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Best linear model to explain variability in the growth in Blanco Orejinegro cattle and effect of the serological status for bovine viral diarrhea and bovine leukosis

Melhor modelo linear para explicar a variabilidade no crescimento de bovinos Blanco Orejinegro e efeito do status sorológico para diarreia viral bovina e leucose bovina

Alejandro Saldarriaga-Saldarriaga[1*]; Luis Gabriel González-Herrera[2]; Marisol Londoño-Gil[3]; Juan Carlos Rincón Flórez[4]; Albeiro López-Herrera[2]

Highlights:
The inclusion of contemporary group improves the fit of the model for the traits assessed.
Assessing growth traits is useful to improve the performance of Blanco Orejinegro (BON) animals.
Being seropositive for Bovine Viral Diarrhea and Leukosis had no effect growth traits in BON cattle.

Abstract

The cattle breed Blanco Orejinegro (BON) is an important animal genetic resource in Colombia that needs to be studied to identify its productive benefits for Colombian livestock. The aim of this work was to establish the best linear model that explains the variability for birth weight, weaning weight and yearling weight, and estimate the effect of the serological status for Bovine Viral Diarrhea (BVD) and Bovine Leukosis (BL) in BON cattle in Colombia. The information on animal weighings belonging to 14 BON cattle herds, was collected and cleansed. Using the least squares method, 12 linear models were evaluated including as fixed effects, factors such as herd, sex, weighing month, birth order, season (rainy or dry), birth year, and contemporary group (formed by the concatenation of the factors herd, sex, and birth year). The weighing age was included as a covariate for weaning and yearling weights. For the selection of a model that best describes each parameter, the criteria for choosing models, such as Akaike information criterion (AIC), Bayesian Information criterion (BIC), coefficient of determination (R^2), and the sum of squares of the error (SSE), were considered. The model that included the contemporary group showed the best fit, being also the best to describe the three parameters evaluated, since, of the four criteria considered for its evaluation, AIC and SSE showed the lowest values and the highest R^2. With this model, weight predictions with higher precision were able to be performed. Employing indirect ELISA screening tests of blood plasma, the serological status of each animal was estimated for BVD and BL viral infections. The serological status of these two viral infections was included in the best-fit model. There was no significant effect of the serological status on the parameters evaluated, so there are indications that animals that came in contact with the virus were not affected during growth.

Key words: Environmental effects. Growth models. Creole race. Serology.

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[1] Discente do Curso de Mestrado do Programa de Pós-Graduação em Ciência Agrária, Universidad Nacional de Colombia sede Medellín, Grupo de Investigación BIOGEM, Medellín, Ant, Colombia. E-mail: asaldarriagas@unal.edu.co

[2] Profs. Drs., Universidad Nacional de Colombia sede Medellín, Grupo de Investigación BIOGEM, Medellín, Ant, Colombia. E-mail: luggonzalezhe@unal.edu.co. alherrera@unal.edu.co

[3] Discente do Curso de Mestrado do Programa de Pós-Graduação em Ciências da Biotecnologia, Universidad Nacional de Colombia sede Medellín, Grupo de Investigación BIOGEM, Medellín, Ant, Colombia. E-mail: malondonogi@unal.edu.co

[4] Prof. Dr., Universidad Tecnológica de Pereira Grupo de Investigación BIOPEC, Universidad Nacional de Colombia sede Palmira Grupo de Investigación BIOGEM, Palmira, Valle, Colombia. E-mail: jcrincon@unal.edu.co

[*] Author for correspondence

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Resumo

A raça bovina Blanco Orejinegro (BON) é um importante recurso genético animal da Colômbia que requer estudos que identifiquem seus benefícios produtivos para a bovinocultura colombiana. O objetivo deste trabalho foi identificar o melhor modelo linear que explique a variabilidade do peso ao nascimento, ao desmame e ao ano e estimar o efeito do status sorológico para diarréia viral (BVD) e leucose bovina (BL) em gado BON da Colômbia. As informações sobre a pesagem de animais pertencentes a 14 fazendas dedicadas à criação de BON foram coletadas e depuradas. Utilizando o método dos mínimos quadrados, foram avaliados 12 modelos lineares nos quais foram incluídos como efeitos fixos fatores de rebanho, sexo, mês de pesagem, ordem de parição, época de nascimento (chuvosa ou seca), ano de nascimento e grupo de contemporâneos; a idade no momento da pesagem foi incluída como covariável para as características peso ao desmame e peso ao ano. Para a escolha do modelo que melhor descreve cada característica, foram considerados os critérios para escolha dos modelos AIC, BIC, coeficiente de determinação (R^2) e soma dos quadrados dos erros (SCE). Verificou-se que o modelo que incluía o grupo de contemporâneos apresentou o melhor ajuste, sendo o melhor para descrever as três características avaliadas, uma vez que, dentre os quatro critérios levados em consideração para a sua avaliação, o AIC e a SCE apresentaram os menores valores e os R^2 mais altos. Com este modelo, foi possível fazer predições de peso com maior acurácia. Os testes ELISA de rastreamento indireto estimaram o status sorológico de cada animal para infecções virais por BVD e BL. O efeito do status sorológico nessas duas infecções virais foi incluído no modelo que apresentou melhor ajuste. Não houve efeito do status sorológico sobre as características avaliadas, portanto há indicações de que os animais que tiveram contato com o vírus não foram afetados durante o crescimento.

Palavras-chave: Efeitos ambientais. Modelos de crescimento. Raça crioula. Sorologia.

Introduction

Blanco Orejinegro (BON) cattle descend from European cattle that were introduced to the Americas by the Spanish in the fifteenth century; however, the characteristics of the animals of that time do not correspond to those shown by the breed today due to the adaptations undergone for more than 500 years in Colombia (Martinez, 1992; Gutiérrez, 2003). The name of the BON breed refers to one of its main characteristics. It has white fur on black skin throughout the body, with black ears and snout. Nonetheless, it has been criticized for not having good body balance because of the size of the head, a saddled back, low haunch and high tail insertion, thoracic weakness, low body depth, and udder defects (Buitrago & Gutiérrez, 1999). However, these defects are compensated with their adaptation and rusticity, as well as by their ease at the time of delivery and by their ability to walk through steep terrains (Gutiérrez, 2003). These characteristics translate into vigor at birth, resistance, adaptability, and reproductive ability.

BON cattle, as well as other Creole breeds, have high rusticity, longevity, fertility, and resistance to diseases (Buitrago & Gutiérrez, 1999). This last aspect has attracted the attention of researchers, as it can be an essential tool for the control of diseases that affect the livestock. Research has been conducted to establish the resistance of BON cattle to some diseases. A study of *in vitro* cell cultures of BON cattle found that 93% of the animals were resistant to the A24 Cruzeiro subtype virus, and 52.8% to the foot-and-mouth disease virus (FMD) O1 subtype (López, Arango, Zuluaga, Barrera, & Ossa, 2000). Similarly, Ruiz, Ossa, Barrera, Rugeles and López (2015), working with *in vitro* culture of BON cattle fibroblasts infected with FMD, found that *in vitro* cells with high resistance showed a low level of integrin αV- β3 expression, a protein postulated as an FMD cell receptor. Furthermore, supernatants from cell cultures with high antiviral activity (to control replication of vesicular stomatitis virus), belonged to fibroblast cultures that under *in vitro* conditions, were highly resistant to the FMD A24 subtype or highly to moderately resistant to the O1 subtype. These findings show the resistance of the BON breed to diseases of high economic impact for livestock such as foot-and-mouth disease. However, research should be conducted around other diseases of viral origin that affect livestock such as Bovine Leukosis (BL) and Bovine Viral Diarrhea (BVD). BL is a disease caused by a retrovirus of the *Deltaretrovirus* genus (Murakami et al., 2011), characterized by infecting B lymphocytes of the acquired immune system (Frie & Coussens, 2015), making animals more susceptible to other diseases, such as mastitis, metritis, diarrhea, with high somatic cell count (Organización Mundial de Salud Animal [OIE], 2018).

On the other hand, BVD is caused by the *Flaviviridae* virus family (Fray, Paton, & Alenius, 2000), associated with enteric and respiratory lesions (OIE, 2015). The virus has high tropism for reproductive organs such as ovaries, oviducts, and granulose cells (Brownlie, 1991; Brodersen, 2014). This generates economic losses for cattle herds derived from reduced milk production, lower reproductive performance, lower weight gain, increased mortality, premature discards, and higher veterinary costs (Houe, 2003; Thomann et al., 2017). Consequently, it is crucial to estimate the effect of the serological status of these diseases on the growth parameters in the BON breed, so that guidelines can be established to select animals with better zoo-technical behavior and, in turn, take advantage of this important Colombian genetic resource efficiently. Therefore, the aim of this work was to identify the best linear model that explains the variability of birth weight, weaning weight, and yearling weight of Colombian BON cattle and estimate the effect of the serological status for BVD and BL on these parameters.

Materials and Methods

This work was endorsed by the Ethics Committee of Universidad Nacional de Colombia, Medellin campus [CICUA 005 of 2016].

Herds and regions

Weighing records of BON animals from 14 Colombian herds located in 6 departments of Colombia, Antioquia, Caldas, Risaralda, Cundinamarca, Tolima, and Meta were analyzed. In all production systems, the animals were maintained under rotational grazing with mineral supplementation and natural mating.

Registries

The information on the weights of the BON specimens was obtained from databases of each herd, from the year 1992 up to the year 2018. The following growth traits were considered: birth weight (BW), weaning weight (WW), and yearling weight (YW). The information was digitized in spreadsheets of the Office 365 package, and subsequently cleansed and statistically analyzed using the statistical program R version 3.4.3 (R Core Team [R], 2019), eliminating information outside the normal biological range or with extreme values. For BW, the reported weighings were included in the herd databases. For WW, values between 180 and 330 days with more than 100 kg of weight were considered; and for YW, weight values among 330 and 396 days were considered, as not all the animals had an exact weight at 12 months of age in the databases. Animals that had complete information related to the identification of the production system, identification of the animal and the mother, birth number, birth date and weight, sex, weaning date and weight, and the date and weight after 12 months were included. The final database analyzed included 1,086 records for BW, 688 records for WW and 323 records for YW. For the evaluation of the models, the factors considered as fixed effects included the following: herd, sex, the month of birth, and birth order (from the first to the sixth, and in the seventh, the animals with seven births or more were grouped). Furthermore, also the weighing seasons that included two rainy periods, the first between April and June, and the second, between

October and December; and two dry periods, the first between January and March, and the second between July and September. Moreover, the year of birth included values between the years 2001 and 2018, because, for previous years, the information was not well represented, and the contemporary group was comprised of at least five observations per group (formed by the concatenation of the herd, sex and year of birth factors). Weighing age was included as a covariate for WW and YW features.

Selection of the model for the traits birth weight, weaning weight and yearling weight

Twelve models were evaluated using the least squares method, starting with a simple model that included a single factor, and subsequently, incorporating the factors mentioned above. For the choice of the model that best described each particular situation, the criteria for the selection of the models AIC, BIC, coefficient of determination (R^2), and the sum of squares of the error (SSE) were considered. The residual graphs were also elaborated with the lattice package of the R software version 3.4.3 (R, 2019), to verify the fit of the models used for the description of the variability of the studied traits. Once the best model was identified, measured in terms of lower AIC and BIC, higher R^2, lower SSE, and better prediction based on the adjustment of the residuals, the normality assumptions were evaluated using the Shapiro Wilk's test and the homoscedasticity of the residual employing Levene's test. Below, the general model of fixed effects (equation 1) that includes all the environmental factors considered in this analysis, is shown using WW as an example.

$$Y_{ijklmnpqr} = \mu + S_i + H_j + Md_k + Ad_l + Np_m + CG_n + Ep_p + Ed_q + \varepsilon_{ijklmnpqr} \quad (1)$$

Where: $Y_{ijklmnpqr}$: weaning weight of the r-th animal of sex i, belonging to the j-th herd, k-th weaning month, l-th weaning year, born in the m-th birth, belonging to the n-th contemporary group, in the p-th season and with a q-th weaning age. μ: general mean; S_i: effect of sex i (male = 1; female = 2); Hj: effect of j-th herd (j= 1, 2…14); Md_k: effect of the k-th weighing month (k = 1, 2, …, 12); Ad_l: effect of the l-th weighing year (l = 2000, …, 2018); Np_m: effect of m-th birth (m = 1, 2, …, 6 and 7 or more grouped in this last birth group); CG_n: effect of the n-th contemporary group (n = 1, 2, ... 92, 65 and 39 for BW, WW and YW, respectively); Ep_p: effect of the p-th weighing season (p = 1, 2, 3, 4); Ed_q: effect of the q-th age as a covariate for the traits weaning weight (WW) and yearling weight (YW); and $\varepsilon_{ijklmnpqr}$: random error associated with each observation.

Serological status assessment

A blood sample of 4 mL was taken from each of the 498 BON animals randomly selected from 14 Colombian herds located in 6 departments of Colombia, Antioquia (135 animals), Caldas (72 animals), Risaralda (137 animals), Cundinamarca (13 animals), Tolima (94 animals) and Meta (47 animals). The population included 116 males and 382 females from all age groups, with body weights between 25 kg and 700 kg that were selected for the serological study. Each sample was taken from the middle coccygeal vein in a tube with EDTA anticoagulant. Then, in all samples, the blood plasma was separated by centrifugation at 3,000 rpm for 10 minutes in the field; subsequently, these were transported under refrigeration conditions to the Animal Biotechnology laboratory of Universidad Nacional de Colombia, Medellin campus, where they were kept at -20 °C until processing. Indirect ELISA screening tests were performed for the detection of antibodies against BL using the SVANOVIR® BLV gp51-Ab kit, which has a sensitivity of 100% and a specificity of 99.8%. Likewise, for the detection of antibodies against BVD, the SVANOVIR® BVDV-Ab kit was used, which has a sensitivity of 100% and a specificity of 98.2%. The manufacturer's instructions of the kits to carry out the ELISA test procedure were followed for each of the tests. To wash each of the plates, the MultiWash III Tricontinent model 844 1-11 was used, and the final reading of the plates was done at 450 nm using the Biotek Instrument Inc model ELX 800 equipment. Once the results per animal and test were obtained, these were tabulated in spreadsheets for further analysis.

Statistical analysis

To assess the effect of the serological status on BW, WW, and YW traits, the effect of the serological m-diagnosis was included in the best model as a new fixed effect, as described in equation 2. Initially, the analysis, including the separate diagnosis of each disease was carried out, and then, the diagnosis of the two diseases for each animal was included in the analysis.

$$Y_{ijklm} = \mu + Npi + CG_j + Ep_k + Ed_l + Dx_{m\,+}\,\varepsilon_{ijklmn} \quad (2)$$

Where: Y_{ijkl}: weight of the animal born in the i-th birth, belonging to the j-th contemporary group, in the k-th weighing time and with a l-th weaning and yearling ages. μ: general mean for each trait; Np_i: effect of the m-th birth (m = 1, 2, …, 6 and 7 or more grouped in this last birth); CG_j: effect of the n-th contemporary group (n = 1, 2, ... 92, 65 and 39 for BW, WW and YW, respectively); Ep_k: effect of the last weighing period (p = 1, 2, 3, 4); Ed_l: effect of the q-th age as a covariate for the traits weaning weight (WW) and yearling weight (YW); Dx: effect of the serological m-diagnosis, i.e., m = 0 (negative), 1 (positive) for BL and BVD, and for the joint effect of the two diseases, the following categories were considered: A = (BVD = 0 and BL = 1), B = (BVD = 1 and BL = 0), C = (BVD = 0 and BL = 0) and D = (BVD = 1 and BL = 1); ε_{ijklmn}: random error associated with each observation.

It should be noted that to construct the initial model, that is, without considering the effect of the diagnosis for the three characteristics, a higher number of records were available for each trait, as historical information was included on the animals that were supplied by the herd owners. In this sense, by including the effect of the diagnosis in the model, the number of records for BW, WW, and YW was reduced, given that for this effect, the only animals considered were those that during blood sampling, belonged to the herds assessed. Additionally, in the case of BVD, some of the herd managers had contemplated the application of the vaccine for this disease within their sanitary scheme; therefore, these herds were not included in the analysis. The final database for BL was comprised of 250, 168, and 69 records for BW, WW, and YW, respectively, meanwhile for BVD, there were 143, 114, and 48 records for BW, WW, and YW, respectively. However, each of the factors in the model was checked to have at least three records per level to ensure a minimum representation within the factor.

Using the lm function of the stats package included in the R software version 3.5.3 (R, 2019), the model described in equation 2 was evaluated, including the serological diagnostic factor of BVD, BL and for the joint effect of the two (BVD + BL, i.e., those animals that showed antibody titers against the two diseases) in each of the BW, WW and YW traits. In this case, the emphasis of building a model is to verify if the serological status was related to the higher or lower weight of the animals in each of the traits evaluated. The other factors were included to reduce the error, and thus, be able to know more precisely the effect that the contact with the virus has on animal growth. Using the Anova function of the Car package included in the R software version 3.5.3 (R, 2019), the model described in equation 2 was evaluated for each of the traits. Then, the significance of each of the factors included was verified, particularly the effect of the serological diagnostic factor of the diseases.

Results and Discussion

For the BW in the Colombian BON cattle was obtain an average of 32.47 ± 4.11 kg, and for the WW, an average of 198.19 ± 39.85 kg. Even for the BON breed, no average values have been reported for the YW, in this study was found an average of 222.91 ± 38.44 kg for this parameter. The variability obtained in this study in terms of standard deviation for the traits studied, may be reflect the environmental and management differences of each of the herds where animals are maintained, e.g., for birth weight, animals show values from 28.36 kg up to 36.58 kg. In Colombia, some studies have been carry out for these traits in BON and other creole breeds. Martínez andGallego (2012) founded in the BON cattle a BW value of 27.54 ± 3.72 kg, while Ossa, Suárez and Pérez (2007) reported a BW of 30.65 ± 3.79 kg for the Romosinuano breed, both values lower than the obtained in the present research. On the other hand, for the trait WW Martínez and Gallego (2012) showed an average of 165 ± 29.16 kg adjusted to 240 days for the BON race, this is 57 kg lowest than the obtained for us for WW. Although YW reports for the BON cattle have not been reported, some studies have found weight averages in the 16 months of 215.38 ± 30.57 kg in this cattle (Martínez & Gallego, 2012); being lower than that obtained in the present studio for YW despite the difference of age, while, for Romosinuano cattle, Ossa et al. (2007) founded weight average for the 16 months of age of 247.18 ± 0.78 Kg showing less variability compared to the YW get in this studio for the BON animals from Colombia.

The lowest values for the AIC and SSE evaluation criteria, the highest R^2 values, and the best predictions were obtained with the use of model 10; consequently, this is the model that best describes the variability for the three features studied (Table 1). Although for birth weight, the AIC value for this model is not the lowest, it is within the lowest values found among all models. On the other hand, model 10 presented the maximum BIC value for the three features; this is understandable since the BIC criterion penalizes the model with the highest number of parameters (Núñez & Zimmerman, 2000; Múnera, Herrera, & Cerón, 2013)

Table 1
AIC, BIC, R^2 and SSE values obtained for the criteria used in choosing the best model to evaluate three growth traits in BON cattle in Colombia

No.	Model	Birth weight				Weaning weight				Yearling weight			
		AIC	BIC	R^2	SSE	AIC	BIC	R^2	SSE	AIC	BIC	R^2	SSE
1	$Y_{ij} = \mu + H_i + \varepsilon_{ij}$	5945	5980	18.4	14971	6752	6779	21.4	724130	3143	3166	22.1	391422
2	$Y_{ij} = \mu + H_i + S_j + \varepsilon_{ijk}$	5912	5952	21.0	14495	6727	6758	24.5	696153	3118	3144	28.4	282375
3	$Y_{ijk} = \mu + H_i + S_j + Ep_k + \varepsilon_{ijkl}$	5916	5971	21.1	14468	6717	6763	26.1	680781	3120	3158	29.2	279184
4	$Y_{ijk} = \mu + H_i + S_j + Mn_k + \varepsilon_{ijkl}$	5913	5958	21.0	14492	6723	6760	25.0	690865	3118	3149	28.7	281080
5	$Y_{ijk} = \mu + H_i + S_j + An_k + \varepsilon_{ijkl}$	5913	5958	21.0	14489	6711	6748	26.3	678965	3103	3133	32.0	268162
6	$Y_{ijkl} = \mu + H_i + S_j + An_k + Np_l + \varepsilon_{ijklm}$	5887	5962	23.8	13987	6673	6736	31.6	630710	3101	3154	34.9	256651
7	$Y_{ijkl} = \mu + H_i + S_j + Mn_k + Np_l + \varepsilon_{ijklm}$	5887	5962	23.7	13993	6687	6750	30.1	643694	3115	3168	32.1	267843
8	$Y_{ijkl} = \mu + H_i + S_j + Mn_k + Np_l + An_m + \varepsilon_{ijklmn}$	5889	5969	23.8	13985	6669	6737	32.1	625330	3103	3159	35.0	256409
9	$Y_{ijklm} = \mu + H_i + S_j + Ep_k + Np_l + Ed_m + \varepsilon_{ijklmn}$	5890	5975	23.8	13979	6617	6694	37.4	576792	3113	3177	33.6	261619
10	$Y_{ijklm} = \mu + Npi + Gc_j + Ep_k + Ed_l + \varepsilon_{ijklm}$	5902	6411	34.1	12083	6441	6786	59.2	376212	3064	3253	53.5	183241
11	$Y_{ijklmno} = \mu + H_i + Ep_j + Np_k + Md_l + Ad_m + Ed_n + \varepsilon_{ijklmno}$	5893	5988	23.9	13962	6643	6724	35.2	596757	3125	3193	31.6	269656
12	$Y_{ijklmno} = \mu + H_i + Ep_j + Np_k + S_l + Ad_m + Ed_n + \varepsilon_{ijklmno}$	5891	5981	23.9	13968	6603	6685	38.9	563423	3099	3167	37.0	248488

No.: model number. R^2: coefficient of determination, SSE: sum of squares of the error. AIC: Akaike information criterion, BIC: Bayesian information criterion. H: herd; S: sex; Ep: birth time; Mn: birth month; An: birth year; Np: birth number; Gc: contemporary group; Md: weighing month; Ad: weighing year; Ed: age as a covariate for WW and YW.

In this work, the evaluation of the models for the traits BW, WW, and YW, improves with the inclusion of the contemporary group (CG), based on the selection criteria of the models considered. Showing the WW as an example, when model 12 was evaluated, which included the factors herd, sex, and year, independently, it presented lower SSE, AIC, BIC, and higher R^2 compared to model 11 (Table 1). However, when the model 10 that included the contemporary group was evaluated, the lowest AIC and SSE values of all the evaluated models were found; furthermore, also the highest values for R^2 (59.2%) and BIC were found. When considering the contemporary group with the three factors, i.e., herd, sex and year (both for weaning and yearling) and in turn, each of these three factors with their own levels and interactions, the number of parameters of the model increases, also obtaining an increase in the value for this last criterion. However, the conformation of the CG in model 10 reduced the degrees of freedom of the error, the sum of squares of the error, and consequently, the average square of the error, which translates into an increase in R^2, i.e., a higher variability percentage for the three traits is explained by model 10.

In this sense, the results coincide with those of Pascoa et al. (2013), who pointed out in a study carried out in Nelore cattle, that the models that included the effect of the sex of the offspring as a random effect separated from the CG were much better. Further, in those that the CG was the concatenation of herd, year and time of birth, the best data fit was found. This is because these allowed the formation of CG with a higher number of individuals facilitating the genetic connections between CG, and in turn, increasing the prediction accuracy of genetic evaluations.

Particularly for the WW trait, some studies in which models considering factors common to those of this work were evaluated, found R^2 values of 46% (Biffani, Martins, Martini, Bozzi, & Lima, 1999), 64% (Silveira et al., 2004), and 42% (Ossa et al., 2004). In the current work, for the WW characteristic with the inclusion in the CG model, it had an R^2 of 59%, which implies a 21% increase in the R^2 concerning model 12, highlighting the effect of the inclusion of the CG as a source of important variation in the model. In this way, the model that included the CG explains 59.2% of the variability of weaning weight in BON cattle under the conditions evaluated. Other studies found values of R^2 of 59.59% in pre-weaning traits of Nelore cattle, including in the model the effect of the CG (Santiago & Dantas, 2013).

Concerning YW, model 10 had a similar behavior explaining 53.5% of the variation for this trait; meanwhile, for BW, it only explains 34.1%. Silva, Fraga, Espíndola and Pedrosa (2008) evaluated three models with factors common to those considered in this research (i.e., sex, herd, year, and birth month). These authors found that the best model explained 61% of the variability for BW traits, which in turn, showed the lowest value for the degrees of freedom of the error and a low mean square; moreover, this translates into lower SSE compared to the other two models. However, other reports show an R^2 of 23% for the BW trait, considering within the model, the effects of the year, birth month, number of birth and sex of the animal (Ossa et al., 2007). That is, for this trait, there are other factors not included, which provide variability and have an important effect on its expression, such as the availability of fodder in quantity and quality for pregnant cows, animal management, climatic factors, and maternal ability of females, which are often not considered within the models (Silva et al., 2008).

For the choice of the best model for the three traits evaluated, the lowest R^2 values were those that included only the herd factor for the three characteristics. Specifically, for BW the initial R^2 value was 18.4% and the increase was maximum 5.5 percentage points including the other factors; on the contrary, when the CG was included, the increase between the simplest model and the one that included this factor was 15.7 percentage points when the R^2 value increased from 18.4% to 34.1%.

Likewise, for WW, the increase between the worst and the best model was 37.8 percentage points in the R^2 value, ranging from 21.4% to 59.2%; meanwhile, for YW, the increase between the worst and the best model was 31.4 percentage points ranging from 22.1% to 53.5% in the R^2 value.

Figures 1a and 1b show the boxplot of the standardized residuals for the WW characteristic of models 10 and 12 obtained using the analysis of variance, whose only difference is the inclusion or not of the CG. It is possible to observe that in model 10 (which includes the CG), the means of the boxplot, which represent the distribution of the estimated residues for each group of animals, are closer to zero. That is, there is a lower dispersion of the residues among animal groups, which translates into higher precision of the estimated values for weaning weight for each animal by contemporary group. On the other hand, when using model 12, a lower homogeneity of the estimates includes the individual effects of the factors that comprise the CG. These verifications were also made for the other models for the three traits (data not shown).

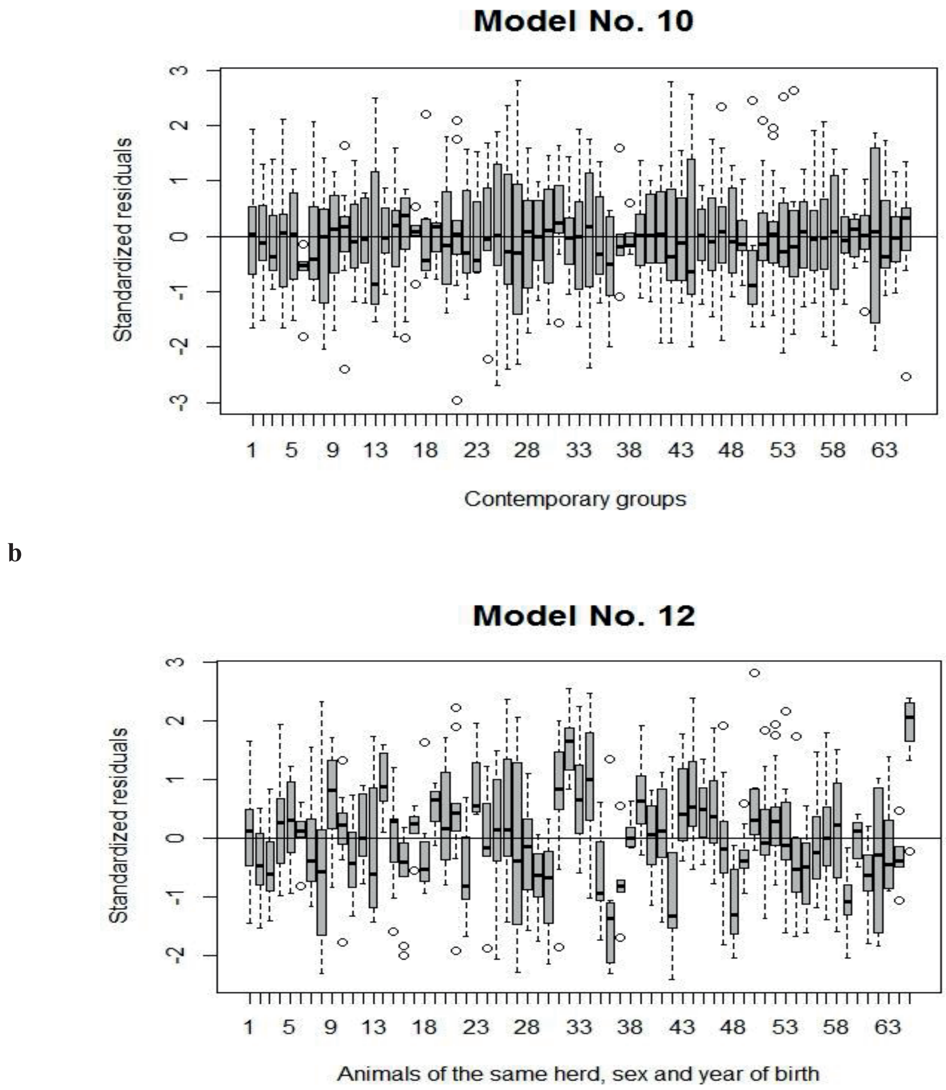

Figure 1. Standardized residuals for the weaning weight (WW) trait, including a) the contemporary group (CG) (Model No. 10), and b) the factors that comprise the CG independently (Model No. 12).

Tables 2 to 4 show the results of the analysis of variance constructed for the traits BW, WW, and YW, including the effect of the serological status for each disease, as well as for the joint effect of the two diseases evaluated in the best model found. As can be seen, the serological status of BON animals did not have a significant effect on the traits evaluated. When the effect of serological diagnosis to BL was included in the model, was obtain a p value of 0.9765 for BW, 0.3004 for WW and 0.8749 for YW. Likewise, when the effect of serological diagnosis to BVD, was found a p value of 0.524 was found for BW, 0.8511 for WW and 0.1654 for YW. When the joint effect of BL and DVB serological diagnosis was includes in the model was found a p value for BW of 0.308, 0.993 for WW and 0.476 for YW.

Table 2

Results of the analysis of variance for the traits birth weight (BW), weaning weight (WW) and yearling weight (YW), including the seropositivity for Bovine Leukosis (BL) in the model

	Birth weight				**Weaning weight**				**Yearling weight**			
Factor	**SS**	**DF**	**F value**	**p value**	**SS**	**DF**	**F value**	**p value**	**SS**	**DF**	**F value**	**p value**
Birth number	138.72	6	1.875	0.0877	12766	6	3.650	0.0024	16641.5	6	3.572	0.0068
Weaning age/year	NA	NA	NA	NA	9110	1	15.629	0.0001	373.2	1	0.480	0.4923
CG	938.21	36	2113	0.0007	70572	26	4.656	7.64 e-9	20612	12	2.212	0.0320
Season	145.11	3	3.923	0.0096	2137	3	1.222	0.3053	3730.6	3	1.601	0.2054
DxBL	0.01	1	0,0009	0.9765	631	1	1.082	0.3004	19.5	1	0.025	0.8749
Residual	2083.56	169			61785	106			28722.3	37		
R^2	38.75				67.76				66.53%			

DxBL: serological diagnosis for Bovine Leukosis; DF: degrees of freedom; NA: factor not included in the traits; SS: sum of squares; CG: Contemporary group.

Table 3

Results of the analysis of variance for the traits birth weight (BW), weaning weight (WW) and yearling weight (YW), including the seropositivity for Bovine Viral Diarrhea (BVD) in the model

	Birth weight				**Weaning weight**				**Yearling weight**			
Factor	**SS**	**DF**	**F value**	**p value**	**SS**	**DF**	**F value**	**p value**	**SS**	**DF**	**F value**	**p value**
Birth number	73.2	6	0.846	0.537	7411	6	2.2071	0.0506	18042.1	6	5.063	0.0014
Weaning age/year	NA	NA	NA	NA	5495	1	9.8200	0.0024	1.3	1	0.0021	0.9637
CG	502	28	1.243	0.214	62303	22	5.0606	3.92e-8	14176.2	10	2.387	0.0364
Season	90.5	3	2.090	0.105	2183	3	1.3005	0.28007	2334.6	3	1.310	0.2921
DxBVD	5.9	1	0.406	0.524	20	1	0.0354	0.8511	1209.2	1	2.036	0.1654
Residual	1500	104			44769	80			15440.4	26		
R^2	34.86				69.11				77.33			

DxBVD: serological diagnosis for Bovine Viral Diarrhea; DF: degrees of freedom; NA: factor not included in the traits; SS: sum of squares; CG: Contemporary group.

Table 4

Results of the analysis of variance for the traits birth weight (BW), weaning weight (WW) and yearling weight (YW), including the seropositivity for the joint effect of Bovine Leukosis plus Bovine Viral Diarrhea (BL + BVD) in the model

	Birth weight				Weaning weight				Yearling weight			
Factor	SS	DF	F value	p value	SS	DF	F value	p value	SS	DF	F value	p value
Birth number	70.41	6	0.823	0.554	7061	6	2.051	0.068	16666.3	6	4.43	0.0037
Weaning age/year	NA	NA	NA	NA	5513	1	9.611	0.002	0.6	1	0.001	0.974
CG	544.36	28	1.363	0.133	60744	22	4.081	1.19e-07	11963.5	10	1.909	0.094
Season	79.40	3	1.856	0.141	1895	3	1.101	0.353	2193.1	3	1.166	0.343
DxBL + DxBVD	51.96	3	1.215	0.308	49	3	0.028	0.993	1612	3	0.857	0.476
Residual	1453.9	102			44739	78			15037.6	24		
R^2	36.87				69.11				77.92			

DxBL + DxBVD: serological diagnosis for Bovine Leukosis and Bovine Viral Diarrhea; DF: degrees of freedom; NA: factor not included in the traits; SS: sum of squares; CG: Contemporary group.

The fact of not finding an effect of the serological status of BL on these traits (Table 2), leaves us with several hypotheses. In the first instance, when the diagnosis of seropositivity to BL infection was carried out, the exact contact moment of the animal with the virus was not known, that is, it could have occurred long before the serological analysis was done or recently. Consequently, the effects of the serological status on these characteristics were not evident if the infection was recent. The second hypothesis lies in the fact that many of the animals diagnosed with antibody titers for BLV infection do not carry the virus since a screening kit was used for each disease. Although this kit has a sensitivity of 100% and a specificity of 99.8% for BL, a new analysis should ideally be carried out using a confirmatory kit or using a molecular technique to detect proviral DNA. Another aspect to consider is that the final database for BL included up of 250, 168, and 69 records for BW, WW, and YW, respectively. If the size of this sample increases, the association of growth traits with seropositivity to BL may be found.

Although this study did not find a significant effect of the serological status of the BL on growth traits such as BW, WW, and YW in the evaluated animals of the BON breed, other studies have found an important effect of seropositivity to BL in specialized breeds, such as Holstein, on productive parameters such as milk production. In a study carried out by Nekouei, VanLeeuwen, Stryhn, Kelton and Keefe (2016), seropositive cows were found to have a shorter lifespan in the herd, being discarded much earlier compared to the seronegative cows; this was one of the leading causes of premature discarding, leading in turn, to obtaining lower milk production per cow in its productive life. In this sense, Bartlett et al. (2013) found that cows that showed to have antibodies against BL had a higher risk of leaving the herd approximately 1.6 years after diagnosis, while Erskine et al. (2012), found evidence that subclinical infection may be associated with a decrease in milk production. In Colombia, Úsuga, Echeverri and López-*Herrera* (2018) reported that cows infected with Bovine Leukosis had lower production of lactation milk (7.67%) and less protein (15.37 kg/lactation), which ultimately affects the profitability of the herds.

As in the case of BL, no significant effect of the serological status was found for BVD, which may be due to the reasons given for the case of BL, and especially considering that the sample sizes for this trait were smaller (143 records for BW, 114 for WW and 43 for YW). This is because the information from some herds was eliminated from this analysis, as these were vaccinated against this pathogen. In the case of the joint effect of BVD plus BL, the proportion of animals positive to the two diseases within each characteristic was relatively low, i.e., 13.9% for BW, 13.1% for WW, and 18.7% for YW. This could have influenced the fact of not finding a significant effect of the joint seropositivity on each of the characteristics assessed. Another reason may be that there is no effect of seropositivity to both infections on these growth parameters in BON cattle.

Although the serological diagnosis of BVD was not significant for the BW, YW, and WW traits of BON cattle, important effects have been found on other features, such as those related to fertility in females and males, decreased milk production, higher risk of contracting other diseases, and lower weight gain (Yarnall & Thrusfield, 2017). Likewise, Campbell (2004) reported that the animals that were detected with persistent infection (PI) of BVD did not perform well at weaning, showing an adjusted weight of 43 kg below the animals that were not diagnosed as PI. Similarly, Martin, Nagy, Armstrong, and Rosendal (1999) reported that BVD infection was related to the risk of respiratory diseases and lower weight gain in a batch of calves that entered a feedlot system; on the other hand, Richter et al. (2017) found on average, higher economic losses due to BVD infection in milk production systems compared to meat production systems. In this sense, Heuer, Healy and Zerbini (2007) reported that the economic losses per cow per year in herds affected by BVD could be around NZ $ 87, without considering other aspects such as the higher incidence of other immunosuppression diseases that the animals experience.

Another hypothesis that is posed for not finding a significant effect of the diagnosis of these two viral infections on the growth traits studied may lie in the resistance that the BON cattle breed may have to the infection and/or disease caused by these viruses (BL and/or BVD). In this sense, animals could come in contact with the virus but not develop the disease, as it has been found in this breed for other types of viral infections such as foot-and-mouth disease and vesicular stomatitis (López et al., 2000; López, Salazar, Restrepo, Zuluaga, & Ossa, 2002). However, more thorough research is necessary to establish a possible resistance effect for these diseases.

Conclusions

The best model to describe the variability of the traits birth weight (BW), weaning weight (WW) and yearling weight (YW) in BON cattle in Colombia, is the one which includes the contemporary group (CG), formed by the concatenation of the herd, sex, and birth year factors. This significantly improves the adjustment of linear models to explain the variability for growth traits. This finding is important if the first step is the acquisition of tools when looking for strategies that seek to increase the performance of the animals and to be able to use these models in genetic evaluations, which allows identifying BON animals with superior genetic merit.

For the BW trait, other models that include additional variables that allow finding a better fit for the model must be evaluated.

There was no significant effect of the serological status for BL and BVD on the growth traits assessed, such as BW, WW, and YW, in the BON cattle-breed evaluated in this study, so it is essential to continue with studies that allow elucidating possible resistance mechanisms to these diseases in the BON breed.

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