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GEOREFERENCED EVALUATION OF GENETIC PATTERNS OF MONTANA TROPICAL® CATTLE

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SUMMARY

The influence of environmental (normalized difference vegetation index (NDVI), rainfall, minimum, maximum and average temperatures, altitude, relative humidity and temperature and humidity index) and socioeconomic (gross domestic product, number of inhabitants, municipal area and human development index) factors on the genetic distribution of Montana Tropical® beef composite cattle located in 41 counties. Expected progeny differences (EPD) of 455,175 animals for weights at weaning and at 14 months of age, post-weaning weight gain, scrotal circumference and muscle score were used to group the counties into five clusters by SAS® PROC FASTCLUS. Discriminant analysis identified significant differences between the clusters due to altitude, NDVI and maximum and minimum temperatures, by t-Student test. However, it was not possible to identify a clear relation between the cluster means for these factors and the genetic distribution of Montana® herd. Using environmental and socioeconomic information to classify the counties into the previously formed groups, the percentage of correct classifications was much lower than the classification based on EPD, which reinforces the weak influence of those factors on the genetic clustering proposed.

INTRODUCTION

The Montana Tropical® beef composite cattle, raised in Brazil since 1994, aims to exploit the benefits of heterosis and complementarity between breeds by crossing four biological groups. In this system, animal's racial composition is not fixed, which allows the customization of herds according to the conditions of each region. Hermuche *et al.* (2012, 2013) and Costa *et al.* (2014) demonstrated that environmental and socioeconomic factors can influence the dynamics of animal production and the genetic structure of populations in sheep and Holstein cattle, respectively. Manel *et al.* (2003) proposed combine molecular data and environmental conditions information for a better understanding of how geographical and environmental factors can influence the genetic structure of populations, an approach called landscape genetics. Costa *et al.* (2014) highlighted that many of these studies were done using molecular information, while few were conducted based on the genetic value of animals.

In view of racial diversity of Montana Tropical® herd and its diffusion throughout the Brazilian territory, the present study aimed to analyze the influence of environmental and socioeconomic conditions of counties in its genetic distribution.

MATERIALS AND METHODS

The analysed data consisted of 455,175 animals from 57 farms located in 41 cities placed in nine Brazilian federal states (Espírito Santo, Goiás, Minas Gerais, Mato Grosso do Sul, Mato Grosso, Pará, Rondônia, Rio Grande do Sul and São Paulo) located in Central-West, North, South and Southeast regions. Estimated progeny differences (EPD) for weights at weaning and 14 months of age, post-weaning weight gain, scrotal circumference and muscle score, which are the traits considered in selection index of Montana® breeding program, were evaluated.

These animals belong to the genetic breeding program of Montana Tropical® cattle managed by CFM-Leachman Pecuaria Ltda., whose genetic evaluations are conducted by the Animal Breeding and Biotechnology Group of the College of Animal Science and Food Engineering of University of Sao Paulo.

Environmental and socioeconomic data were obtained from different sources: NASA (National Aeronautics and Space Administration), IBGE (Brazilian Institute of Geography and Statistics) and INMET (National Meteorological Institute).

The environmental variables evaluated were: normalized difference vegetation index (NDVI), rainfall, minimum, maximum and average temperatures, altitude, relative humidity and temperature and humidity index. Additionally, the socioeconomic variables considered were: gross domestic product, number of inhabitants, municipal area and human development index.

The 41 cities were grouped into five clusters by PROC FASTCLUS procedure of SAS® software, being the cluster 1 composed by the counties with highest mean EPD values for studied traits and cluster 5 by the lowest ones. The determination of environmental and socioeconomic factors that differ between the clusters was performed by PROC GLM procedure of SAS® software. Additionally, discriminant analyses were performed by PROC STEPDISC and PROC DISCRIM procedures of SAS® software.

RESULTS AND DISCUSSION

The 41 counties, where the evaluated Montana Tropical® herd is raised, were grouped into five clusters and the mean EPD for analyzed traits per cluster were presented in Table 1. The clusters differed on the mean EPD values for weaning (WW) and 14 months of age (W14) weights, post-weaning weight gain (PWG), scrotal circumference (SC) and muscle score (MS). Cluster 1 was composed by the counties with highest mean EPD values and cluster 5 by the lowest ones. The number of counties (animals) per cluster was 3 (4,893), 4 (81,553), 16 (238,141), 12 (123,818) e 6 (6,770), in this order.Analysing the differences between clusters due the environmental and socioeconomic factors, only NDVI (p=0.08) and altitude (p=0.05) were significant by test F. However, the comparison of the mean values between clusters for the same factors, under t-Student test, revealed additional significant differences by maximum and minimum temperatures (Table 2). Although, the t-test is less rigorous than the F test, it was chosen to present these results in view of the pioneering nature of the present study in the search for environmental and socioeconomic variables that explain the genetic distribution of Montana Tropical® animals in the country. The analysis of the mean values for these four environmental factors by cluster (Table 2) didn’t allow a clear identification of their influence on the genetic distribution of Montana Tropical® beef cattle.

Using all the environmental and socioeconomic information to classify the counties into the previously formed groups (Table 3), the percentage of correct classifications was much lower than the classification based on EPDs (Table 4), which reinforces the weak influence of those factors on the genetic clustering proposed.

Table 1. Descriptive statistics of EPD by cluster for weaning (WW) and 14 months of age (W14) weights, post-weaning weight gain (PWG), scrotal circumference (SC) and muscle score (MS).

Cluster	Trait	Mean	STD	Minimum	Maximum
1	WW (kg)	3.78	1.29	2.99	5.27
	W14 (kg)	6.02	1.36	4.58	7.29
	PWG (kg)	1.74	1.12	0.65	2.88
	SC (cm)	0.32	0.05	0.29	0.38
	MS (unit)	0.14	0.02	0.13	0.16
2	WW (kg)	2.63	0.65	1.93	3.45
	W14 (kg)	2.40	0.61	1.66	3.11
	PWG (kg)	0.31	0.16	0.13	0.51
	SC (cm)	0.15	0.05	0.08	0.20
	MS (unit)	0.06	0.01	0.04	0.07
3	WW (kg)	1.25	0.39	0.54	1.90
	W14 (kg)	1.06	0.33	0.53	1.62
	PWG (kg)	0.24	0.21	-0.22	0.56
	SC (cm)	0.06	0.03	0.02	0.12
	MS (unit)	0.03	0.01	0.01	0.05
4	WW (kg)	-0.08	0.42	-0.63	0.54
	W14 (kg)	-0.11	0.46	-0.89	0.47
	PWG (kg)	-0.06	0.27	-0.48	0.42
	SC (cm)	-0.01	0.04	-0.11	0.03
	MS (unit)	0.00	0.01	-0.03	0.01
5	WW (kg)	-1.33	0.14	-1.53	-1.13
	W14 (kg)	-1.01	0.40	-1.76	-0.69
	PWG (kg)	-0.11	0.07	-0.18	0.02
	SC (cm)	-0.06	0.02	-0.09	-0.04
	MS (unit)	-0.02	0.00	-0.03	-0.02

STD: standard deviation.

Table 2. Mean values of environmental factors that presented significant effects between clusters.

Cluster	Altitude (m)	NDVI	Tmin (°C)	Tmax (°C)
1	393.47 ^{a,b}	0.57 ^{a,b}	25.34 ^{a,b}	34.81 ^{a,b}
2	458.91 ^{b}	0.53 ^{a}	23.43 ^{a,b}	32.09 ^{a,b}
3	289.50 ^{a}	0.61 ^{b}	26.04 ^{b}	35.30 ^{b}
4	399.09 ^{b}	0.58 ^{a,b}	25.11 ^{a,b}	34.01 ^{a,b}
5	484.97 ^{b}	0.54 ^{a}	22.95 ^{a}	31.34 ^{a}

NDVI: normalized difference vegetation index; Tmax: maximum temperature; Tmin: minimum temperature.

Means followed by different letters in columns differ ($P < 0.05$) by the t-Student test.

Table 3. Percentage of counties classified into each cluster using environmental and socioeconomic factors.

Cluster	1	2	3	4	5
1	33,33	0,00	33,33	0,00	33,33
2	25,00	50,00	0,00	0,00	25,00
3	6,25	6,25	75,00	0,00	12,50
4	16,67	8,33	16,67	33,33	25,00
5	0,00	16,67	0,00	0,00	83,33

Table 4. Percentage of counties classified into each cluster using the expected progeny differences of evaluated traits.

Cluster	1	2	3	4	5
1	100,00	0,00	0,00	0,00	0,00
2		75,00	25,00	0,00	0,00
3			100,00	0,00	0,00
4				100,00	0,00
5					100,00

These results can be explained by the fact that this breed is been raised in Brazil for only 22 years, which could be too short for the environmental and socioeconomic factors exert any influence on the genetic distribution of the Montana Tropical® herd. Moreover, the use of reproductive biotechnologies, such as artificial insemination (around 80% of the cows), could be masking the environmental and socioeconomic effects, since it allows the transference of genetic material between regions.

In conclusion, there were differences in the genetic merit of animals among the counties where Montana Tropical® beef composite cattle are raised. However, the only environmental factors were significantly different between clusters without a clear influence on the genetic distribution of these animals in Brazil.

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