] T2M, T2M_MIN, T2M_MAX= average mean, maximum and minimum temperature; WS2M, WS2M_MIN= mean and minimum wind speed; SNODP= snow depth; RH2M= relative humidity; PRECTOTCORR= total precipitation. https://power.larc.nasa.gov/parameters/

classified by their average of cos_s^2 in each season over the period. We classified cos_s^2 into five groups, dividing the range cos_s^2 of each season into five equal intervals. The estimated heritability (h^2) from Model (1) was 0.50 (±0.003). From Model (2), the h^2 estimates were highest at the extreme values of cos_s^2 and ranged from 0.66 to 0.74 (±0.007). From the interval [0.1, 0.9] of cos_s^2, the h^2 estimates decrease continuously from 0.60 (± 0.006) to 0.39 (± 0.007).

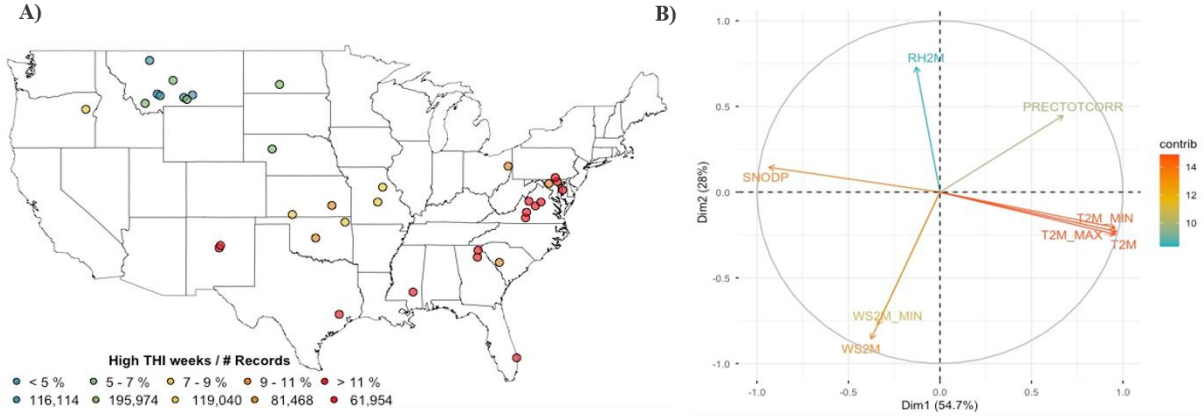

Figure 1. (A) Geographical distribution of herds classified by climate group, and amount of information contributed by each climate group to the study. (B) Relative contribution of eight climate variables[1] considered in the PCA to the first and second principal components.

The h^2 estimates were consistent across models; however, they were higher than those reported in previous studies for the direct h^2 in models with maternal effects (Bradford *et al.,* 2016; Jang *et al.,* 2022). In particular, h^2 estimates at intermediate values were more similar to those reported in the literature. The genetic correlations among breeding values at 10 equidistant points of cos_s^2 (ranging from 0 to 1) varied from 0.98 to -0.19. In general, the lowest correlations were observed between more extreme values of cos_s^2; however, even at lower values of cos_s^2 (<0.4), the genetic correlations decreased to 0.92, 0.77, and 0.43, indicating substantial GxE interactions (Figure 2.D). Bradford *et al.* (2016) used a heat load function as a covariate in a reaction norm model. The authors reported genetic correlations below 0.50 for large differences in heat load in WWT (direct genetic effects). In the present study, we sought to go beyond the already-studied effect of heat stress, incorporating multiple climatic variables to better characterize the environments experienced by animals across contemporary groups. The proposed methodology is well-suited for integration into genetic evaluation models; however, its biological interpretation is less straightforward. The average farming environment was defined by a combination of eight climatic variables, and extreme values of the environmental index may correspond to different climatic situations, as illustrated in Figures 2A and 2B. A relatively low number of phenotypic records under extreme climatic conditions limits the precision of estimates, and caution is needed when interpreting the results. However, the correlations between breeding values at intermediate cos_s^2 levels decreased as the environmental gradient increased. This pattern might indicate GxE interactions, even within the range of conditions most commonly represented in the data.

Conclusions

Incorporating multiple meteorological variables into genetic evaluation models enabled more detailed characterization of non-genetic effects and GxE interactions. Moreover, accounting for such information on GxE interactions can improve the accuracy of selection decisions, by enabling a better choice of those selection candidates best suited to specific environmental conditions.

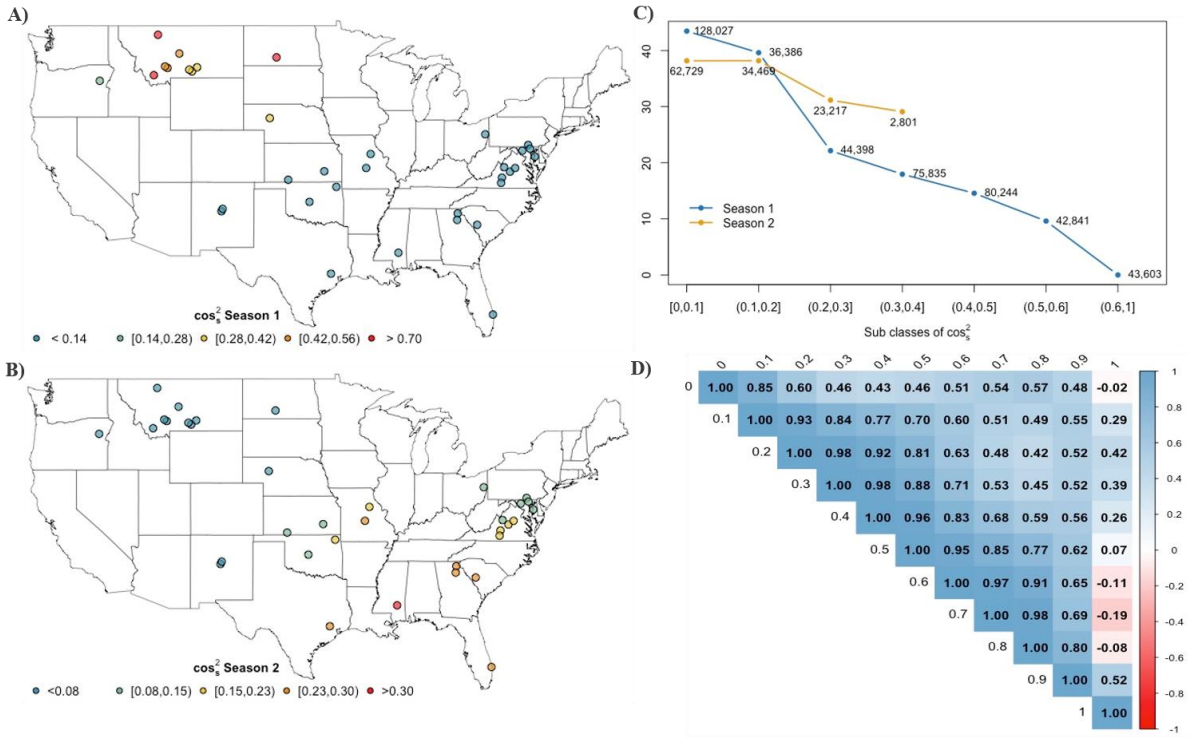

Figure 2. A) and B) Geographical distribution of the herds classified by group of cos_s^2 in seasons 1 (S1) and 2 (S2). C) Effect of cos_s^2 on WW205 in seasons 1 and 2 from model (1). D) Genetic correlations between breeding values at different cos_s^2 from model (2).

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