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Ramírez Toro EJ[1], Burgos Paz WO[2], Elzo MA[3] ⓘ, Martínez Sarmiento RA[2] ⓘ, Cerón-Muñoz MF[4] ⓘ

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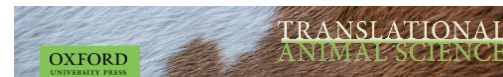❝ Get citation

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Abstract

Since 1940, efforts have been made to preserve the Blanco Orejinegro (BON) cattle breed by maintaining gene banks. Nine years ago, a BON genetic improvement program was implemented to increase genetic gain based on control of productivity and the use of performance tests, polygenic and genomic evaluations, and selection indices. The objective of this study was to estimate genetic parameters and trends for growth traits by using polygenic (PM) and genomic-polygenic (GPM) models. Productive information from the years 1980 to 2019 was used. The following data were used: 7,304 birth weight (BW) records, 1,281 records of body weight adjusted to 120 days (W120), 4,791 records of weight adjusted to 240 days (W240), 3,339 records of weight adjusted to 480 days (W480), and 1,364 records of weight adjusted to 720 days (W720). The relationship matrix included 13,612 pure animals belonging to the Colombian Corporation for Agricultural Research - AGROSAVIA and the Producer Network program. A total of 1,224 individuals were genotyped with chips of different densities and all were imputed up to 50,932 SNPs. Polygenic and genomic-polygenic models were used to estimate genetic parameters and correlations between the genetic values estimated by each model. A generalized additive model with smoothing was used to estimate trends of genetic values from 1980 to 2019. Heritabilities between 0.29 and 0.40, genetic correlations between 0.13 and 0.94, and phenotypic correlations between 0.23 and 0.72 were observed. Close-to-zero genetic growth was observed for BW and W120. Genetic trends for the other traits were positive, with higher growth in the last 7 years. The heritabilities observed in this population indicate that the traits measured would respond to selection. Greater genetic progress can be achieved in W240, W480, and W720 by continuing with genetic evaluations and developing performance tests and strategies to make genetic material readily available to producers.

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Genetic parameters and trends for growth traits in Blanco Orejinegro cattle

Edison J Ramírez Toro,[1,2] William O Burgos Paz,[3] Mauricio A Elzo,[4] Rodrigo A Martínez Sarmiento,[3] and Mario F Cerón-Muñoz[2]

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Since 1940, efforts have been made to preserve the Blanco Orejinegro (BON) cattle breed by maintaining gene banks. Nine years ago, a BON genetic improvement program was implemented to increase genetic gain based on control of productivity and the use of performance tests, polygenic and genomic evaluations, and selection indices. The objective of this study was to estimate genetic parameters and trends for growth traits by using polygenic (PM) and genomic–polygenic (GPM) models. Productive information from the years 1980 to 2019 was used. The following data were used: 7,304 birth weight (BW) records, 1,281 records of body weight adjusted to 120 days (W120), 4,791 records of weight adjusted to 240 days (W240), 3,339 records of weight adjusted to 480 days (W480), and 1,364 records of weight adjusted to 720 days (W720). The relationship matrix included 13,612 pure animals belonging to the Colombian Corporation for Agricultural Research - AGROSAVIA and the Producer Network program. A total of 1,224 individuals were genotyped with chips of different densities and all were imputed up to 50,932 SNPs. Polygenic and genomic-polygenic models were used to estimate genetic parameters and correlations between the genetic values estimated by each model. A generalized additive model with smoothing was used to estimate trends of genetic values from 1980 to 2019. Heritabilities between 0.29 and 0.40, genetic correlations between 0.13 and 0.94, and phenotypic correlations between 0.23 and 0.72 were observed. Close-to-zero genetic growth was observed for BW and W120. Genetic trends for the other traits were positive, with higher growth in the last 7 years. The heritabilities observed in this population indicate that the traits measured would respond to selection. Greater genetic progress can be achieved in W240, W480, and W720 by continuing with genetic evaluations and developing performance tests and strategies to make genetic material readily available to producers.

Keywords: Genetic evaluations, beef cattle, genetic improvement

INTRODUCTION

Blanco Orejinegro (BON) is a *Bos taurus* breed with white body hair and black ears. The BON has fully adapted to the conditions of the region (characterized by low nutritional quality pastures, outstanding topography, and extensive management), which is an advantage compared to foreign cattle breeds. As a result, BON is an ideal animal for local farming systems seeking to increase productivity (López et al., 2001).

Growth traits are of utmost importance since they directly influence the productive efficiency of the farm (Ferraz et al., 2002). They are also fundamental in a genetic improvement program, as they can be included as selection targets due to their medium to high heritabilities (Cienfuegos-Rivas et al., 2006).

The estimation of the genetic values allows to identify superior individuals for each character and, through selection, increase the frequency of desirable alleles in the population (Ferraz et al., 2002). Using a single-step genomic BLUP methodology proposed by Aguilar et al. (2010) it is possible to combine genomic, genealogical, and productive information to predict the genetic values of animals in a simple manner (Lourenco et al., 2015). This increases the accuracy of the predictions of young animals (Crossa et al., 2010) and increases genetic gains (Meuwissen and Goddard, 1996). Incorporating genomic evaluation methods is also important when there is a loss of kinship information (Christensen et al., 2012; Legarra and Ducrocq, 2012), as is the case in BON. To assess the impact of the selection process, it is important to monitor the genetic trends, which allow us to know the effectiveness of the breeding program (Hintz, 1978).

In the case of the genetic improvement program in BON cattle, it is necessary to know the genetic parameters of the population to establish strategies in the coming years. Based on the above, the present study aimed to estimate the genetic parameters and trends for growth traits in BON cattle by using polygenic (PM) and genomic–polygenic (GPM) models.

MATERIALS AND METHODS

Ethic statement

No direct interventions on the animals were performed in this study; only databases of the AGROSAVIA National Genetic Improvement Program were used, under the guidelines of the Colombian Ministry of Agriculture and Rural Development (Resolution 000327-2018 and contract 003 of the year 1994, accepting the Convention on Biological Diversity of the year 1992). The information provided by the AGROSAVIA databases is obtained from routine farm management activities based on the International Animal Registration Committee.

Traits

Animals and data.

We used productive and genealogical information of a pure BON database. These data include animals of the Conservation Program, the production nucleus of Nus Research Center (Colombian Corporation for Agricultural Research - AGOSAVIA), and 24 cattle farms in different regions of Colombia. All of them are included in the productive control program of AGROSAVIA Producers Network. The number of growth records per farm varied between 3 and 3708 and all farms contributed to the genetic connectivity of the population.

The following productive information was used: 7,304 birth weight (BW) records, 1,281 records of weight adjusted to 120 days (W120), 4,791 records of weight adjusted to 240 days (W240), 3,339 records of weight adjusted to 480 days (W480), and 1,364 records of weight adjusted to 720 days (W720),). Records spanned from the year 1980 to 2019 (between 40 and 493 records per year). The relationship matrix included 13,612 animals, 719 sires, and 3,675 dams, where 6,629 animals were inbred with an average inbreeding coefficient of 4.7%. The weights were adjusted according to the methodology proposed by the Beef Improvement Federation (2018).

Blood sampling and genotyping.

Animals were chosen according to convenience depending on availability at the time of sampling and their economic relevance in the herd. Blood samples from 1,224 animals (1,147 of them with phenotypic records) were obtained from the coccygeal vein using vacuum 4 mL tubes with EDTA. After collection, the samples were refrigerated at 4 °C and sent to AGROSAVIA'S animal genetics laboratory in Bogotá, Colombia for genotyping. The DNA was extracted with a commercial kit (MoBio Laboratories, Inc., Carlsbad, CA, USA). The samples were genotyped with the BovineLD (97), GGP Bovine LD (542), and BovineSNP50 (585) chips from Illumina. SNPs with call rates lower than 90% or MAF lower than 5%, and SNPs located in sex chromosomes as well as individuals with more than 10% missing SNP were excluded from the analysis. All genotypes were imputed to the highest density chip using the Fimpute program (Sargolzaei et al., 2014). The final genotype file contained 917 animals with 50,932 SNPs per animal.

Genetic parameters and (co)variance components were estimated with PM and GPM by the maximum restricted likelihood method based on an animal model (Corbeil and Searle, 1976; Harville, 1977) using the AIREMLF90 package (Tsuruta, 2014) of the BLUPF90 program system of the University of Georgia (Misztal, 2006; Misztal et al., 2018).

The analysis was performed with a multi-trait model that included the five traits under evaluation. The fixed effects for each trait were: contemporary group (farm, season, and year of weighing) and sex (male and female) and age of dam at calving as a covariate for BW, W120, and W240 traits. The weighing seasons were formed according to the region's rainfall regime, as follows: *Dry* = December, January, February, June, July, and August; *Rainy* = March, April, May, September, October, and November.

In matrix notation the PM was as follows:

$$y_i = X_i\beta_i + Z_ia_i + Q_im_i + e_i$$

where is the vector of observations for trait *i* (BW, W120, W240, W480, and W720); is the vector of fixed effects for trait *i* (BW, W120, W240, W480, and W720); is the vector of direct animal additive genetic random effects for trait *i* (BW, W120, W240, W480, and W720); is the vector of maternal dam additive genetic random effects for trait *i* (BW, W120, and W240); is the vector of residual effects for trait i (BW, W120, W240, W480, and W720); X_i is an indicator matrix relating records in y_i to fixed effects in β_i, Z_i is and indicator matrix relating records in y_i to direct animal additive genetic effects in vector a_i, and matrix Q_i is an indicator matrix relating records in y_i to maternal dam additive genetic effects in vector m_i.

The model assumed that $E[y] = X\beta$, $Var(e) = I \otimes R$ and the matrix of direct and maternal genetics covariances are:

$$Var\begin{bmatrix} a_1 \\ a_2 \\ a_3 \\ a_4 \\ a_5 \\ m_1 \\ m_2 \\ m_3 \end{bmatrix} = \begin{bmatrix} A\sigma^2_{a_{11}} & A\sigma_{a_{12}} & A\sigma_{a_{13}} & A\sigma_{a_{14}} & A\sigma_{a_{15}} & A\sigma_{a_1m_1} & A\sigma_{a_1m_2} & A\sigma_{a_1m_3} \\ A\sigma_{a_{21}} & A\sigma^2_{a_{22}} & A\sigma_{a_{23}} & A\sigma_{a_{24}} & A\sigma_{a_{25}} & A\sigma_{a_2m_1} & A\sigma_{a_2m_2} & A\sigma_{a_2m_3} \\ A\sigma_{a_{31}} & A\sigma_{a_{32}} & A\sigma^2_{a_{33}} & A\sigma_{a_{34}} & A\sigma_{a_{35}} & A\sigma_{a_3m_1} & A\sigma_{a_3m_2} & A\sigma_{a_3m_3} \\ A\sigma_{a_{41}} & A\sigma_{a_{42}} & A\sigma_{a_{43}} & A\sigma^2_{a_{44}} & A\sigma_{a_{45}} & 0 & 0 & 0 \\ A\sigma_{a_{51}} & A\sigma_{a_{52}} & A\sigma_{a_{53}} & A\sigma_{a_{54}} & A\sigma^2_{a_{55}} & 0 & 0 & 0 \\ A\sigma_{m_1a_1} & A\sigma_{m_1a_2} & A\sigma_{m_1a_3} & 0 & 0 & A\sigma^2_{m_{11}} & A\sigma_{m_{12}} & A\sigma_{m_{13}} \\ A\sigma_{m_2a_1} & A\sigma_{m_2a_2} & A\sigma_{m_2a_3} & 0 & 0 & A\sigma_{m_{21}} & A\sigma^2_{m_{22}} & A\sigma_{m_{23}} \\ A\sigma_{m_3a_1} & A\sigma_{m_3a_2} & A\sigma_{m_3a_3} & 0 & 0 & A\sigma_{m_{31}} & A\sigma_{m_{32}} & A\sigma^2_{m_{33}} \end{bmatrix}$$

where 1 = BW, 2 = W120, 3 = W240, 4 = W480, and 5 = W720, A is the matrix of polygenic genealogical kinship among all individuals, $\otimes$ is the Kronecker product, I is an identity matrix, and R is a (co)variance matrix of residual effects. The maternal environment permanent effect was not considered because in preliminary analyses this variance was close to zero.

For GPM, the single-step genomic BLUP methodology proposed by Aguilar et al., (2010) was used, replacing matrix A with the genomic-genealogical kinship matrix of animals with and without genotypes (H), where:

$$H = \begin{bmatrix} A_{11} + A_{12}A_{22}^{-1}(G_{22} - A_{22})A_{22}^{-1}A_{21} & A_{12}A_{22}^{-1}G_{22} \\ G_{22}A_{22}^{-1}A_{21} & G_{22} \end{bmatrix}$$

where A_{11} is a matrix of additive relationships among animals without genotypes. A_{12} is a matrix of additive relationships among animals with and without genotypes. A_{22}^{-1} is an inverse of the matrix of additive relationships among animals with genotypes (Legarra et al., 2009; Aguilar et al., 2010). G_{22} is a matrix of genomic relations, calculated as:

$$G_{22} = MM'/2\sum p_j(1 - p_j)$$

where M is a matrix of dimension equal to the number of genotyped animals (rows) by the number of SNPs (columns). Its elements were calculated as follows: $(0 - 2p_j)$ if the genotype was homozygous (1-1); $(1 - 2p_j)$ if the genotype was heterozygous (1–2 or 2-1); and $(2 - 2p_j)$ if the genotype was homozygous (2–2). p_j = current allele frequency of the second allele at locus j (VanRaden, 2008). The convergence criterion for the estimation of variance and covariance components was 1x10^-12.

Once the variance and covariance components were obtained, heritability, genetic correlations (r_g) and phenotypic correlations (r_p) were estimated. Spearman's correlation was calculated between the genetic values (GV) estimated by PM and those estimated by GPM, using all animals, and 5, 10, and 50% of superior individuals.

Genetic trends.

Genetic trends in the evaluated period were estimated by the relationship of the GV obtained by GPM with the non-parameterized smoothed effect of the year of birth, using a generalized additive model (gam). Only GVs with an accuracy (formula described by Elzo et al., 2017) greater than 0.3 were considered. The gam was:

$$y_{ijk} = \beta_0 + X_i + s(BY_j) + e_{ijk}$$

where y_{ijk}= Genetic value of the animal, of the *i-th* sex, born in the *j-th* year, with the *k-th* error; β_0= Intercept; X_i= Effect of sex, i = 1,2; $s(BY_j)$ = non-parameterized smoothed function of the *j-th* year of birth, j = 1980: 2019; e_{ijk}= residual effect, $N(0, \sigma_e^2)$.

The mgcv library (Wood, 2011) of the R-project statistical software (R core team, 2017) was used for this analysis.

Table 1 shows a description of the data, with mean, standard deviation, range and number of records used. Table 2 shows the variance components for the five traits, as well as direct and maternal heritability. Direct heritabilities were between 0.29 and 0.39 for PM, and between 0.29 and 0.40 for GPM. W720 was the trait with the highest heritability in both models. The heritabilities estimated in this study were moderate to high, indicating that these traits respond to selection processes in both direct and maternal effects.

Table 1.

Statistical description for weight traits in BON cattle[1]

Trait	N	Mean (kg)	Minimum (kg)	Maximum (kg)	CV
Birth weight	7304	28.74±3.14	21.00	34.50	10.92
Weight adjusted to 120 days	1281	100.72±12.58	70.78	154.00	12.49
Weight adjusted to 240 days	4791	169.81±26.77	102.80	291.09	15.76
Weight adjusted to 480 days	3339	217.10±31.48	129.56	335.22	14.50
Weight adjusted to 720 days	1364	309.15±37.07	241.77	555.85	11.99

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[1]N=number of records; CV=coefficient of variation

Table 2.

Variance components and genetic parameters for growth traits in BON cattle[1]

	Birth weight		Weight adjusted 120 days		Weight adjusted 240 days		Weight adjusted 480 days		Weight adjusted 720 days	
	PM	GPM	PM	GPM	PM	GPM	PM	GPM	PM	GPM
σ_a^2	2.37 (0.03)	2.44 (0.03)	55.18 (0.67)	52.87 (0.64)	124.65 (1.51)	123.99 (1.15)	239.66 (2.91)	238.19 (2.89)	337.69 (4.10)	339.54 (4.11)
σ_m^2	0.78 (0.01)	0.74 (0.01)	42.46 (0.52)	40.62 (0.49)	41.44 (0.50)	37.17 (0.45)				
σ_e^2	4.53 (0.06)	4.48 (0.06)	86.17 (2.56)	87.41 (2.58)	268.91 (4.23)	271.22 (4.25)	389.55 (3.96)	390.81 (3.98)	524.83 (6.70)	518.22 (6.62)
σ_p^2	7.68 (≈0)	7.66 (0.06)	183.81 (2.62)	180.89 (2.64)	435.00 (4.66)	432.38 (4.67)	629.21 (4.90)	629.00 (4.89)	862.52 (7.82)	857.76 (7.75)
h_d^2	0.31 (≈0)	0.32 (≈0)	0.30 (0.01)	0.29 (≈0)	0.29 (≈0)	0.29 (≈0)	0.38 (≈0)	0.38 (≈0)	0.39 (≈0)	0.40 (≈0)
h_m^2	0.10 (≈0)	0.10 (≈0)	0.23 (0.01)	0.22 (≈0)	0.10 (≈0)	0.09 (≈0)				

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[1]PM= polygenic model, GPM= genomic-polygenic model, = direct additive genetic variance, = maternal additive genetic variance, = phenotypic variance, = residual variance, = direct heritability, = maternal heritability. Values in parentheses are standard errors.

Table 3 shows the genetic correlations between growth traits for each model (PM and GPM). They ranged between 0.13 and 0.96 for PM, and between 0.17 and 0.94 for GPM. The highest genetic correlations were between W720 and W480, and between W240 and W480. Genetic correlations are greater between consecutive weights; correlations decrease as weighing times move away. BW had a positive genetic correlation (between 0.13 and 0.32) with all the traits. The lowest genetic correlations were between BW and W240, and also between BW and W120. Phenotypic correlations were between 0.23 and 0.72 for PM, and between 0.23 and 0.71 for GPM (Table 4).

Table 3.

Genetic correlations between growth traits in BON cattle estimated by polygenic and genomic-polygenic models[1]

	BWd		BWm		W120d		W120m		W240d		W240m		W480
	PM	PGM	PM	PGM	PM	PGM	PM	PGM	PM	PGM	PM	PGM	PM
BW$_d$			-0.28 (0.01)	-0.28 (0.01)			0.04 (0.01)	0.04 (0.01)			0.27 (0.01)	0.25 (0.01)	
BW$_m$							0.11 (0.01)	0.05 (0.01)			-0.08 (0.01)	-0.08 (0.01)	
W120$_d$	0.18 (0.01)	0.18 (0.01)					-0.63 (0.01)	-0.62 (0.01)			0.02 (0.01)	0.03 (0.01)	
W120$_m$											0.55 (0.01)	0.52 (0.01)	
W240$_d$	0.13 (0.01)	0.17 (0.01)			0.51 (0.01)	0.55 (0.01)					0.24 (0.01)	0.29 (0.01)	
W480	0.25 (0.01)	0.50 (0.01)			0.44 (0.01)	0.52 (0.01)			0.85 (≈0)	0.87 (≈0)			
W720	0.27 (0.01)	0.34 (0.01)			0.40 (0.01)	0.43 (0.01)			0.77 (≈0)	0.75 (≈0)			0.96 (≈0)

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[1]BW$_d$ = direct genetic effect of birth weight, BW$_m$ = maternal genetic effect of birth weight, W120$_d$ = direct

weight adjusted to 720 days, PM = polygenic model, GPM = genomic-polygenic model. Values in parentheses are standard errors.

Table 4.

Phenotypic correlations between growth traits in BON cattle estimated by polygenic and genomic-polygenic models[1]

	Birth weight		Weight adjusted 120 days		Weight adjusted 240 days		Weight adjusted 480 days	
	PM	GPM	PM	GPM	PM	GPM	PM	GPM
Weight adjusted to 120 days	0.27 (0.01)	0.26 (0.01)						
Weight adjusted to 240 days	0.26 (0.01)	0.26 (0.01)	0.65 (≈0)	0.65 (≈0)				
Weight adjusted to 480 days	0.23 (≈0)	0.23 (≈0)	0.48 (≈0)	0.48 (≈0)	0.71 (≈0)	0.71 (≈0)		
Weight adjusted to 720 days	0.25 (0.02)	0.25 (0.02)	0.48 (≈0)	0.48 (≈0)	0.57 (≈0)	0.57 (≈0)		

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[1]PM= polygenic model, GPM= genomic-polygenic model. Values in parentheses are standard errors.

Correlations between GV estimated by PM and GPM were high for the direct effects in all traits. Correlations were between 0.65 and 0.93 for the top 5% GV; between 0.87 and 0.95 for the top 50% GV; and between 0.94 and 0.98 for 100% of GV (Table 5). Figure 1 shows the genetic trends of direct and maternal effects, expressed as the change in GVs over time. These changes were highly significant (P <0.01) for all genetic effects, except for W120 maternal effects.

Table 5.

Spearman correlations between genetic values and accuracy changes of genetic values estimated by polygenic (PM) and polygenic-genomic (PGM) models for growth traits in BON cattle

Trait	Genetic effect	Accuracy changes[1]		Spearman correlations[2]		
		G	U	5%	50%	All
Birth weight	Direct	2.62	2.69	0.81	0.91	0.96
	Maternal	1.30	-4.07	0.77	0.89	0.95
Weight adjusted to 120 days	Direct	3.15	18.53	0.83	0.87	0.94
	Maternal	2.25	4.48	0.65	0.89	0.95
Weight adjusted to 240 days	Direct	3.60	1.63	0.91	0.95	0.98
	Maternal	0.69	-0.95	0.85	0.92	0.96
Weight adjusted to 480 days	Direct	2.06	0.58	0.93	0.95	0.95
Weight adjusted to 720 days	Direct	0.76	-4.10	0.91	0.94	0.94

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[1]Median accuracy change percentage = ((PGM-PM)*100)/PM; G = genotyped; U = Ungenotyped.

[2]5% and 50% of the best genetic values.
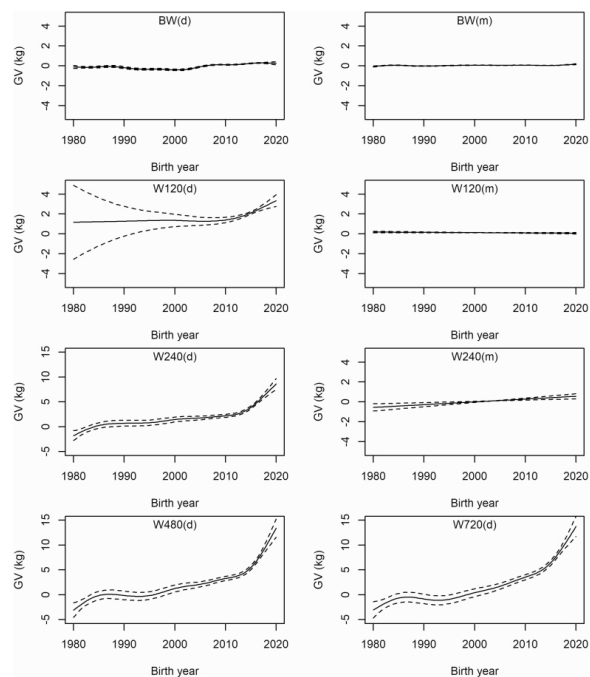
Figure 1.

Direct (d) and maternal (m) genetic trends expressed in genetic values (GV) of birth weight (BW) and weight adjusted of 120, 240, 480 and 720 days (W120, W240, W480 and W720, respectively) in BON cattle, obtained by genomic-polygenic models. The dotted lines represent two standard errors above and below the estimate of smoothness.

DISCUSSION

The means of body weight were within the ranges reported for Colombian creole cattle (Vásquez et al., 2006; Rojas et al., 2011). The main advantages of BON is that there is a low frequency of dystocia, resistance to diseases and good weight gains despite poor nutritional conditions. Its performance is similar to that of other Creole, Zebu and European breeds in the region (Vásquez et al., 2006; Baldi et al., 2010; Martínez et al., 2017; Palacios-Espinosa et al., 2019). A wide range was found for the different traits, and coefficients of variation were between 10.92 and 15.76, which may be explained by the diverse pasture, the grazing periods and type of pastures used to feed the animals in the different herds.

The estimated direct heritability for BW was lower than those reported by Gallego et al. (2006) and Ramirez et al. (2019) in a BON conservation nucleus where they estimated 0.38 and 0.36, respectively. Maternal heritabilities were higher than those reported by Gallego et al. (2006). In a previous study, Ramírez et al. (2019) used genomic information from the BON conservation nucleus finding heritabilities similar to those of this study. Regarding W240, the estimated heritabilities for direct and maternal effects were lower than those found by Cañas et al. (2008) who reported 0.63 and 0.22, respectively. Differences between results here and those from previous authors are likely due to the fact that they used different statistical models and information from a single herd. Although the maternal heritabilities for BW, W120 and W240 were lower than the corresponding direct heritabilities, it is necessary to carry out a joint selection for the two genetic effects because grazing production systems require a balance between the ability of calves to grow and the ability of dams to raise them appropriately.

Regarding W480, the estimated heritabilities were higher than the 0.09 reported by Gallego et al. (2006), but lower than the 0.73 by Fragomeni et al. (2013) in Nellore breed in Brazil for weight at 550 days. As for W720, heritability was higher than the estimated by Baldi et al. (2010) in Canchim breed.

The highest phenotypic correlations were between W480 and W240, and also W720, suggesting that W240 is an indicator of W480, and that W480 is a good indicator of W720. The lowest phenotypic correlations were between BW and the other traits, suggesting that this weight does not have an important relationship with weight at later ages. Both genetic and phenotypic correlations estimated at early ages were lower than those estimated at older ages.

The estimated correlations indicate that animals with high GV in PM have a high value in GPM, keeping the GV for all the groups, and the correlation being greater as the number of individuals in the group increases. These correlations were similar to those reported by Elzo et al. (2013, 2017) in Angus x Brahman cattle, who calculated 0.89 and 0.99 between polygenic and genomic-polygenic models. Although moderate and high correlations were found between predicted GV from PM and GPM, reclassification of animals was evident (especially among animals with the highest GV, which may become future dams or sires).

Therefore, although the GV accuracies for maternal BW and W240 and for direct W720 for non-genotyped animals were lower for GPM than for PM (**Table 5**), it would be advisable to use GPM in this population because the predicted GV from GPM had a higher accuracies than those from PM for genotyped animals (median values of 0.76% to 3.60% for all traits), possibly because the genomic relationship matrix accounted for relationships that were not recorded in the genealogy, as indicated by Christensen et al. (2012) and Amaya et al. (2020).

The direct and maternal genetic values for BW were stable over time. Maintaining low BW is desirable in cattle, since high birth weight can result in calving difficulties (Laster et al., 1973; Burfening et al., 1978). The BON breed is recognized by its calving ease, not requiring assistance during calving; therefore, it is important to keep birth weight

from year 2011. This trend was similar to that reported by Gallego et al. (2006) in a BON conservation population.

As for W240 (maternal), a tendency to stay stable was observed during the evaluation period. In W240 (direct), W480 and W720 the genetic trend increased slowly until around year 2000. The increase was greater later, especially in the last years of study.

Genetic gains of W240 and W480 until year 2000 were similar to those reported by Gallego et al. (2006) in BON, which had low and positive genetic trends between 1980 and 2004. The trend between 2011 and 2019 -period with the highest values in genetic gains- coincides with the start of BON performance tests on grazing and the strengthening of the Creole Genetic Improvement Program of AGROSAVIA and its network of producers, which increased the use of sires with high genetic value, for quality and quantity of meat and milk (Bolívar et al., 2010; Quiceno et al., 2012).

CONCLUSIONS

A high genetic effect was observed for the traits evaluated in the BON breed, thus selection for multiple traits is possible. The maternal genetic effect of W120 and W240 should be considered, as no genetic progress was found. Greater genetic progress can be achieved for W240, W480 and W720 by continuing with genetic evaluations and developing performance tests and strategies to make genetic material readily available to producers.

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