

Genetic-Quantitative Uni- and Bi-Trait Analysis for Growth Traits in the Colombian Creole Breed Blanco Orejinegro (BON)

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

3

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16

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21

22 Abstract

23 The Blanco Orejinegro (BON) is a Colombian creole cattle breed that is not genetically well characterized
24 for growth traits. The aim of this work was to estimate genetic parameters for birth weight (BW), weaning weight
25 (WW), yearling weight (YW), daily weight gain between birth and weaning (DWG), time to reach 120 kg of live
26 weight (T120), and time to reach 60% of adult weight (T60%), and establish the selection criteria for growth traits
27 in the BON population of Colombia. Genealogical and phenotypic information for BW, WW, YW, DWG, T120,
28 and T60% traits of BON animals from 14 Colombian herds were used. These traits were analyzed with the
29 AIREML method in a uni- and bi-trait animal model including the maternal effect for BW, WW, DWG, and T120.
30 The direct heritability estimates values were 0.22 ± 0.059 (BW), 0.20 ± 0.057 (WW), 0.20 ± 0.153 (YW), $0.17 \pm$
31 0.07 (DWG), 0.26 (T120), and 0.44 ± 0.03 (T60%). The maternal heritability estimates values were 0.14 ± 0.040
32 (BW), 0.15 ± 0.039 (WW), 0.25 ± 0.06 (DWG), and 0.16 (T120). The direct genetic correlations were high
33 ($>|0.60|$) among all the traits, except between T60% with BW, WW, YW, and DWG (ranged from -0.02 to -0.51),
34 all in a favorable direction. The results showed that there is genetic variation in the growth traits associated with
35 the additive genetic effect and they might respond to selection processes. Furthermore, genetic gains would
36 improve through selection, especially for YW and T60% when WW is used as criterion.

37

38 **keywords:** productive performance, quantitative analysis, animal breeding, genetic parameters, animal genetic
39 resource.

40 Introduction

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

45 Despite its good performance for some traits, for 2018 there were only 2003 pure BON animals (FAO, 2018).
46 The information available about the genetic bases controlling aspects related to its growth parameters is limited.
47 Furthermore, there is not information about the genetic variability in the BON population, that allow to establish
48 if selection can be made in the breed. Gallego et al., (2006), Cañas et al., (2008), and Ramírez-Toro et al., (2019),
49 have carried out studies genetically evaluating the breed, with information from a single herd in each case,
50 preventing the generalization of their results to the entire population.

51 Studying the growth traits in BON cattle is necessary since usually, in beef cattle, these traits are considered
52 selection criteria (Chud et al., 2014). Besides, they can be easily estimated as they are calculated directly with

53 phenotypic data and are measured several times in the animal's life as part of the routine management. Likewise,
 54 due to their heritability estimates of moderate to high magnitude, have a good response to direct selection (Chud
 55 et al., 2014; Moreira et al., 2015)

56 Therefore, the aim of this work was to estimate genetic parameters for the growth traits birth weight (BW),
 57 weaning weight (WW), yearling weight (YW), daily weight gain between birth and weaning (DWG), time to reach
 58 120 kg of live weight (T120), and time to reach 60% of adult weight (T60%), of the Blanco Orejinegro (BON)
 59 breed from Colombia, to verify if there is sufficient genetic variability to make selection and determine the
 60 selection criteria to be utilized —according to genetic correlations— to provide selection tools for better
 61 performance and most intensive use of the breed.

62 **Materials and methods**

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

65

66 *Data*

67 Historical phenotypic and pedigree data (from 2000 to 2018), belonging to 8 Colombian BON herds located
 68 in the states of Antioquia, Caldas, Meta, and Risaralda were used. Each herd had its own edaphoclimatic and
 69 pasture conditions. The growth traits considered were BW, WW, YW, DWG, T120, T60%. The traits T120 and
 70 T60% were calculated from the growth curve parameters obtained by the Brody model: $Y_{ij} = \beta_0 + (1 - \beta_1 e^{-\beta_2 t})$
 71 cited by Dominguez Viveros et al., (2017), using the consecutive weights in the animal's life, and the BW as a
 72 starting point. Animals with at least four weighings and 800 days of age were employed. In this model, Y_{ij}
 73 corresponds to the j -th weight of the i -th animal at a time (t); β_0 corresponds to the asymptotic value when t tends
 74 to infinity, β_1 corresponds to an adjustment parameter when $Y_{ij} \neq 0$, and when $Y_{ij} \neq 0$, β_2 is the growth rate;
 75 expressed as a proportion of the total weight. Finally, t is the age in days.

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

$$77 \quad T(120) = \frac{\log \left(1 - \left(\frac{120}{\beta_0} \right) \right)}{\beta_2} + \frac{\left(\log \left(\frac{1}{\beta_1} \right) \right)}{-\beta_2}$$

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

$$79 \quad T60\% = \frac{\log (\beta_0 - (\beta_0 * 0,6)) - \log (\beta_0 * \beta_1)}{-\beta_2}$$

80 The information was depurated using the R Project program (R Core Team, 2020), where records with data
 81 above or below three standard deviations according to the mean of each trait were eliminated. Moreover, animal
 82 records that had complete information related to the identification of the animal, dam, and herd, calving number,
 83 sex, date, BW, and BW and YW, were included in the analyzes. The final dataset included 3218 records for BW,
 84 2265 for WW, 496 for YW, 2287 for DWG, 325 for T120, and 408 records for T60%.

85

86 *Model*

87 Table 1 shows the data structure used for the growth traits genetic analyzes in the BON cattle. Although
 88 pedigree individuals were 7799, from 14 herds, there was a reduction in the number of animals in the kinship
 89 matrix, according to the connectivity and animals number associated with phenotypic records.

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

96 A uni-trait animal model was used to estimate genetic parameters; in addition, bi-trait analyses was performed
 97 to estimate the genetic and phenotypic correlations between the BW, WW, YW, DWG, T120, and T60% traits.
 98 The genetic parameters were estimated through the frequentist Average Information Restricted Maximum
 99 Likelihood (AIREML) methodology, using the Wombat software (Karin Meyer, 2007), with a 10^{-9} convergence
 100 criterion. For the BW, WW, DWG, and T120 traits, maternal additive genetic effects were included. Difficulties
 101 in reaching the convergence criterion for direct (h_d^2) and maternal (h_m^2) heritability estimates obtained through
 102 univariate analysis for trait T120 were observed, due to the limited amount of data available. Mean values obtained
 103 through a bivariate analysis were considered in this case. The general animal model used was:

104

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{u} + \mathbf{W}\mathbf{m} + \mathbf{e}$$

105

106

107

108

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

109

The assumptions considered for the general model were the following:

110

$$[\mathbf{a}'\mathbf{m}'\mathbf{e}'] \sim N[0, \text{Var}]; \text{Var}(\mathbf{a}) = \mathbf{A}\sigma_a^2; \text{Var}(\mathbf{m}) = \mathbf{A}\sigma_m^2; \text{Var}(\mathbf{e}) = \mathbf{I}\sigma_e^2; \text{Cov}(\mathbf{a}, \mathbf{m}) = \mathbf{A}\sigma_{am}^2$$

111 Where σ_a^2 is the additive genetic variance, σ_m^2 is the maternal additive genetic variance, σ_e^2 is the residual
 112 variance, and σ_{am}^2 is the covariance between the direct additive and maternal additive genetic effects. \mathbf{A} is the
 113 numerator of the additive kinship matrix, and \mathbf{I} is an identity matrix. The bivariate animal model used was the one
 114 employed by Koetz Junior et al., (2019).

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

$$117 \quad \Delta G = h_1^2 i \sigma_1 \quad CR_2 = r_a h_1 h_2 i_1 \sigma_2 \quad RE = (CR_2 / \Delta G) \times 100$$

118 Where, ΔG is the genetic progress by direct selection for each trait (BW, WW, YW, DWG, T120, and T60%),
 119 h_i^2 is the heritability for the i -th trait, i is the selection intensity for the trait in standard deviation units, and σ_i is
 120 the phenotypic standard deviation for the i -th trait. CR_2 is the correlated response for the i -th trait when selected
 121 for the j -th trait, r_a is the genetic correlation between the traits, h_i is the square root of the heritability for the i -th
 122 trait and i_i is the selection intensity for the i -th trait. RE is the relative efficiency of the selection.

123 **Results**

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

127 The genetic parameters of direct (h_d^2) and maternal heritabilities (h_m^2) and correlations between direct
 128 and maternal additive genetic effects (r_{am}) are shown in Table 2. A large proportion of the growth traits variation
 129 was associated with direct additive genetic variance, finding h_d^2 estimates of 0.22 ± 0.059 (BW), 0.20 ± 0.057
 130 (WW), 0.17 ± 0.07 (DWG), 0.202 ± 0.153 (YW), 0.26 (T120), and 0.44 ± 0.03 (T60%). Another significant
 131 proportion of the variation for the pre-weaning traits was associated with maternal additive genetic variance, thus
 132 the h_m^2 estimates were 0.14 ± 0.040 (BW), 0.15 ± 0.039 (WW), 0.25 ± 0.06 (DWG), and 0.15 (T120). The
 133 correlations between direct and maternal additive genetic effects ranged between -0.39 and 0.19

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

140 and would have a favorable impact for the T60% trait. Finally, the genetic correlation between T120 and T60%
141 was high (0.60),

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

144 **Discussion**

145 The population inbreeding coefficient mean found was lower than Cañas et al., (2008) reported in a single
146 BON herd (24.5%). However, the population mean was moderate; this should be highlighted when considering
147 the small size of the BON population that currently exists (Martínez et al., 2012). Therefore, the magnitude of this
148 coefficient must be controlled within the BON population through strategies, such as directed mating that considers
149 the degree of kinship and inbreeding of individuals.

150 In the genetic parameters estimates, the results indicate the existence of sufficient additive genetic variability,
151 in which the growth traits would exhibit selection response. Nevertheless, the maternal heritability value must be
152 interpreted carefully, since it was not possible to separate the permanent environment effect; therefore, the maternal
153 additive genetic variance could be overestimated. These results indicate that the growth traits evaluated before
154 weaning in BON breed can respond to selection for both direct and maternal genetic effects, considering their
155 genetic correlations which were of low magnitude, probably because very few genes influence direct and maternal
156 additive genetic effects simultaneously, also are indicating the lack of correlation, given by a high variation
157 between sires and dams, either due to a higher genetic variance or confusion between the environmental effects
158 (Meyer, 1992; Vergara et al., 2009). On the other hand, post-weaning traits should be selected based on their direct
159 breeding values.

160 For BW, the h_d^2 estimate was lower than the ones found for BW by Gallego et al., (2006) and Ramírez-Toro
161 et al., (2019) of 0.38 ± 0.017 and 0.36 , respectively, in BON breed populations from a single herd. The h_m^2 for this
162 trait was higher than the reported by Gallego et al., (2006) with a value of 0.03 ± 0.015 , and lower than the found
163 by Ramírez-Toro et al., (2019) of 0.20 . This difference may be due to the variable number of herds under study
164 and the phenotype and pedigree information of the various herds

165 The h_d^2 values for WW of this research are similar to those found in the BON breed by Gallego et al., (2006)
166 of 0.18 ± 0.022 and Ramírez-Toro et al. (2019) of 0.17 , but lower than those found by Cañas et al. (2008) of 0.63
167 ± 0.36 . The h_m^2 estimate is superior to the ones found by Gallego et al. (2006) of 0.0599 ± 0.025 and Ramírez-
168 Toro et al. (2019) of 0.11 , and lower than the one found by Cañas et al. (2008) of 0.22 ± 0.19 . This may indicate
169 that the dams of the current BON breed population from Colombia have a maternal effect on the WW of their

170 calves, higher than the one found previously in the studies mentioned above. This may be due to postnatal
171 influences, mainly nutritional, such as milk production (Quijano & Echeverri-Zuluaga, 2015). Negative and very
172 high correlations between h_d^2 and h_m^2 of -0.78 ± 0.21 in a single Colombian BON breed herd was reported by Cañas
173 et al. (2008), contrary to what was found in the current study.

174 In the DWG trait, the h_d^2 and h_m^2 estimates indicate that the genetic component is influenced by the growth
175 ability of the offspring and the ability of the BON dams to raise a calf; however, the maternal genetic effect is
176 higher than the direct one on the total phenotypic variance. This may be due to the maternal effect given by the
177 milk production of the dam that influences more the variability of the trait at this growth stage. In this sense, it is
178 widely known that the dam is responsible for 60% of the weaning growth (Amaral et al., 2014). In Nelore breed,
179 lower estimates of direct heritability (0.12 ± 0.04) and higher estimates of maternal heritability (0.29 ± 0.09) have
180 been found, with a high and negative correlation between the direct and maternal genetic effect of -0.77 (Rocha et
181 al., 2003). For these authors, the maternal effect is much higher than the direct one, as in the current study,
182 explained by the high dependence of the calf on the dam between birth and weaning.

183 For YW, similar results were found in Brahman (0.22 ± 0.02) (Manuel et al., 2019) and in Nelore breed, these
184 the estimates varied between 0.17 and 0.44 (Moreira et al., 2015; Teixeira et al., 2018; Koetz Junior et al., 2019).
185 In the BON breed, there are no reports in the literature of genetic parameters for YW. This trait is economically
186 important as it shows the genetic potential of the animal to develop and gain weight (Hernández-Hernández et al.,
187 2015).

188 The h_d^2 and h_m^2 for T120 have not been previously reported in BON breed. This trait measures growth speed
189 and is important because it can be used as a selection criterion for the growth precocity or earliness of the animals
190 and the maternal ability to produce milk. This shows that shorter the time to reach 120 kg, animal precocity and
191 maternal ability are greater, with higher weights expected at future ages as weaning weight (Garnero et al., 2001a),
192 and the animals have the potential to respond to selection for precocious growth (Santana et al., 2017). There are
193 reports of growth speed of days to reach 160 kg (T160) and 180 kg (T180) in Nelore breed, where estimates of
194 direct heritability for T160 vary between 0.12 and 0.42, and maternal heritability from 0.0 to 0.07 (Garnero et al.,
195 2001a; Garnero et al., 2001b; Henrique et al., 2005), and for T180, the values recorded were 0.45 and 0.04,
196 respectively (Santana et al., 2017).

197 For T60% trait, the animals reach 60% of adult live weight at around 18 months, but with high variability for
198 the animals sampled. Therefore, care must be taken when interpreting this result, given the low amount of data. It
199 is expected that as new information is obtained for the trait, the estimates will be more accurate. This is an indicator
200 trait of growth speed and sexual maturity, since the faster the growth rate, the animal will reach puberty faster.

201 This precocity can lead to better reproductive parameters of the animal and greater longevity or useful life of the
202 animals in the herd (Ramírez et al., 2009). Similar results have been found in Brahman breed (0.42) for the puberty
203 age and in Indubrasil breed, and Nelore breed (0.35 ± 0.05) for weight at 550 days; these are considered estimates
204 of moderate heritability for the trait (Vargas et al., 1998; De Souza et al., 2018). Higher estimates for this trait
205 (0.75) have also been reported in Nelore breed (Gonçalves et al., 2011).

206 The genetic correlations for the direct additive genetic effect between the BW, WW, YW, and DWG traits
207 indicate that a large part of the genes with additive action that influence one of the traits also influence the others.
208 Furthermore, animals with superior genetic merit for BW will also have higher genetic merit for DWG, and even
209 higher genetic merit at weaning and at one year of age, and vice versa. These results indicate that selecting
210 individuals with genetic potential for higher birth weight will be reflected in a correlated response in the other
211 traits. Thus, the selection of young individuals may reduce the generational interval, showing a faster response to
212 selection. These results are superior to the low genetic correlations reported between BW and WW traits of 0.30
213 adjusted at 240 days in BON breed by Ramírez-Toro et al., (2019). In the Costeño Con Cuernos and Romosinuano
214 creole breeds, high correlations have been reported between pre-weaning traits, like what was found in the current
215 study (Martínez & Pérez, 2006; Martínez Rocha et al., 2018). Similar genetic correlations have also been found
216 by Martins et al., (2000) in Nelore breed.

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

223 For T60% and BW, the genetic correlations suggests that genes that affect the BW of differ slightly from
224 those responsible for the growth of genes involved in T60%, these results indicate that the selection of animals for
225 BW would have essentially no impact for T60%. A genetic correlation close to zero (-0.04) between pre and post-
226 weaning traits was also reported by Vergara et al., (2009) in cattle crossbred with BON.

227 The genetic correlation between T120 and T60% shows that a large part of additive genes that are expressed
228 in the pre-weaning growth speed trait T120 are still being expressed in another post-weaning growth speed trait
229 (T60%) that is indicative of sexual maturity and precocity. A moderate genetic correlation (0.23) was obtained in
230 Nelore breed by Santana et al., (2017) between the pre-weaning trait T180 (days to reach 180 kg) and the post-
231 weaning trait T300 (days to reach 300 kg). The analysis of these results suggests that the traits should not be used

232 simultaneously in selection indices since, due to the high genetic correlations found, selection for one will cause a
233 similar magnitude-correlated response in the other.

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

238 According to the response to selection analysis, selection for T120 might be the better option when looking
239 for genetic progress in the other traits, as it has better-correlated responses (CR_2). Therefore, moderate responses
240 correlated to selection will be expected for WW (+7.26 kg), YW (+8.50 kg), DWG (+0.028 kg/day), and T60% (-
241 49 days). Nevertheless, caution should be exercised when using the response to selection data, since the estimates
242 found for the T120 trait showed difficulties when converging, given the limited number of phenotypic
243 observations. Consequently, for all traits, it is recommended to use WW as a selection criterion, since it is a trait
244 from which a relative efficiency to selection (RE) close to and even higher than 100% is expected when it is used
245 as a selection criterion to obtain genetic progress, more similar to in the case of carrying out a direct selection (0.62
246 kg, 7.30 kg, 0.025 kg/day, -6.11, and -26.13 days for BW, YW, DWG, T120, and T60% respectively). Besides,
247 WW is a trait recorded in most herds and that the producer has at hand to carry out selection. The contrary occurs
248 with T120, which must be calculated and implies new procedures that producers must carry out to have information
249 for this trait.

250 These results are different from those found by Garner et al. (2001a) in the Nelore breed, where the trait
251 weight at 550 days showed a higher correlated response compared to weights at lower ages or times to reach a
252 certain weight. For authors as Ortiz Peña et al., (2004), when using T160 as a selection criterion, a higher response
253 correlated to selecting pre-weaning traits is obtained. They even recommend this type of selection criterion, since,
254 in animal industries that use traits like T160 (time to reach certain weights), they have achieved a remarkable
255 degree of production uniformity, allowing *all in-all out* systems.

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

262 **Declarations**

263 **Conflicts of interest**

264 The authors of this work declare that there are no conflicts of interest that jeopardize the validity of the results
265 obtained.

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270 **Ethical approval**

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

274 **Consent to participate**

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

276 **Consent to publish**

277 The owners of the herds and animals signed a consent so that the data could be published, provided it was done
278 anonymously.

279 **Availability of data and material**

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

282 **Code availability**

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

284 **Authors' contributions**

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

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