Genetic-quantitative uni- and bi-trait analysis for growth traits in the Colombian creole breed Blanco Orejinegro (BON)

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Abstract
The Blanco Orejinegro (BON) is a Colombian creole cattle breed that is not genetically well characterized for growth traits. The aim of this work was to estimate genetic parameters for birth weight (BW), weaning weight (WW), yearling weight (YW), daily weight gain between birth and weaning (DWG), time to reach 120 kg of live weight (T120), and time to reach 60% of adult weight (T60%), and establish the selection criteria for growth traits in the BON population of Colombia. Genealogical and phenotypic information for BW, WW, YW, DWG, T120, and T60% traits of BON animals from 14 Colombian herds were used. These traits were analyzed with the AIREML method in a uni- and bi-trait animal model including the maternal effect for BW, WW, DWG, and T120. The direct heritability estimates values were $0.22 \pm 0.059$ (BW), $0.20 \pm 0.057$ (WW), $0.20 \pm 0.153$ (YW), $0.17 \pm 0.07$ (DWG), $0.26$ (T120), and $0.44 \pm 0.03$ (T60%). The maternal heritability estimates values were $0.14 \pm 0.040$ (BW), $0.15 \pm 0.039$ (WW), $0.25 \pm 0.06$ (DWG), and $0.16$ (T120). The direct genetic correlations were high ($>0.60$) among all the traits, except between T60% with BW, WW, YW, and DWG (ranged from $-0.02$ to $-0.51$), all in a favorable direction. The results showed that there is genetic variation in the growth traits associated with the additive genetic effect, and they might respond to selection processes. Furthermore, genetic gains would improve through selection, especially for YW and T60% when WW is used as criterion.

Keywords Productive performance · Quantitative analysis · Animal breeding · Genetic parameters · Animal genetic resource

Introduction
The Colombian Creole cattle breed Blanco Orejinegro (BON) has a natural selection process of ~500 years to the Colombian tropic conditions. Phenotypically, it has a white coat and black ears, skin, and snout (López-Herrera et al. 2001). Its economic importance lies in its rusticity, longevity, ability to reproduce, survive, and because it is a triple purpose animal (milk, meat, and work) (Bedoya et al. 2001, López-Herrera et al. 2001).

Despite its good performance for some traits, for 2018, there were only 2003 pure BON animals (FAO 2018). The information available about the genetic bases controlling aspects related to its growth parameters is limited. Furthermore, there is no information about the genetic variability in the BON population that allows to establish if selection can be made in the breed. Gallego et al. (2006); Cañas et al. (2008); Ramírez-Toro et al. (2019) have carried out studies genetically evaluating the breed, with information from a single herd in each case, preventing the generalization of their results to the entire population. Just Ramírez Toro et al. (2020) have used multiple herds information with a few growth traits.

Studying the growth traits in BON cattle is necessary since usually, in beef cattle, these traits are considered selection criteria (Chud et al. 2014). Besides, they can be easily estimated as they are calculated directly with phenotypic data and are measured several times in the animal’s life as part of
the routine management. Likewise, due to their heritability estimates of moderate to high magnitude, they have a good response to direct selection (Chud et al. 2014, Moreira et al. 2015).

Therefore, the aim of this work was to estimate genetic parameters for the growth traits birth weight (BW), weaning weight (WW), yearling weight (YW), daily weight gain between birth and weaning (DWG), time to reach 120 kg of live weight (T120), and time to reach 60% of adult weight (T60%), of the Blanco Orejinegro (BON) breed from Colombia, to verify if there is sufficient genetic variability to make selection and determine the selection criteria to be utilized — according to genetic correlations — to provide selection tools for better performance and most intensive use of the breed.

Materials and methods

The Ethics Committee for the Care and Use of Animals of Universidad Nacional de Colombia, Medellín campus, has approved this work (CICUA-005 of 2016).

Data

Historical phenotypic and pedigree data (from 2000 to 2018), belonging to 8 Colombian BON herds located in the states of Antioquia, Caldas, Meta, and Risaralda, were used. Each herd had its own edaphoclimatic (16 to 27 °C average temperatures) and pasture conditions (pastures as Cynodon plectostachyus, Brachiaria spp., and Cenchrus clandestinus). In all herds, the animals were under rotational grazing with mineral supplementation, and natural mating as the predominant mating method.

The growth traits considered were BW, WW, YW, DWG, T120, and T60%. The traits T120 and T60% were calculated from the growth curve parameters obtained by the Brody model: \( Y_{ij} = \beta_0 + (1 - \beta_1 e^{-\beta_1 t}) \) cited by Dominguez Viveros et al. (2017), using the consecutive weights in the animal’s life, and the BW as a starting point. Animals with at least four weighings and 800 days of age were employed. In this model, \( Y_{ij} \) corresponds to the \( j \)th weight of the \( i \)th animal at a time \( t \); \( \beta_0 \) corresponds to the asymptotic value when \( t \) tends to infinity; \( \beta_1 \) corresponds to an adjustment parameter when \( Y_{ij} \neq 0 \), and when \( Y_{ij} = 0 \); and \( \beta_2 \) is the growth rate, expressed as a proportion of the total weight. Finally, \( t \) is the age in days.

T120 was obtained by clearing the time from Brody’s equation, as follows:

\[
T(120) = \frac{\log \left( 1 - \left( \frac{120}{\beta_0} \right) \right)}{-\beta_2} + \left( \frac{\log \left( \frac{1}{\beta_1} \right)}{-\beta_2} \right)
\]

The equation of Ramírez et al. (2009) was used to calculate the time to reach 60% of adult weight, as follows:

\[
T60% = \frac{\log (\beta_0 - (\beta_0 * 0, 6)) - \log (\beta_0 * \beta_1)}{-\beta_2}
\]

The information was depurated using the R Project program (R Core Team 2021), where records with data above or below three standard deviations according to the mean of each trait were eliminated. In this sense, data for BW were considered between 20 and 45 kg, the ones for WW between 120 and 300 kg, the values for YW between 140 and 320 kg, for DWG between 0.25 and 1.3 kg/day, for T120 between 100 and 300 days, and for adult weight between 300 and 600 kg. Moreover, animal records that had complete information related to the identification of the animal, dam, and herd, calving number, sex, date, BW, and BW and YW, were included in the analyses. The final dataset included records of 3218 animals for BW, 2265 for WW, 496 for YW, 2287 for DWG, 325 for T120, and records of 408 animals for T60%.

Model

Table 1 shows the data structure used for the growth traits genetic analyzes in the BON cattle. Although pedigree individuals were 7799, there was a reduction in the number of animals in the kinship matrix, according to the connectivity and animal number associated with phenotypic records.

For each trait, the fixed effects were contemporary group (CG — composed by herd, sex, and weighing year for BW, WW, YW, and DWG, and herd and year for T60% and T120), weighing season distributed in four periods (dry season 1: January to March, rainy season 1: April to June, dry season 2: July to September, rainy season 2: October to December), calving number (CN: 1–7 with 7, grouping ≥7 calvings), sex (T120 and T60%), and weaning or yearling age as covariates for the WW and YW traits, respectively. As random effects, direct and maternal additive genetic effects were considered.

A uni-trait animal model was used to estimate genetic parameters; in addition, bi-trait analyses were performed to estimate the genetic and phenotypic correlations between the BW, WW, YW, DWG, T120, and T60% traits. The genetic parameters were estimated through the frequentist Average Information Restricted Maximum Likelihood (AIREML) methodology, using the Wombat software (Meyer 2007), with a 10^-5 convergence criterion. For the BW, WW, DWG, and T120 traits, maternal additive genetic effects were included. Difficulties in reaching the convergence criterion for direct (\( h^2_d \)) and maternal (\( h^2_m \)) heritability estimates obtained through univariate analysis for trait T120 were observed, due to the limited amount of data available. Mean values obtained through a bivariate analysis were considered in this case. The general animal model used was:
Table 1 Data structure used for the genetic evaluation of the growth traits BW, WW, YW, DWG, T120, and T60% in bovines of the Blanco Orejinegro breed from Colombia

| Item                      | BW     | WW     | YW     | DWG    | T120   | T60%   |
|---------------------------|--------|--------|--------|--------|--------|--------|
| n                         | 3,211  | 2,254  | 496    | 2,280  | 329    | 408    |
| Mean±se                   | 31.8±0.06 | 202.06±0.72 | 230.54±1.67 | 0.645±0.003 | 136.38±1.52 | 541.07±12.99 |
| Standard deviation        | 3.52   | 34.23  | 37.26  | 0.126  | 27.49  | 262.41 |
| Animals in the kinship matrix | 4,329 | 3,398  | 1,237  | 3,430  | 1,058  | 1,162  |
| Known bulls               | 285    | 267    | 131    | 259    | 169    | 127    |
| Known dams                | 1,390  | 1,235  | 464    | 1,248  | 580    | 456    |
| Contemporary groups       | 161    | 141    | 68     | 140    | 42     | 49     |

BW birth weight, WW weaning weight, YW yearling weight, DWG daily weight gain between birth and weaning, T120 time to reach 120 kg of live weight, T60% time to reach 60% of adult weight, se standard error

\[ y = X\beta + Zu + Wm + e \]

where \( y \) is a vector of observations for each trait, \( \beta \) is a solution vector of fixed effects, and \( u \) is a solution vector for direct additive genetic random effects. Furthermore, \( m \) is a solution vector for maternal additive genetic random effects (for BW, WW, DWG, and T120), and \( e \) is a vector of random residuals. \( X, Z, \) and \( W \) are the incidence matrices associated with their respective effects for \( y \).

The assumptions considered for the general model were the following:

\[ [u \ m \ e^\top] \sim N(0, \begin{bmatrix} \text{Var}(u) & \text{Cov}(u,m) & \text{Var}(e) \\ \text{Cov}(u,m) & \text{Var}(m) & \text{Cov}(m,e) \\ \text{Var}(e) & \text{Cov}(m,e) & \text{Var}(e) \end{bmatrix}) = \begin{bmatrix} \sigma^2_a & \alpha & \sigma^2_e \\ \alpha & \sigma^2_m & \sigma^2_{am} \\ \sigma^2_e & \sigma^2_{am} & \sigma^2_e \end{bmatrix} \]

where \( \sigma^2_a \) is the additive genetic variance, \( \sigma^2_m \) is the maternal additive genetic variance, \( \sigma^2_e \) is the residual variance, and \( \sigma^2_{am} \) is the covariance between the direct additive and maternal additive genetic effects. \( A \) is the numerator of the additive kinship matrix, and \( I \) is an identity matrix. The bivariate animal model used was the one employed by Koetz et al. (2019).

The genetic progress and the expected correlated response for the studied traits were also calculated, considering the same selection intensity (equal to 1). The formulas used were the following:

\[ \Delta G = h^2_i \sigma^2_i \quad CR_2 = r_{ij}h_1h_2i \sigma^2 \quad RE = (CR_2/\Delta G) \times 100 \]

where \( \Delta G \) is the genetic progress by direct selection for each trait (BW, WW, YW, DWG, T120, and T60%), \( h^2_i \) is the heritability for the \( i \)th trait, \( i \) is the selection intensity for the trait in standard deviation units, and \( \sigma^2_i \) is the phenotypic standard deviation for the \( i \)th trait. \( CR_2 \) is the correlated response for the \( i \)th trait when selected for the \( j \)th trait, \( r_{ij} \) is the genetic correlation between the traits, \( h_1 \) is the square root of the heritability for the \( i \)th trait, and \( i_j \) is the selection intensity for the \( i \)th trait. \( RE \) is the relative efficiency of the selection.

**Results**

According to the genealogy information (7799 individuals), the total inbred animals in the BON population \( (F>0) \) were 3705, and the inbreeding coefficient mean was 4.41%, although considering only the population of inbred animals, it was 9.29%.

The genetic parameters of direct \( (h^2_d) \) and maternal \( (h^2_m) \) heritabilities and correlations between direct and maternal additive genetic effects \( (r_{am}) \) are shown in Table 2. A large proportion of the growth traits variation was associated with direct additive genetic variance, finding \( h^2_d \) estimates of 0.22±0.059 (BW), 0.20±0.057 (WW), 0.17±0.07 (DWG), 0.202±0.153 (YW), 0.26 (T120), and 0.44±0.03 (T60%). Another significant proportion

Table 2 Estimates of direct \( (h^2_d) \) and maternal \( (h^2_m) \) heritabilities and correlation between direct and maternal genetic effects \( (r_{am}) \) with their respective standard errors for growth traits in Blanco Orejinegro breed from Colombia

| Trait   | \( h^2_d \)         | \( h^2_m \)         | \( r_{am} \)    |
|---------|---------------------|---------------------|-----------------|
| BW      | 0.22±0.059          | 0.14±0.040          | 0.10±0.256      |
| WW      | 0.20±0.057          | 0.15±0.039          | -0.03±0.313     |
| YW      | 0.20±0.153          | NA                  | NA              |
| DWG     | 0.17±0.07           | 0.25±0.06           | -0.39±0.228     |
| T120    | 0.26                | 0.16                | -0.15           |
| T60%    | 0.44±0.03           | NA                  | NA              |

BW birth weight, WW weaning weight, YW yearling weight, DWG daily weight gain between birth and weaning, T120 time to reach 120 kg of live weight, T60% time to reach 60% of adult weight, NA not applicable. The heritability and correlation estimates between genetic and maternal variances for the T120 trait were challenging to find by the univariate methodology due to the low amount of data available and its difficulty to converge; therefore, the value reported is the mean of the estimates found in the bivariate analyses.
of the variation for the pre-weaning traits was associated with maternal additive genetic variance; thus, the $h^2_m$ estimates were $0.14 \pm 0.040$ (BW), $0.15 \pm 0.039$ (WW), $0.25 \pm 0.06$ (DWG), and $0.15$ (T120). The correlations between direct and maternal additive genetic effects ranged between $-0.39$ and $0.19$.

The genetic and phenotypic correlations between the growth traits analyzed in the BON breed from different regions of the Colombian tropics are presented in Table 3. The genetic correlations for the direct additive genetic effect between the BW, WW, YW, and DWG traits were high and positive, varying from $0.82$ to $0.99$. Between the BW, WW, YW, and DWG traits and T120% were high and negative (ranging from $-1$ to $-0.67$). Concerning to T60% and the BW, the correlation was $-0.02$, being classified as null. Between T60% and WW, YW, and DWG traits, the correlations were negative and ranged from $-0.51$ to $-0.32$, being classified as moderate and would have a favorable impact for the T60% trait. Finally, the genetic correlation between T120 and T60% was high ($0.60$).

The response to selection is presented in Table 4. For most cases, the best option is to use T120 or WW as a selection criterion.

### Discussion

The objectives of this work were to estimate genetic parameters for growth traits in the Blanco Orejinegro (BON) breed from Colombia, to verify if there was sufficient genetic variability to make selection, and to determine the selection criteria to be utilized, providing selection tools for better performance and most intensive use of the breed.

In consequence, a percentage of inbred animals was found. Nevertheless, the population inbreeding coefficient mean found was lower than Cañas et al. (2008) reported in a single BON herd (24.5%), using genealogical data as well. Moreover, the population mean was moderate; this should be highlighted when considering the size of the BON population that currently exists (Martínez et al. 2012). Therefore, the magnitude of this coefficient must be controlled within the BON population through strategies, such as directed mating that considers the degree of kinship and inbreeding of individuals.

In the genetic parameters estimates, the results indicate the existence of sufficient additive genetic variability, in which the growth traits would exhibit selection response. Nevertheless, the maternal heritability value must be interpreted carefully, since it was not possible to separate the permanent environment effect; therefore, the maternal additive

### Table 3

| Trait | BW (kg) | WW (kg) | YW (kg) | DWG (kg/day) | T120 (days) | T60% (days) |
|-------|---------|---------|---------|--------------|-------------|-------------|
| BW    | $0.84 \pm 0.118$ | $0.82 \pm 0.354$ | $0.86 \pm 0.139$ | $-0.67 \pm 0.411$ | $-0.02 \pm 0.33$ | $-0.02 \pm 0.33$ |
| WW    | $0.30 \pm 0.024$ | $0.98 \pm 0.086$ | $0.99 \pm 0.05$ | $-0.93 \pm 0.200$ | $-0.32 \pm 0.328$ | $-0.32 \pm 0.328$ |
| YW    | $0.22 \pm 0.056$ | $0.77 \pm 0.021$ | $0.91 \pm 0.141$ | $-1.00 \pm 0.306$ | $-0.51 \pm 0.374$ | $-0.51 \pm 0.374$ |
| DWG   | $0.19 \pm 0.025$ | $0.99 \pm 0.001$ | $0.69 \pm 0.027$ | $-0.98 \pm 0.178$ | $-0.48 \pm 0.313$ | $-0.48 \pm 0.313$ |
| T120  | $-0.20 \pm 0.00$ | $-0.87 \pm 0.019$ | $-0.79 \pm 0.035$ | $-0.84 \pm 0.019$ | $0.60 \pm 0.463$ | $0.60 \pm 0.463$ |
| T60%  | $0.08 \pm 0.066$ | $-0.36 \pm 0.057$ | $-0.30 \pm 0.073$ | $-0.34 \pm 0.052$ | $0.58 \pm 0.045$ | $0.58 \pm 0.045$ |

*BW* birth weight, *WW* weaning weight, *YW* yearling weight, *DWG* daily weight gain between birth and weaning, *T120* time to reach 120 kg of live weight, *T60%* time to reach 60% of adult weight

### Table 4

| Trait | ΔG | RC2 (ER %) | WW (kg) | YW (kg) | DWG (kg/day) | T120 (days) | T60% (days) |
|-------|-----|------------|---------|---------|--------------|-------------|-------------|
| BW (kg) | 0.78 | 6.03 | $88.05$ | 6.41 | 86.00 | 0.023 | 98.34 | -4.41 | -61.66 | -1.63 | -1.41 |
| WW (kg) | 6.85 | 0.62 | 79.52 | 7.30 | 98.00 | 0.025 | 107.94 | -6.11 | -85.59 | -26.13 | -22.63 |
| YW (kg) | 7.45 | 0.61 | 77.62 | 6.71 | 97.94 | 0.023 | 99.22 | -6.57 | -92.03 | -41.65 | -36.06 |
| DWG (kg/day) | 0.02 | 0.59 | 75.06 | 6.25 | 91.22 | 6.25 | 83.90 | -6.44 | -90.19 | -39.20 | -33.94 |
| T120 (days) | 7.14 | -0.56 | 72.31 | -7.26 | -105.97 | -8.50 | -114.02 | -0.028 | -121.83 | 49.00 | 42.43 |
| T60% (days) | 115.49 | -0.022 | -2.81 | -3.25 | -47.44 | -5.64 | -75.65 | -0.018 | -77.63 | 3.81 | 53.38 |

*BW* birth weight, *WW* weaning weight, *YW* yearling weight, *DWG* daily weight gain between birth and weaning, *T120* time to reach 120 kg of live weight, *T60%* time to reach 60% of adult weight
genetic variance could be overestimated. These results indicate that the growth traits evaluated before weaning in BON breed can respond to selection for both direct and maternal genetic effects, considering their genetic correlations which were of low magnitude, probably because few genes influence direct and maternal additive genetic effects simultaneously, also are indicating a lack of correlation, given by a high variation between sires and dams, either due to a higher genetic variance or confusion between the environmental effects (Meyer 1992; Vergara et al. 2009). On the other hand, post-weaning traits should be selected based on their direct breeding values.

For BW, the direct heritability estimate was lower than the ones found for BW by Gallego et al. (2006); Ramírez-Toro et al. (2019), in BON breed populations from a single herd, and the ones reported by Ramírez Toro et al. (2020), using multiple herds information. On the other hand, the maternal estimate was higher than the ones reported by Gallego et al. (2006); Ramírez Toro et al. (2020), and lower than the ones found by Ramírez-Toro et al. (2019). In comparison with other specialized breeds infused in the tropics, as the Angus, these direct and maternal estimates were superior (Donoghue et al. 2016; Moore et al. 2005, Torres-Vázquez et al. 2018). These differences may be due to the variable number of herds under study, distinct gene frequencies, and the different phenotype and pedigree information of the herds. Selection for this trait is significant, since hefty animals at birth have been associated with a higher incidence of mortality and calving difficulty (Schmidek et al. 2013), as well as subsequent reproductive problems for cows (Ossa et al. 2011).

In beef cattle genetic breeding, WW is an economic important trait that contributes to selecting males and females through the prediction of the breeding value at this age. The direct estimate for WW of this research is similar to those found in the BON breed by Gallego et al. (2006); Ramírez-Toro et al. (2019), but lower than those found by Cañas et al. (2008); Ramírez Toro et al. (2020). Likewise, the maternal estimate is superior to the ones found by Gallego et al. (2006); Ramírez-Toro et al. (2019), and Ramírez-Toro et al. (2020), and lower than the one found by Cañas et al. (2008). In comparison to Australian Angus, these direct and maternal estimates were similar to the found by Donoghue et al. (2016), but lower than the ones reported by Moore et al. (2005). Likewise, the Herford cattle used in Brazil and Uruguay had lower heritability estimates for this trait (Teixeira et al. 2018b).

Regarding the DWG trait, the direct and maternal heritability estimates indicate that the genetic component is influenced by the growth ability of the offspring and the ability of the BON dams to raise a calf; however, the maternal genetic effect is higher than the direct one on the total phenotypic variance. This may be due to the maternal effect given by the milk production of the dam that influences more the variability of the trait at this growth stage. In this sense, it is widely known that the dam is responsible for 60% of the weaning growth (Amaral et al. 2014). In Nelore breed, lower estimates of direct heritability (0.12 ± 0.04) and higher estimates of maternal heritability (0.29 ± 0.09) have been found (Rocha et al. 2003). Similar behavior for pre-weaning gain trait in Hereford cattle has been found (Pardo et al. 2020). For these authors, the maternal effect is higher than the direct one, due to the high dependence of the calf on the dam between birth and weaning.

For YW, similar results were found in Brahman (Manuel et al. 2019) and in Nelore breed, these estimates varied between 0.17 and 0.44 (Moreira et al. 2015, Teixeira et al. 2018a, Koetz et al. 2019). In the Australian Angus breed, the estimate was superior to the one found in this study (Donoghue et al. 2016). In the BON breed, there are no reports in the literature of genetic parameters for YW. This trait is economically important as it shows the genetic potential of the animal to develop and gain weight (Hernández-Hernández et al. 2015).

The direct and maternal heritability estimates for T120 have not been previously reported in BON breed. This trait measures growth speed and is meaningful because it can be used as a selection criterion for the growth precocity or earliness of the animals and the maternal ability. This shows that shorter the time to reach 120 kg, animal precocity and maternal ability are greater, with higher weights expected at future ages as weaning weight (Garnero et al. 2001a), and the animals have the potential to respond to selection for precocious growth (Santana et al. 2017). There are reports of growth speed of days to reach 160 kg (T160) and 180 kg (T180) in Nelore breed, with direct estimates ranging between 0.12 and 0.45, and maternal ones from 0.0 to 0.07 (Garnero et al. 2001a, Garnero et al. 2001b, Henrique et al. 2005, Santana et al. 2017).

For T60% trait, the animals reach 60% of adult live weight at around 18 months, but with high variability for the animals sampled. Therefore, care must be taken when interpreting this result, given the low amount of data. It is expected that as new information is obtained for the trait, the estimates will be more accurate. This is an indicator trait of growth speed and sexual maturity, since the faster the growth rate, the animal will reach puberty faster. This precocity can lead to better reproductive parameters of the animal and greater longevity or useful life of the animals in the herd (Ramírez et al. 2009). Similar results have been found in Brahman breed (0.42) for the puberty age and in Indubrasil breed, and Nelore breed (0.35 ± 0.05) for weight at 550 days; these are considered estimates of moderate heritability for the trait (Vargas et al. 1998, De Souza et al. 2018).

The genetic correlations for the direct additive genetic effect between the BW, WW, YW, and DWG traits indicate...
that a large part of the genes with additive action that influence one of the traits also influence the others. Furthermore, animals with superior genetic merit for BW will also have higher genetic merit for DWG, and even higher genetic merit at weaning and yearling, and vice versa. These results indicate that selecting individuals with genetic potential for higher birth weight will be reflected in a correlated response in the other traits. Thus, the selection of young individuals may reduce the generational interval, showing a faster response to selection. These results are superior to the low genetic correlations reported between BW and WW adjusted at 240 days in BON breed by Ramírez-Toro et al. (2019) and Ramírez-Toro et al. (2020). In the Costeño Con Cuernos and Romosinuano creole breeds, high correlations have been reported between pre-weaning traits, like what was found in the current study (Martínez and Pérez 2006, Martínez Rocha et al. 2018). Similar genetic correlations have also been found by Boligon et al. (2009) in Nelore breed.

The genetic correlations for the direct genetic effect between the BW, WW, YW, and DWG traits with T120% indicate that a large part of the genes with additive action that make individuals show positive genetic merit for those traits influence these individuals to present favorable genetic merit with negative breeding values for T120, which is desirable in beef cattle. The contrary was found by Koetz Júnior et al. (2017); Santana et al. (2017), where the genetic correlations were high and positive between the speed of growth traits (T180 or T160) with daily weight gains before and after weaning.

For T60% and BW, the genetic correlations suggest that genes that affect the BW differ slightly from those responsible for the growth of genes involved in T60%, and these results indicate that the selection of animals for BW would have essentially no impact on T60%. Low genetic correlations between pre- and post-weaning traits were also reported by Vergara et al. (2009) in cattle crossbred with BON, by Ramírez Toro et al. (2020) in other BON populations, and Pardo et al. (2020) in Hereford Cattle.

The genetic correlation between T120 and T60% shows that a large part of additive genes that are expressed in the pre-weaning growth speed trait T120 are still being expressed in another post-weaning growth speed trait (T60%) that is indicative of sexual maturity and precocity. A moderate genetic correlation (0.23) was obtained in Nelore breed by Santana et al. (2017) between the pre-weaning trait T180 (days to reach 180 kg) and the post-weaning trait T300 (days to reach 300 kg). The analysis of these results suggests that the traits should not be used simultaneously in selection indices since, due to the high genetic correlations found, selection for one will cause a similar magnitude-correlated response in the other.

The phenotypic correlations exhibited a similar behavior regarding the signs of the genetic correlations, but different in relation to the magnitude. This difference is expected, since the phenotypic correlation has an intrinsic combination of additive, non-additive, and environmental genetic effects affecting the trait (Quijano et al. 2015).

According to the response to selection analysis, selection for T120 might be the better option when looking for genetic progress in the other traits, as it has better-correlated responses (CR2). Therefore, moderate responses correlated to selection will be expected for WW (+ 7.26 kg), YW (+ 8.50 kg), DWG (+ 0.028 kg/day), and T60% (− 49 days). Nevertheless, caution should be exercised when using the response to selection data, since the estimates found for the T120 trait showed difficulties when converging, given the limited number of phenotypic observations. Consequently, for all traits, it is recommended to use WW as a selection criterion, since it is a trait from which a relative efficiency to selection (RE) close to and even higher than 100% is expected when it is used as a selection criterion to obtain genetic progress, more similar to the case of carrying out a direct selection (0.62 kg, 7.30 kg, 0.025 kg/day, − 6.11, and − 26.13 days for BW, YW, DWG, T120, and T60% respectively). Besides, WW is a trait recorded in most herds and that the producer has at hand to carry out selection. The contrary occurs with T120, which must be calculated and implies new procedures that producers must carry out to have information for this trait.

These results are different from those found in the Nelore breed by Garnero et al. (2001a), where the trait weight at 550 days showed a higher correlated response compared to weights at lower ages or times to reach a certain weight, or the ones reported by Faria et al. (2007), where the YW was the most recommendable as selection criteria due to a greater direct effect with decreasing influence of maternal effects. For authors as Ortiz Peña et al. (2004), when using T160 as a selection criterion, a higher response correlated to selecting pre-weaning traits is obtained. They even recommend this type of selection criterion, since, in animal industries that use traits like T160 (time to reach certain weights), they have achieved a remarkable degree of production uniformity, allowing all in-all out systems.

Therefore, these results showed that a large proportion of the variation of the traits was associated with the direct additive genetic term, and another large percentage was associated with the maternal genetic term, except for YW and T60%. The growth traits assessed in this study exhibited significant genetic variability and could respond appropriately to the selection process if this is done based
on breeding values. High correlated responses are expected through selection for growth traits in BON breed based on genetic breeding, especially for YW and T60% when WW is used as a selection criterion.

**Author contribution** All authors contributed to the conception and design of the study. The preparation of the material, the data collection, and the analysis were carried out by all the authors. Marisol Londoño Gil wrote the first draft of the manuscript, and the other authors made their contributions to later versions. All authors read and approved the final manuscript.

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**Data availability** The data sets generated and/or analyzed during the current study are available through the corresponding author upon reasonable request.

**Code availability** The code generated during this study is available through the corresponding author upon reasonable request.

**Declarations**

**Ethical approval** The study complies with current Colombian laws. This work was approved by a research ethics committee at the Universidad Nacional de Colombia—Medellín campus, CICUA 005 of 2016, and followed all applicable international, national, and institutional guidelines for animal care.

**Consent to participate** Herd and animal owners signed a consent to participate in the project that generated this article.

**Consent to publish** The owners of the herds and animals signed a consent so that the data could be published, provided it was done anonymously.

**Conflict of interest** The authors declare no competing interests.

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