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1 Phenotypic and genetic trends in American Angus associated with climate variability

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3 G. Rovere^{1*}, B.C.D. Cuyabano², B. Makanjuola¹, S. Kelly³, C. Gondro¹

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5 ¹ Department of Animal Science, Michigan State University, 474 S Shaw Ln, East Lansing, MI
6 48824, USA; ² Université Paris Saclay, INRAE, AgroParisTech, GABI, Domaine de Vilvert,
7 78350 Jouy-en-Josas, France. ³ BEACON Center, East Lansing, MI 48824, USA.

8 [*roverega@msu.edu](mailto:roverega@msu.edu)

9 10 Abstract

11 Climate change is expected to not only increase the frequency of extreme weather events, but
12 to also increase the variability of climate conditions within geographical locations. Within the
13 context of climate, livestock genetics research has mostly focused on GxE interactions and on
14 selection for specific environments. This approach, however, does not address the sensitivity of
15 animals to unstable environmental conditions, a likely scenario due to climate change. In this
16 study, we explored the association between the variation in climate variables and the historical
17 trends of growth traits in American Angus beef cattle. Analyses were performed using historical
18 climate data, and phenotypic records of birth, weaning and post-weaning weights from Ameri-
19 can Angus beef cattle over the last three decades, from herds covering a wide area of the United
20 States of America (USA). Results suggest a greater variation of both phenotypic and genetic
21 trends in regions with high climate variability.

22 23 Introduction

24 One of the most pressing issues that humanity faces is the challenge of feeding a continuously
25 growing population in an environment that is being disrupted by climate change. Due to the
26 current concerns related to climate change there is an immediate need for breeding programs to
27 reduce the environmental footprint of animal production (*e.g.* methane emission) and at the
28 same time increase the resilience of animals to environmental changes. This is particularly rel-
29 evant for beef cattle production systems which are largely extensive, and animals are constantly
30 exposed to a broad range of environments (*e.g.* heat stress, which has a negative effect on com-
31 mercial traits in beef cattle (Bradford et al., 2016)). In terms of climate, livestock genetic re-
32 search has mostly focused on estimation of GxE interactions (Fennewald et al., 2018) and on
33 selection for specific environments, viz recent studies that evidenced within-breed genetic diver-
34 sity associated with different ecoregions in the USA that were defined based on the historical
35 means of several climate variables and topography (Blackburn et al., 2017; Braz et al., 2021;
36 Rowan et al., 2021). However, one of the frequently noted outcomes of climate change is the
37 increasing climate variability and frequency of extreme events (Trenberth et al., 2015; Stott,
38 2016). It may be the case that subregions within these ecoregions suffer differently the effect
39 of climate variability over the years. The objective of this study was to explore the association
40 between the variability of climate conditions and the historical growth traits trends in American
41 Angus beef cattle.

42 43 Materials & Methods

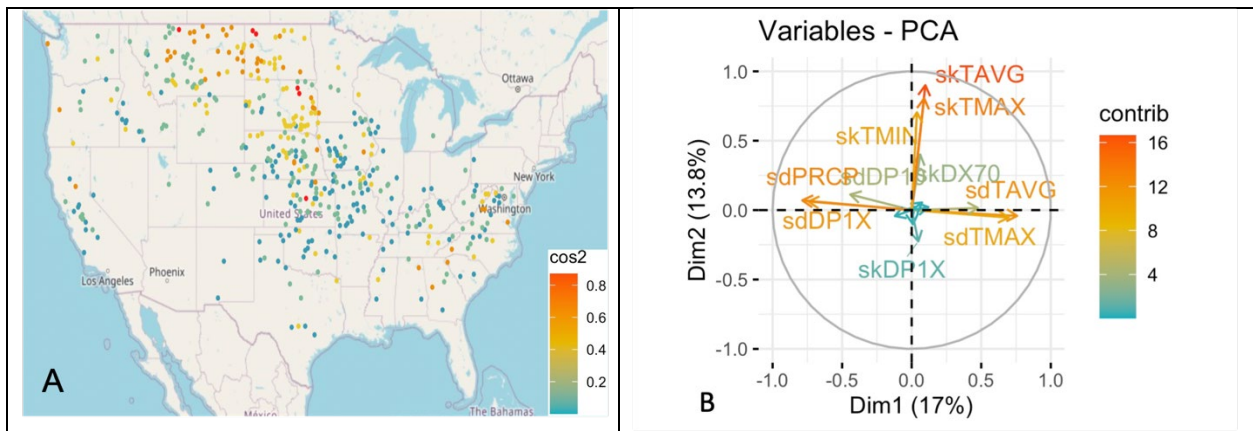
44
45 **Animal performance data.** Phenotypic and pedigree information was provided by the Ameri-
46 can Angus Association. We performed the analysis on phenotypes recorded between 1990 and
47 2019 from 448 herds, all herds with at least 25 years of records and a minimum of 10 records
48 per year-season (two seasons defined). Birth weight (BW), weaning weight (WW) and post-
49 weaning weight (PWW) were recorded for a total of 1,754,310 Angus cattle.

50 **Climate data.** We used historical time-series climate data from 2,334 weather stations spread
 51 across the continental USA (Menne et al., 2012). Eight variables¹ based on temperature and
 52 precipitation were selected from weather stations with at least 25 years of records between 1990
 53 and 2019. A Principal Component Analysis (PCA) was carried out using the standard deviation
 54 and skewedness of each of the eight variables for each station during the period of interest.
 55 From this PCA, we used the squared cosine (COS2) of the components to calculate the distance
 56 of a given observation (station) from the center of the system. COS2 was then used as a proxy
 57 for each station's climate variability (ClimVar). Finally, we classified the weather stations into
 58 five ClimVar groups using the values of COS2 as: low [0-0.2], medium-low (0.2-0.4], medium
 59 (0.4-0.6], medium-high (0.6-0.8] and high (0.8-1]. Using GPS coordinates, the herds used in
 60 this study were associated to each weather station and their corresponding ClimVar group.

61
 62 **Genetic evaluation model.** Variance components and estimated breeding values (EBV) were
 63 obtained using a single trait model $\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}\mathbf{a} + \mathbf{e}$, where \mathbf{y} are the phenotype records (of
 64 BW, WW or PWW); \mathbf{b} are the coefficients of the fixed effects (herd-year-season – 16,047 lev-
 65 els; sex – two levels, male or female; age of the dam at calving – four levels, 2yo, 3-5yo, 6yo,
 66 or 7-12yo; for WW and PWW the linear and quadratic effects of the age of the animal was
 67 included as well) and \mathbf{X} is their design matrix; $\mathbf{a} \sim N(\mathbf{0}, \mathbf{A}\sigma_a^2)$ are the breeding values and \mathbf{Z} is
 68 their design matrix, with \mathbf{A} as the numerator relationship matrix based on the pedigree;
 69 $\mathbf{e} \sim N(\mathbf{0}, \mathbf{I}_n\sigma_e^2)$ are n random residuals. \mathbf{A} was built tracing three generations back from the ani-
 70 mal with records and comprised 2,208,105 animals. The analyses were implemented using
 71 airemlf90 which is part of the BLUPF90 family of programs (Miszta et al., 2014).

72
 73
 74

Results

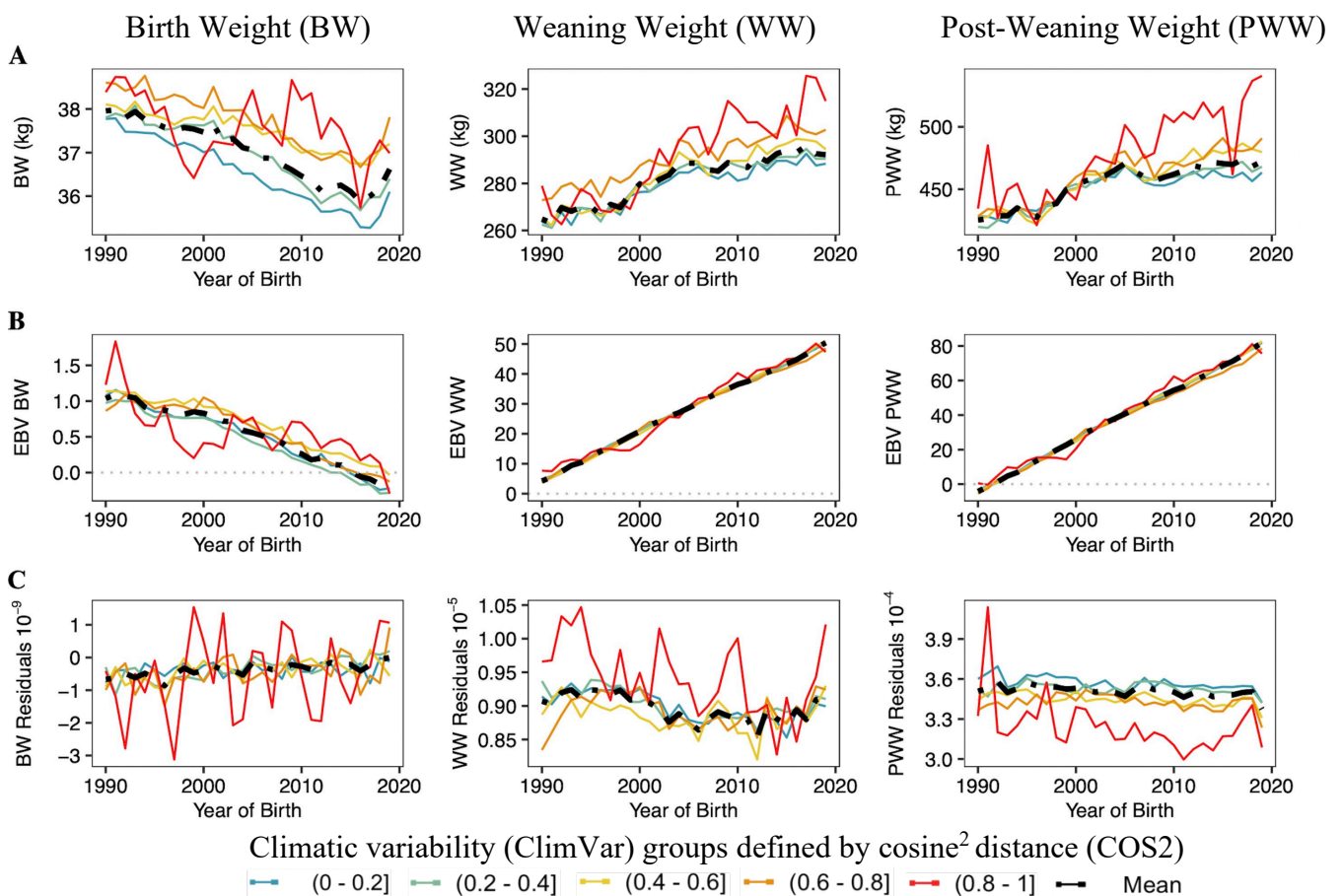


75 **Figure 1. (A) Location of Angus herds classified by cosine square (COS2) distances; (B)**
 76 **Contribution of the skewness and standard deviation of each climate variable used to**
 77 **build COS2.**

78
 79 Figure 1 shows (A) the geographical location of the herds used in the analysis and their ClimVar
 80 grouping; and (B) the contribution of the skewness and standard deviation of each of the eight
 81 climate variables used to classify the herds into a ClimVar group. We noticed that herds located
 82 in the central-north region of the country were closer to locations with higher ClimVar during
 83 the analyzed period. These locations mostly correspond to the ecoregion denominated 'high

¹ Average mean, maximum and minimum temperature in the year, total precipitation per year, number of days with maximum temperature ≥ 21.1 °C in the year, number of days with maximum temperature ≥ 32.2 °C in the year, number of days with ≥ 2.54 millimeters precipitation in the year, number of days with ≥ 25.4 millimeters precipitation in the year.

84 plains' by Braz et al. (2021). Approximately 40% of the phenotypic records were from herds
 85 classified as medium to high ClimVar. The variables with a higher contribution in the PCA
 86 analysis were the standard deviations of the average and maximum temperature (sdTAVG and
 87 sdTMAX), and the variables related to precipitation, *i.e.* the variability of the total amount of
 88 precipitation per year (sdPRCP) and the number of days with ≥ 25.4 mm of rain in the year
 89 (sdDP1X). We also observed that the skewness of the average, maximum and minimum tem-
 90 peratures (skTAVG, skTMAX, skTMIN) were relevant, although mostly associated with the
 91 second component of the PCA analysis. Figure 2 shows the average phenotypic, genetic, and
 92 residual trends by year of birth, for herds located in the five ClimVar groups. We observed a
 93 decreasing trend for BW, while WW and PWW showed an increasing trend along the years.
 94 These trends are in line with the general emphasis given to selection traits in beef cattle breeding
 95 programs. Herds associated with high ClimVar showed a more irregular trend, especially for
 96 phenotypes.



99

100 **Figure 2. Average (A) phenotypic, (B) genetic, and (C) residual trends by birth year for**
 101 **herds located in the five ClimVar groups, for birth weight (BW), weaning weight (WW)**
 102 **and post-weaning weight (PWW).**

103

104 A greater difference between the extreme ClimVar groups (low and high) was observed for
 105 phenotypic and genetic trends of BW, a rather unexpected result since BW is a phenotype mod-
 106 ulated by the maternal environment and should be less directly influenced by changing weather
 107 conditions. The residual trends of the herds classified as high ClimVar were distinct for all three
 108 traits, however in the three traits residuals were more unstable for herds in the highest ClimVar
 109 locations.

110 **Discussion**

111 The USA uses ~45% of its area for agriculture and livestock production (The World Bank,
112 2021), which spans a large area with very different climate conditions. Previous studies sug-
113 gested that the information from different ecoregions based on historical climate data averages
114 can be useful for beef cattle production (e.g. Blackburn et al., 2017; Braz et al., 2021). Here,
115 instead of considering these different ecoregions, we considered the climate variability over the
116 last 30 years to geographically distinguish herds by classifying them in five climate variability
117 (ClimVar) groups. High ClimVar was detected in several regions of the USA. Our objective
118 was to examine the trends of Angus beef cattle growth traits in herds with 25 to 30 years of
119 records when the environmental conditions are unstable (*i.e.* high ClimVar). These trends
120 showed higher variability across the years when compared to herds in more stable weather
121 conditions, although it should be noted that a smaller number of herds were in these high
122 ClimVar locations. The phenotypic trajectory of the higher ClimVar groups were above the
123 mean trajectory, but it was less obvious for the genetic trends. Then, it is possible that the un-
124 stable climate condition biased mostly to beneficial conditions or that the management system
125 adopted effectively neutralized the climate variability. The model used to obtain EBVs included
126 the environmental effect of the contemporary group, however ClimVar groups showed different
127 patterns indicating that more environmental effects could be accounted for in the model. These
128 results reinforce the idea that the inclusion of climate variables and the development of novel
129 methodologies can be of value for traditional genetic and phenotypic prediction models. Addi-
130 tionally, analyses that account for climate variability may be an alternative method to evaluate
131 resilience to environmental changes instead of the use of specific environmental stressors.

132

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