

Phenotypic variability for conformation traits of BON cattle in Colombia

Hernán Issaías Medina Ríos

Universidad de Antioquía: Universidad de Antioquia

Edison Julián Ramírez Toro

Colombian Corporation of Agricultural Research: AGROSAVIA

Mario Fernando Cerón-Muñoz (✉ grupogamma@udea.edu.co)

Universidad de Antioquia <https://orcid.org/0000-0002-7233-6625>

William Burgos Paz

Corporacion Colombiana de Investigación Agropecuaria: AGROSAVIA

Research Article

Keywords: multivariate analysis, creole cattle, linear type, populations, selection

Posted Date: September 6th, 2022

DOI: <https://doi.org/10.21203/rs.3.rs-1886742/v1>

License: © ⓘ This work is licensed under a Creative Commons Attribution 4.0 International License.

[Read Full License](#)

Abstract

The purpose of this study was to evaluate the variability of conformation traits (CT) in three BON cattle subpopulations with different herd management. For this study, using the nine-point scores of 20 CT as well as breed characterization and final score in 929 cows were analyzed. Descriptive statistics alongside hierarchical cluster analysis were performed. It was found that legs and feet traits had the slightest phenotypic variability whereas traits related to musculature and the fore attach and udder depth traits showed the higher variability. The herarchical clustering revealed relationships that allow analyzing the phenotypic trend between animals according to herd management and breeding objectives.

Introduction

The Blanco Orejinegro (BON) is a colombian creole cattle originated from cattle brought by the Spaniards in the fifteenth century during colonization (Ramírez et al. 2019). It currently has the greatest animal inventory with respect to creole bovine breeds existing in the country (Ocampo et al. 2020), with a production target oriented to growth and meat production (Ramírez et al. 2019, 2020).

The development of this breed in Colombia has occurred through three strategies: 1) The conservation through Colombia's Animal Germplasm Bank (AGB), consisting of a herd without selection processes; 2) The Agrosavia Selection Herd (ASH) formed in 2012 and promotes the use of cattle with superior genetic merit for growth and reproduction maintaining consanguinity as lower as possible, and 3) actions of the Breeders Network (BN), which come from a set of BON breeders whose production targets depend on the dynamics of the bovine sector in the country.

These three production strategies for BON have shown some differences at the molecular level, where the management has been decisive in the conservation and sustainability of this genetic resource for the country (Valderrama et al. 2021). However, the maintenance of the breed's genetic diversity must be consistent with the economic development of the producers and the possibility of generating added value (Schäler et al. 2019). Herein, the production targets and even market demands could decline aspects such as the animal's body conformation in order to stay in high production systems (Sofyan et al. 2020).

Productive monitoring alongside accompaniment to producers resulted in comparisons of either productive or linear classification characteristics that constituted a first point in decision making for the development of the breed. In this regard, breed-oriented work allowed generating genetic parameters and values for growth characteristics (Ramírez et al. 2020). However, the conservation of the breed's phenotypic characteristics, the search for animals with body conformation for meat or the market requirements transferred to producers can define phenotypic aspects that require consideration of a balance between productivity and conservation.

The purpose of this study, was to compare body conformation traits in the Blanco Orejinegro bovine breed under three scenarios: conservation, selection and livestock systems of Colombian breeders.

Materials And Methods

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

Linear classification records of 929 lactating females of the BON breed belonging to the breeders network (BN, n = 11) and to the conservation (AGB) and selection (ASH) subpopulations of the El Nus Research Center of the Colombian Corporation for Agricultural Research – AGROSAVIA were used.

The BN farms are distributed in three departments of Colombia with height ranges oscillating between 100 (Sabana de Torres, Santander) and 1700 (Támesis, Antioquia) m.a.s.l., with valley and hillside topographic conditions.

AGB and ASH animals are located at the El Nus Research Center of the Colombian Corporation for Agricultural Research – AGROSAVIA. For AGB, the herd management is based on conservation through circular mating to minimize consanguinity of herd. Meanwhile, ASH has a mating program based on the use of reproducers with positive genomic estimated breeding values for growth traits and negative values for reproduction traits, limiting consanguinity to 3%.

Through visits to BN herds and the productive monitoring of AGB and ASH between 2014 and 2019, evaluation of the conformation traits was carried out through visual scores of the biological extremes of the linear classification used by Agrosavia for the native bovine breeds of Colombia. The scores used considered the guidelines defined by the International Committee for Animal Registration (ICAR, 2018). Scores (1 to 9) were recorded for 20 traits distributed in four trait groups and racial characterization (Table 1). The final score (FS) variable was evaluated as the rater's assessment of the animal's overall appearance: 60 to 74 poor/insufficient; 75 to 79 good; 80 to 84 better than good; 85 to 89 very good, and 90 to 99 excellent.

Table 1
Description of the conformation traits evaluated in Colombian BON cattle.

Group	Trait	Score 1 to 3	Score 4 to 6	Score 7 to 9
Structure	Chest width (CW)	Narrow	Intermediate	Wide (9)
	Dorsal line (DL)	Concave	Straight (5)	Convex
	Body length (BL)	Short	Intermediate	Long (7)
	Chest depth (CD)	Shallow	Intermediate	Deep (9)
	Height at rump (HR)	Low	Intermediate (6)	Tall
	Rump angle (RA)	High pins	Intermediate (5)	Low pins
	Width at hips (WH)	Narrow	Intermediate	Wide (9)
Musculature	Loin width (LW)	Little musculature	Intermediate musculature	Evident musculature (9)
	Thigh width and depth (TWD)	Little musculature	Intermediate musculature	Evident musculature (9)
	Arm width (AW)	Little musculature	Intermediate musculature	Evident musculature (9)
Legs and feet	Front legs (FL)	Closed	Intermediate (5)	Open
	Hock angle (HA)	Straight	Intermediate (5)	Sickle
	Pasterns angle (PA)	Low	Intermediate (5)	High
	Claw size (CS)	Little	Intermediate (5)	Grande
	Claw angle (CA)	Low	Intermediate (5)	Low
Udder	Fore udder attach (FUA)	Weak	Intermediate	Strong (9)
	Central ligament (CL)	Weak	Intermediate	Strong (9)
	Udder depth (UD)	Tall	Intermediate (5)	Low
	Teat size (TS)	Short	Intermediate (5)	Long
	Teat placement (TP)	Closed	Intermediate (5)	Open
Racial pattern	Racial characterization (RC)	Bad	Acceptable	Good (9)
Values in parentheses indicate the reference value towards the optimum.				

The recorded scores were analyzed independently for BN, AGB and ASH. Descriptive statistics were initially calculated for the variables, while subsequently homogeneous groups of variables were generated (Chavent et al. 2012), which would allow the identification of score patterns among highly-

related variables that can potentially describe groups and variables associated with the productive strategies of each subpopulation. Variable clustering was performed as described by Chavent et al. (2012) and implemented with the `hclustvar` function from the `ClustOfVar` library of the R-project software (R Core Team 2022).

The FAMD and HCPC methods implemented in the `FactoMineR` library (Husson et al. 2015) were used to determine the most probable cluster number, with the graphical representation of the clustering being performed using the hierarchical clustering algorithm.

Results

The conformation traits average scores ranged from 3.26 for UD to 6.14 for BL (Fig. 1). The DL, HR, the set of legs and feet, TL and TP traits had an average score closer to the optimal score.

The body structure traits showed an intermediate trend in body proportions and traits such as CW, related to cardiorespiratory capacity in altitude conditions, did not present maximum scores. Regarding musculature traits, these showed the greatest dispersion and are therefore evidence of the high phenotypic variability for this trait in the BON breed. As expected, leg and foot traits had average scores close to the optimal, because the development of this breed is associated with hillsides or mountainous regions, suggesting a strength in these traits. Low scores were recorded for udder traits, except TL and TP.

Mean scores of the conformation traits obtained independently for the three subpopulations are showed in Table 2. When considering the score mean values, a great similarity was observed in the scores for the three subpopulations. However, all the subpopulations present different levels of variability reflected in the observed standard deviation (Table 2).

Table 2

Conformation traits of BON cows from the breeders network (BN), animal germplasm bank (AGB) and Agrosavia selection herd (ASH) subpopulations in Colombia.

Traits	BN (n = 357)	AGB (n = 314)	ASH (n = 258)
	Mean \pm SD		
Chest width (CW)	5.43 \pm 1.19	5.70 \pm 0.99†	5.62 \pm 1.23
Dorsal line (DL)	5.25 \pm 0.58†	5.30 \pm 0.61	5.34 \pm 0.68
Body length (BD)	5.95 \pm 1.10	6.33 \pm 1.06†	6.18 \pm 1.17
Chest depth (CD)	5.43 \pm 1.15	5.93 \pm 1.02†	5.64 \pm 1.13
Height at rump (HR)	5.64 \pm 1.08	6.07 \pm 0.90†	5.92 \pm 0.96
Rump angle (RA)	5.67 \pm 0.67	5.48 \pm 0.58†	5.82 \pm 0.64
Width at hips (WH)	5.28 \pm 1.14	5.67 \pm 1.03†	5.57 \pm 1.23
Loin (LW)	5.57 \pm 1.16†	5.39 \pm 1.13	5.37 \pm 1.15
Thigt (TWD)	4.28 \pm 1.45	5.29 \pm 1.19†	4.78 \pm 1.43
Arm (AW)	4.05 \pm 1.27	4.65 \pm 1.06†	4.40 \pm 1.24
Front legs (FL)	5.02 \pm 0.31	5.04 \pm 0.31	5.00 \pm 0.24†
Hock angle (HA)	5.08 \pm 0.39†	5.14 \pm 0.63	5.17 \pm 0.45
Pasterns angle (PA)	4.92 \pm 0.47†	4.78 \pm 0.52	4.79 \pm 0.44
Claw size (CS)	5.06 \pm 0.50	5.11 \pm 0.48	5.06 \pm 0.36†
Claw angle (CA)	4.85 \pm 0.47	4.93 \pm 0.52†	4.79 \pm 0.46
Fore udder attach (FUA)	3.25 \pm 1.49	3.42 \pm 1.52†	3.12 \pm 1.35
Central ligament (CL)	4.37 \pm 1.55†	3.61 \pm 1.43	4.16 \pm 1.70
Udder depth (UD)	3.00 \pm 0.87	3.69 \pm 1.00†	3.10 \pm 0.82
Teat size (TS)	5.04 \pm 0.95†	4.78 \pm 0.87	5.21 \pm 1.02
Teat placement (TP)	5.21 \pm 0.60	5.14 \pm 0.61†	5.18 \pm 0.68
Racial characterization (RC)	8.32 \pm 0.89	8.35 \pm 0.91†	8.33 \pm 0.80
Final score (FS)	78.94 \pm 6.81	82.32 \pm 6.50†	80.14 \pm 6.72
SD: standard deviation; † average scores closest to the optimum.			

Initially individuals clustering identified three groups of animals in the population (Fig. 2).

The first cluster grouped 238 animals (25.6%), which presented the lowest average scores in the traits associated with body structure, as well as the lowest number of variables with optimal scores. This group of individuals can be associated with those animals that deviate from the optimal values and that can potentially move away from the phenotypic characterization expected for the breed. The highest percentage of animals belonged to the BN subpopulation (n = 122).

The second cluster grouped 337 (36.3%) cows with the best scores for proper direction, limb angulations and high breed characterization scores. Animals from the BN subpopulation (n = 163) had the highest representation in this group.

The third group (cluster 3) consisted of 354 (38.1%) cows with the best body structure and musculature, as similar members to the previous group, although they presented a better udder development score than the rest of the animal groups, with the AGB subpopulation (n = 197) with the highest representation of this group.

Differences ($p < 0.05$) were found in the final score (FS) averages in the classification of animals associated with the clusters formed. Despite FS depends on the classifier's appreciation, there is a great assertiveness in classifying a cow having optimal phenotypic characteristics regarding those that do not, and this is favorable in the environment of the producers of the BN subpopulation who, in many cases, use the phenotypic characterization aspects as a selection criterion.

In addition to the phenotypic characterization of the animals, relationships between conformation traits within subpopulations were explored in order to establishing homogeneity patterns in the phenotypes associated with management characteristics typical of production systems.

The observed relationships of conformation traits by hierarchical clustering showed different groupings for the three subpopulations (Fig. 3). For the BN subpopulation, four clusters of linear classification variables were identified, while for AGB and ASH, five clusters were identified.

For the group of BN individuals, important variables according to the productive orientation were clustered (Fig. 3A). The first cluster grouped traits related to the muscular development of individuals, highlighting arm span and leg width and depth. Also included in this group are loin width, total score and breed characterization, where producers consider animals with great strength and meat development without departing from the animal's racial pattern. The second and third clusters were related to the body structure traits, where the chest and hip breadth stand out (cluster 2) and legs and feet (cluster 3) have a great interest in the breed due to its adaptation to hillside conditions. Finally, the characteristics associated with udder development and structure formed cluster 4.

As expected, the independent analysis for the AGB subpopulation showed the greatest variability with respect to the trait groups evaluated (Fig. 2B). Two udder traits were grouped with the racial characterization in cluster 1, while the second cluster characterized traits of body structure (i.e., body length and height to the sacrum). The cluster 3 grouped the angulation features of the forelimbs and

hindlimbs. Finally, clusters 4 and 5 were characterized by traits associated with musculature and foot, respectively.

In ASH (Fig. 2C), the first cluster was characterized by cows of good breed pattern with adequate mammary gland strength. The second was characterized by body structure and musculature traits which are the main selection criteria established for this subpopulation. Cluster three and five grouped traits related to limb and pelvic angulations. However, cluster 4 grouped hoof size and haunch angle, variables that may be associated with hillside management.

Discussion

In general, the results obtained showed that BON cows have some characteristics that determine the racial pattern (RC) and breeders identify individuals that fitted to the breed profile. In turn, the average FS observed in the three subpopulations was similar (Table 2), and is supported by the value of 80 points (good) according to ICAR (2018), and suggested that that BON cows correspond to a prototype with desirable phenotype qualification.

There are relevant phenotypic traits for producers over the years. For instance, HR and DL traits showed a rectilinear trend between the withers and the sacrum. This means that BON cows have a strong lumbar-dorsal line and reflects the influence of producers' preferences when selecting their animals, discarding cows with spinal deviations, such as lordosis (Sanchez and Iglesias, 2009).

Creole individuals stand out for their adaptive and reproductive characteristics, where, in some situations, muscle development has been a factor that reduces their use in production environments compared to specialized breeds (Arelovich et al. 2011; Armstrong et al. 2022). Efforts made by Agrosavia in recent animal selection processes generated changes in the musculature traits relationships. It can be seen that these traits in the BN and ASH subpopulations present greater similarity and are grouped with production traits, which in the case of BN include aspects related to the udder. Some producers see in this breed an ideal genetic component for milk production, as well as in crossbreeding with dairy breeds such as Holstein (Cañas et al. 2009).

An interesting result of this study for the ASH subpopulation of cows (Fig. 3C) was the clustering of body structure traits (WH, CW, HR, BL, and CD) and musculature (LW, TWD, and AW), reflecting management of the joint selection of characteristics associated with meat production. Berry et al. (2019) mentioned that the evaluation of the external view of the animal's musculature and size, in terms of structure, should have some relationship with carcass yield, which may seem reasonable that these subjectively scored traits correlate with primal cut yields.

Historically, BON cattle have adapted to the environment of the inter-Andean valleys of Colombia, especially in Antioquia region (Martínez et al. 2012), characterized by altitudes between 1500 and 2200 m.a.s.l., and one of the mountainous regions of the country. In this sense, the BON animals presented a good to excellent posture conformation for hillside grazing.

In fact, the optimal or desirable average scores of the set of legs and feet corroborate that the animals presented a normal and adequate direction of the limbs in their entire length or of the different regions separately, which allows a good physical support (de Faria et al. 2007), and symmetrical locomotion without problems when walking long distances to feed or in the time of reproduction (Góes and Pierre, 2018). Zhang et al. (2015) mentioned that animals with simple, reliable and strong legs adapt very well to the terrain in which they feed, mate and avoid predators. It should be noted that some problems or defects in the legs and feet can worsen, causing pain and suffering that implies low feed intake, loss of body condition, low fertility and production. All this involves animal welfare and, therefore, functionality (Roveglia et al. 2019). As such, care must be taken with the tolerance of certain defects at limb level (de Faria et al. 2007).

Low average udder trait scores indicated weakness in insertion and suspensory ligament, with high udders. Having poor insertion and fixation of the udder (score from 1 to 3 points) predisposes cows to abandon the herd more frequently, given that, as the anterior lobes of the udder are very close together, there is lower productivity (García-Ruíz et al. 2016; Palii et al. 2020). However, TL and TP were suitable, allowing for adequate milking or for the offspring to grasp the teats correctly at the time of suckling, and also preventing mastitis (Campos et al. 2012). This means that cows with functional udders, which are extended under the abdomen, well attached, with thin and short teats, should be selected (Simčič et al. 2021).

García-Ruíz et al. (2016) mentioned that cows with the udder floor slightly above the hock have a lower risk of being discarded than cows with the udder floor below the hock. Therefore, evaluation of cow anatomical attributes, such as udder morphology, provides an opportunity for BON breed selection programs to also target higher milk production (Sinha et al. 2021). Currently, there are no milk production records for genetic evaluations in this breed and, therefore, maternal ability variables are the only indirect criteria for this type of phenotypes.

For the three subpopulations, CW and CD were found to have intermediate scores, reducing the relative risk of discarding cows (Table 2), since those characteristics indicate sufficient space to house vital organs, such as the heart and lungs (García-Ruíz et al. 2016). Thus, for example, cows with high scores indicate broad thorax and sufficient cardiorespiratory capacity. Similarly, the relationship between CW and CD is evident in the clustering of the three BON subpopulations (Fig. 3).

The hierarchical analysis of distances between the analyzed phenotypic variables showed relationships that allow analyzing the phenotypic trend between animals according to management. However, there is clarity in the selection that is made in each subpopulation according to the functional balance in the foot angles so that the animals have an adequate movement in the paddocks.

In each subpopulation studied (BN, AGB and ASH), the selection criteria or animal management can generate differences in the frequency of the scores observed for the conformation traits. For example, some herds in BN have flat terrain whereas other have hillsides and selection criteria at the phenotypic

level may be more oriented towards increasing the frequency of animals with high scores for musculature characteristics such as AW or udder traits (Table 2).

The genetic management model for AGB animals prioritizes conservation and variability over production schemes. In this case, the scores of 14 phenotypic traits are above the expected traits for selection (ASH) or breeder (BN) subpopulations (Table 2).

The animals that have the best body conformation, given the positive contribution for most of the traits, were grouped in cluster three in Fig. 2. According to de Faria et al. (2007), the identification and optimal use of superior animals with morphological evaluation using visual scoring plays a fundamental role in determining trends and promoting the selection of individuals with the appropriate biotype for the market.

Conclusion

In conclusion, the results obtained from the conformation traits showed that the three subpopulations studied are phenotypically homogeneous, maintaining a harmonic size and proportions, as well as correct bone angularities of the body structure and of the legs and feet. In addition, cows have a weak to intermediate mammary gland with adequate teat placement and size. For each subpopulation of BON cows, there are more important traits due to the production and management objectives of each system. The phenotypic variability found for the variables analyzed would justify the inclusion of linear classification in selection programs for the BON breed.

Declarations

Acknowledgments The authors would like to thank the Colombian Corporation for Agricultural Research-AGROSAVIA attached to the Colombian Ministry of Agriculture and Rural Development -MADR for funding this work through its research agenda in projects ID1000684 and ID1001258. Similarly, the Colombian Germplasm Bank System for Food and Agriculture (SBGNAA, project BGA1000882), as well as the producers attached to the Producer Network for the Blanco Orejinegro Breed for supplying part of the information used. The support from the Research Group in Agricultural Sciences, Biodiversity and Territory - GAMMA of the University of Antioquia is also appreciated.

Authors' contribution HMR, WBP and MCM contributed to the design and writing of the manuscript. ERT collected data that was statistically analyzed by HMR. The manuscript has been read and approved by all authors.

Funding: This research was supported by Universidad de Antioquia, GAMMA research group and AGROSAVIA.

Availability of data and material Not applicable.

Code availability Not applicable.

Ethical approval Not applicable, as collected data was used for the analysis.

Consent to participate Not applicable.

Consent for publication Not applicable.

Conflict of interest The authors declare that they have no conflict of interest.

References

1. Arelovich, H., Bravo, R., Martínez, M., 2011. Development, characteristics, and trends for beef cattle production in Argentina. *Animal Frontiers*, 1(2):37–45. <https://doi.org/10.2527/af.2011-0021>
2. Armstrong, E., Rodríguez, F., McIntosh, M., Poli., M., Cibils, A., Martínez-Quintana, A., Félix-Portillo, M., Estell, R., 2022. Genetic and productive background of Criollo cattle in Argentina, Mexico, Uruguay and the United States. *Journal of Arid Environments*, 200:1–10. <https://doi.org/10.1016/j.jaridenv.2022.104722>
3. Berry, D., Pabiou, T., Fanning, R., Evans, R., Judge, M., 2019. Linear classification scores in beef cattle as predictors of genetic merit for individual carcass primal cut yields. *Journal of Animal Science*, 97, 2329–2341. <https://doi.org/10.1093/jas/skz138>
4. Campos, R., Cobuci, J., Costa, C., Braccini, J., 2012. Genetic parameters for type traits in Holstein cows in Brazil. *Revista Brasileira de Zootecnia*, 41(10), 2150–2161. <https://doi.org/10.1590/S1516-35982012001000003>
5. Cañas, J., Restrepo, L., Ochoa, J., Echeverri, A., Cerón-Muñoz, M., 2009. Estimación de las curvas de lactancia en ganado Holstein y BON x Holstein en trópico alto colombiano. *Revista Lasallista de Investigación*, 6(1):35–42. <https://www.redalyc.org/articulo.oa?id=69514350006>
6. Chavent, M., Kuentz, V., Liquet, B., Saracco, J., 2012. ClustOfVar: An R package for the clustering of variables. *Journal of Statistical Software*, 50(2), 1–16. <https://doi.org/10.18637/jss.v050.i13>
7. de Faria, C., Magnabosco, C., Albuquerque, L., de los Reyes, A., Bezerra, L., Lôbo, R., 2007. Utilização de escores visuais de características morfológicas de bovinos Nelore como ferramenta para melhoramento genético. 4ª ed. Planaltina, DF: Embrapa Cerrados. https://ainfo.cnptia.embrapa.br/digital/bitstream/CPAC-2009/28911/1/doc_177.pdf
8. García-Ruiz, A., Ruiz-López, F., Vázquez-Peláez, C., Valencia-Posadas, M., 2016. Impact of conformation traits on genetic evaluation of length of productive life of holstein cattle. *International Journal of Livestock Production*, 7(11), 1–10. <https://doi.org/10.5897/IJLP2016.0301>
9. Góes, A., Pierre, F., 2018. Melhoramento genético: utilização de escores visuais na pecuária de corte. *Tekhne e Logos*, 9(2):36–47. <http://revista.fatecbt.edu.br/index.php/tl/article/viewFile/558/353>
10. Husson, F., 2016 Multivariate exploratory data analysis and data mining, from: <https://cran.r-project.org/web/packages/FactoMineR/FactoMineR.pdf>

11. International Committee for Animal Recording (ICAR), 2018. Guidelines for conformation recording of dairy cattle, beef cattle and dairy goats. Section 5 Conformation Recording. <https://www.icar.org/Guidelines/05-Conformation-Recording.pdf>
12. Martínez, R., Vásquez, R., Gallego, J., 2012. Eficiencia productiva de la raza Bon en el trópico colombiano. 214 p. Editorial Corpoica, Bogotá. Colombia.
13. Ocampo, R., Ramirez, J., Lopera, J., Restrepo, G., Gallego, J., 2020. Genetic diversity assessed by pedigree analysis in the Blanco Orejinegro (BON) cattle breed population from the colombian germplasm bank. *Chilean Journal of Agricultural and Animal Sciences*, 36(1), 69–77. <https://revistas.udec.cl/index.php/chjaas/article/view/1958>
14. Paliy, A., Shkromada, O., Todorov, N., Grebenik, N., Lazorenko, A., Bondarenko, I., Boyko, Y., Brit, O., Osipenko, T., Halay, O., Paliy, A., 2020. Effect of linear traits in dairy cows on herd disposal. *Ukrainian Journal of Ecology*, 10(3), 88–94. https://doi.org/10.15421/2020_138
15. Ramírez, E., Ocampo, R., Burgos, W., Elzo, M., Martínez, R., Cerón-Muñoz, M., 2019. Estimación poligénica y genómico-poligénica para características de crecimiento en ganado Blanco Orejinegro (BON). *Livestock Research for Rural Development*, 31(3), 1–11. <http://www.lrrd.org/lrrd31/3/ceron31030.html>
16. Ramírez, E., Burgos, W., Elzo, M., Martínez, R., Cerón-Muñoz, M., 2020. Genetic parameters and trends for growth traits in Blanco Orejinegro cattle. *Translational Animal Science*, 4(3), 1–9. <https://doi.org/10.1093/tas/txaa174>
17. Roveglia, C., Niero, G., Bobbo, T., Penasa, M., Finocchiaro, R., Visentin, G., Lopez-Villalobos, N., Cassandro, M., 2019. Genetic parameters for linear type traits including locomotion in Italian Jersey cattle breed. *Livestock Science*, 229, 131–136. <https://doi.org/10.1016/j.livsci.2019.09.023>
18. R Core Team 2022 R: A language and environment for statistical computing. R foundation for statistical computing Computing, Vienna, Austria. <https://www.R-project.org/>
19. Sánchez, L., Iglesias, A., 2009. Valoración morfológica en bovino de aptitud cárnica y razas rústicas. En C. Sañudo (Ed), *Valoración morfológica de los animales domésticos* (pp. 271–308). Ministerio de Medio Ambiente y Medio Rural y Marino de España.
20. Schäler, J., Addo, S., Thaller, G., Hinrichs, D., 2019. Exploration of conservation and development strategies with a limited stakeholder approach for local cattle breeds. *Animal*, 13(12): 29222931. <https://doi.org/10.1017/S1751731119001447>
21. Simčič, M., Luštrek, B., Štepec, M., Logar, B., Potočnik, K., 2021. Estimation of genetic parameters of type traits in first parity cows of the autochthonous Cika cattle in Slovenia. *Frontiers in Genetics*, 12, 1–9. <https://doi.org/10.3389/fgene.2021.724058>
22. Sinha, R., Sinha, B., Kumari, R., Vineeth, M., Verma, M., Dayal, I., 2021. Principal component analysis of linear udder type traits and their relationship with milk yield and composition in indigenous Sahiwal cattle. *Animal Bioscience*, 00, 1–10. <https://doi.org/10.5713/ajas.19.0619>
23. Sofyan, H., Sudarnika, E., Satyaningtijas, A., Sumantri, C., Agungpriyono, S., 2020. The economic potential of aceh cattle based on its farmers, traders, and consumers perspective. *Frontiers in*

24. Valderrama, Y., Ramírez, E., Burgos, W., Martínez, R., Ocampo, R., Cerón-Muñoz, M., 2021. Estructura genética de poblaciones de ganado Blanco Orejinegro en Colombia. *Livestock Research for Rural Development*, 33(4), 1–10. <https://lrrd.org/lrrd33/4/3353ceron.html>
25. Zhang, Q., Xu, K., Ding, X., 2017. Investigation of feet functions of large ruminants with a decoupled model of equivalent mechanism. *Biology Open*, 6(4), 407–414. <https://doi.org/10.1242/bio.023630>

Figures

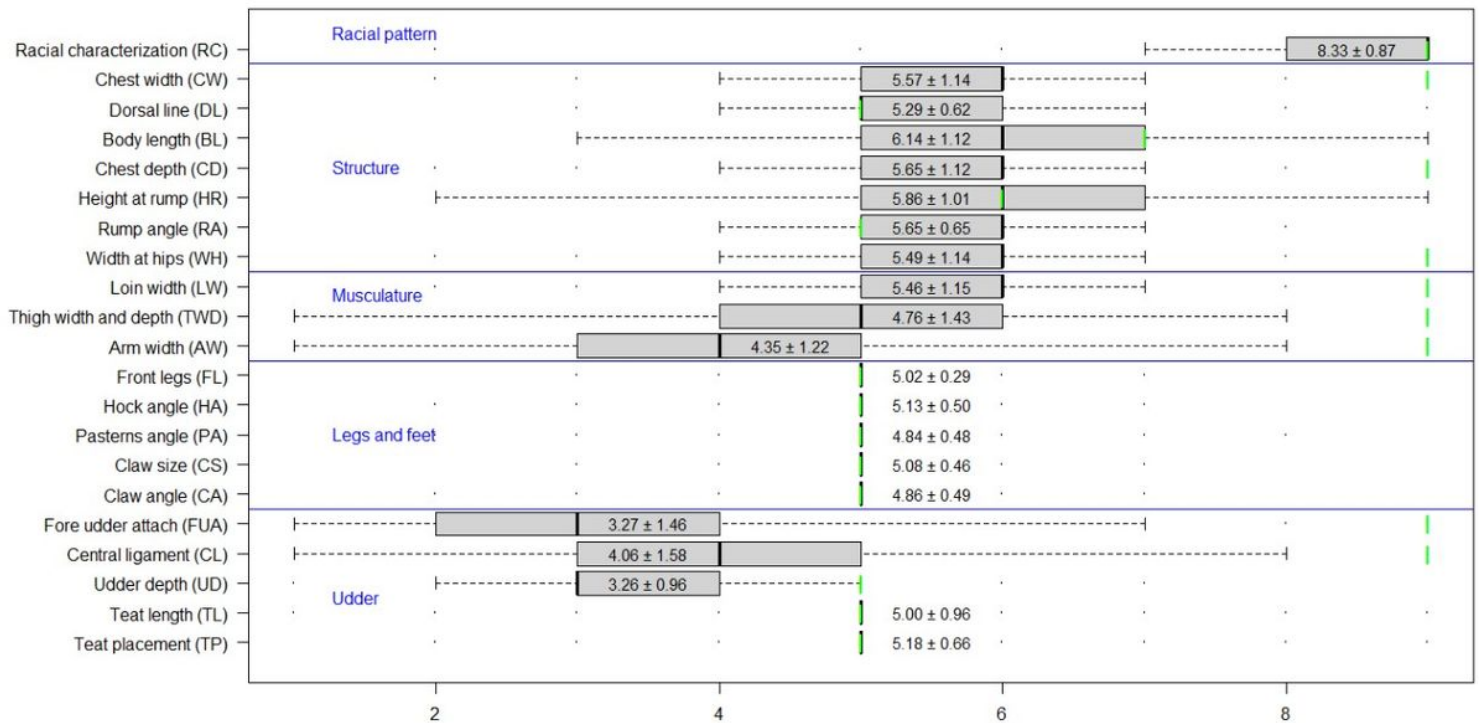


Figure 1

Distribution of conformation trait scores in Blanco Orejinegro cows in Colombia. The green line indicates the reference value towards the optimum.



Figure 2

Influence of conformation traits in groups of Blanco Orejinegro cows in cluster analysis. Values in parentheses indicate the mean and the reference value and red and green colors indicate scores far from or close to the optimum, respectively).

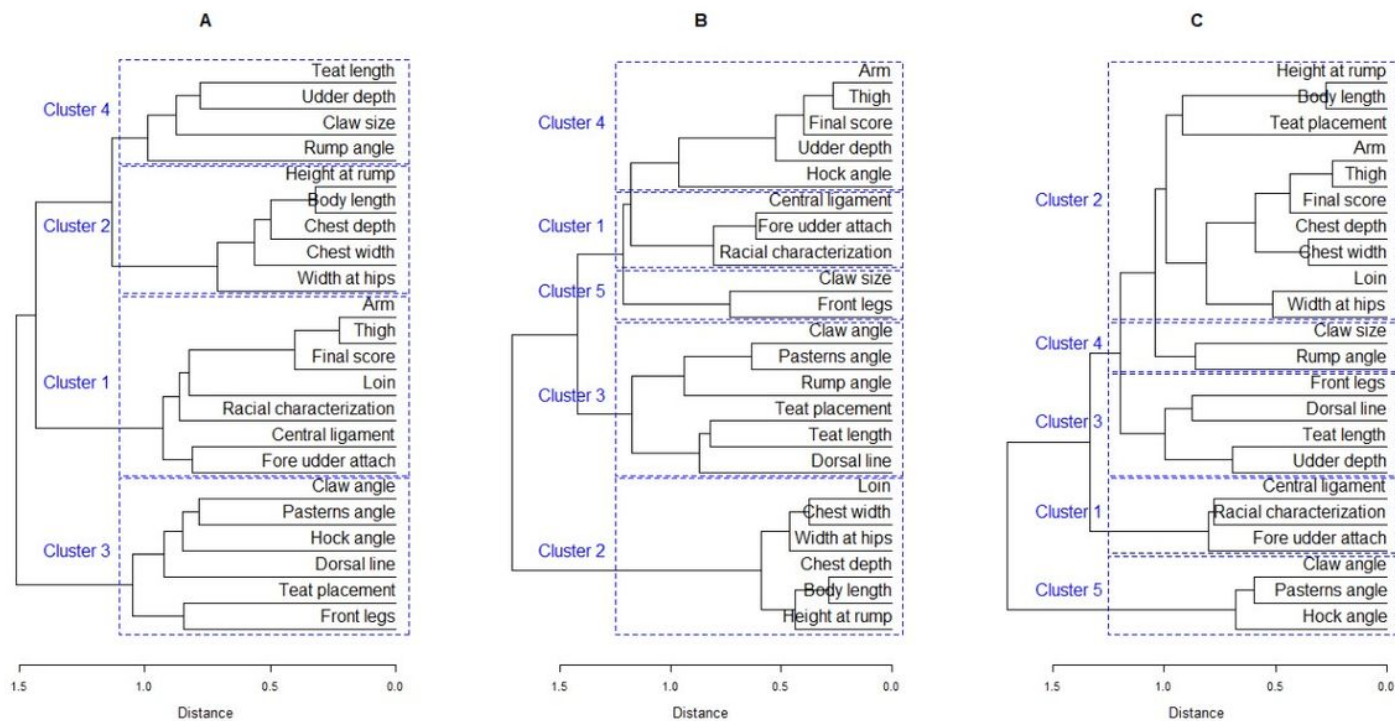


Figure 3

Grouping of conformation variables of Blanco Orejinegro cows in the breeder's network (BN, A), animal germplasm bank (AGB, B) and Agrosavia selection herd (ASH, C) in Colombia, by cluster analysis.