DEMOGRAPHIC AND GENEALOGICAL STRUCTURE OF THE COSTEÑO CON CUERNOS COLOMBIAN CREOLE CATTLE

Jhon Cañas-Alvarez[1a], Jorge Garcés-Blanquiceth[2a], Enoc Paternina[1b], David Quintero[3], Diego Bejarano[4], William Burgos-Paz[2b], and Edison Julian Ramirez Toro[5]*

[1a] Corporación Colombiana de Investigación Agropecuaria – AGROSAVIA. Centro de Investigación Motilonia. Km 5 vía Becerril, Agustín Codazzi, Cesar, Colombia
https://orcid.org/0000-0002-8101-8602

[1b] Corporación Colombiana de Investigación Agropecuaria – AGROSAVIA. Centro de Investigación Motilonia. Km 5 vía Becerril, Agustín Codazzi, Cesar, Colombia
https://orcid.org/0000-0001-9020-5381

[2a] Corporación Colombiana de Investigación Agropecuaria - AGROSAVIA. Centro de Investigación Turipaná. Km 14 vía Montería-Cereté, Córdoba, Colombia
https://orcid.org/0000-0002-4127-3510

[2b] Corporación Colombiana de Investigación Agropecuaria - AGROSAVIA. Centro de Investigación Turipaná. Km 14 vía Montería-Cereté, Córdoba, Colombia
https://orcid.org/0000-0001-6560-4233

[3] Corporación Colombiana de Investigación Agropecuaria - AGROSAVIA. Centro de Investigación Palmira. Diagonal a la intersección de la Carrera 36A con Calle 23, Palmira, Valle del Cauca Colombia
https://orcid.org/0009-0003-3916-0992

[4] Corporación Colombiana de Investigación Agropecuaria - AGROSAVIA. Centro de Investigación Tibaitatá. Km. 14, vía Mosquera – Bogotá, Bogotá, Colombia
https://orcid.org/0000-0002-8981-0274

[5] Corporación Colombiana de Investigación Agropecuaria - AGROSAVIA. Centro de Investigación El Nus. Vereda La ICA, San Roque, Antioquia, Colombia
https://orcid.org/0000-0002-1418-6788

* Corresponding author: ejramirez@agrosavia.co

ABSTRACT

The aim of this study was to assess the demographic structure and genetic diversity of the Costeño con Cuernos (CCC) Colombian creole cattle population using pedigree data. A total of 8,164 genealogical records of the CCC breed, spanning 1958 to 2023, were analyzed to estimate population censuses, effective population size, generational intervals, pedigree completeness, inbreeding coefficient, and effective number of founders. A progressive increase in population size was observed, reaching a population of 1,524 animals by 2022, with an average generational interval of 5.6 and 6.5 years for paternal and maternal lines, respectively. Pedigree completeness has significantly improved since the 1990s, reaching current values close to 100% over six generations. Inbreeding coefficients increased over time and estimates of effective population size were 253 and 89 based on census and inbreeding, respectively. Among the animals analyzed, 852 were found to have both parents unknown. The effective number of founders and ancestors was 69.6 and 42, respectively. The breed conservation strategy has maintained its genetic variability, but there is a need to incorporate new individuals into the Germplasm Bank.

Keywords: effective population size, generation interval, inbreeding.

INTRODUCTION

The Costeño con Cuernos (CCC) is a Colombian creole cattle breed that traces its origins to bovines introduced to America by Spanish colonizers in 1525, which gave rise to the first Colombian cattle nucleus on the Atlantic coast (Primo, 1992). The CCC is well- adapted to the warm and humid conditions of tropical zones, exhibiting excellent reproductive performance and high degree of resistance to ectoparasites (Ossa et al., 2011). Traditionally, this breed has been associated to small- and medium-scale farms dedicated to milk production in the Caribbean region of Colombia.

Several government initiatives have supported the maintenance of a conservation nucleus for the breed, resulting in the presence of both purebred and crossbred CCC herds in Colombia today. In this context, the Corporación Colombiana de Investigación Agropecuaria-AGROSAVIA (www.agrosavia.co) has two populations of the CCC breed, one belonging to the Animal Germplasm Bank (BGA), whose main objective is to preserve the maximum genetic variability of the breed, and the Genetic Improvement Program nuclei (PMG), which uses genetic evaluation to increase productive parameters in economically important traits (Cañas-Alvarez et al., 2020).

Controlling the effects of genetic drift is fundamental for preserving population genetic variability and maintaining a low inbreeding rate (Hammerly et al., 2013). Therefore, studies on genetic variability should be conducted through pedigree analysis or the use of genetic markers (Toro et al., 2014). Recently, the genealogical records of the CCC population were recovered and digitized (Cañas-Alvarez et al., 2023), providing a valuable resource for conservation programs aimed at preserving genetic variability and minimizing inbreeding (Goyache et al., 2003; Gutiérrez et al., 2003).

The objective of this study was to assess the demographic structure and genetic diversity of the Costeño con Cuernos creole cattle population through genealogical analysis.

MATERIALS AND METHODS

Localization and data management

The genealogical information of 8,164 animals spanning from 1958 to 2023 were obtained and analyzed from the herd records of the Germplasm Bank (BGA) and the Genetic Improvement Program (PMG) nuclei of the CCC Colombian creole breed. As this study did not involve animal handling or experimentation, approval from the Institutional Animal Care and Use Committee was not required.

The herds are currently maintained as closed nuclei in a rotational grazing system based on Guinea grass *(Megathysus maximus)* at the Turipaná (Germplasm Bank) and Motilonia (Improvement Nucleus) Research Centers of AGROSAVIA.

Turipaná is located in the Sinú River valley in Cereté, Córdoba (latitude 8º 50' 15.2'' N and longitude 75º 47' 33.9'' W) at 14 meters above sea level, with an average annual temperature of 28ºC, relative humidity ranging from 79 to 87%, and average precipitation of 1,400 mm. Motilonia is located in the Cesar River valley in Agustín Codazzi, Cesar (latitude 10º 00' 06.5'' N and longitude 73º 14' 57.8'' W) at 180 meters above sea level, with an average annual temperature of 31 ºC, relative humidity ranging from 70 to 80%, and average precipitation of 1,250 mm. Fig. 1 illustrates the annual variation in average and maximum temperature (°C) and relative humidity (%) in the Colombian Caribbean from 2013 to 2023. Temperatures remained consistently high throughout the period, with maximum values exceeding 34 °C in most years and average values ranging from approximately 28 to 31 °C. Relative humidity was also persistently high, with average values between 64 and 73% and maximum values frequently exceeding 90 %. These climatic conditions –characterized by sustained high temperatures and humidity– indicate a potential risk of heat stress in animals, highlighting the importance of adaptive livestock management strategies in the region.

Population censuses and effective population size

Population censuses were assessed as the total number of animals, sires, and dams born over time. The effective population size was estimated based on the number of parents under random mating with unequal numbers of males and females, using the Falconer and Mackay (1996) formula $\overline{N_e}Census = 4N_m N_f / N_m + N_f$, where N_m and N_f are the number of male and female, respectively.

Pedigree completeness and generation interval

MaCluer et al. (1983) proposed a pedigree completeness index based on the proportion of known ancestors in each ascending generation $I_d = 4I_{d_{pat}} I_{d_{mat}} / I_{d_{pat}} + I_{d_{mat}}$, and $I_{d_k} = \frac{1}{d}\sum_{i=1}^{d} a_i$; where, represents the paternal (*pat*) or maternal (*mat*) line of an individual, a_i is the proportion of known ancestors in generation i, and d is the number of generations considered in the calculation of the pedigree completeness degree.
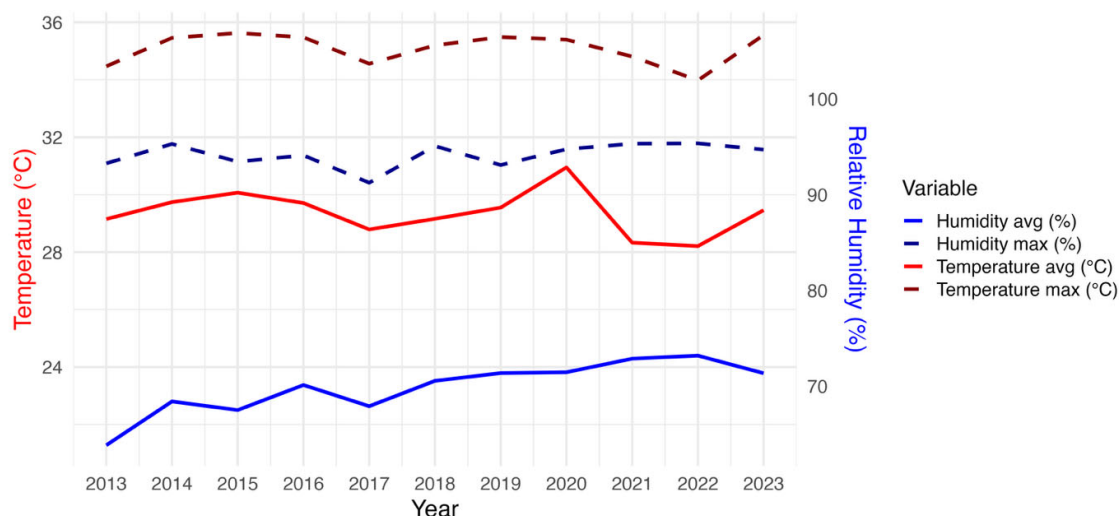
Fig. 1. Annual variation of temperature and relative humidity in the Colombian Caribbean (2013-2023).

Generational interval is defined as the average age of parents at the time of the birth of their offspring maintained for reproduction (James, 1977). This parameter was calculated for the four classic pathways (father-son, father-daughter, mother-son, and mother-daughter) with animals born between 1961 and 2022.

Inbreeding coefficient and coancestry

The inbreeding coefficient (F), as the probability of having two identical genes by descent (Wright, 1922), was estimated for the population as well as for inbred animals. Coancestry (f) is defined as the probability that offsprings from two parents carry two identical alleles by descent. The inbreeding coefficient (F) of an individual is equal to the kinship coefficient between its parents, also referred to as the coancestry coefficient (f), that is, $F_i = f_{sd}$, where i is an individual, s and d are the sire and dam, respectively. Under random mating, the inbreeding rate (ΔF) is equal to the coancestry rate (Δf).

Effective population size

Effective population size (N_e) was estimated based on the inbreeding rate, considering $N_e \Delta F = 1/(2\Delta F)$. The inbreeding rate per generation (ΔF) was calculated using the following equation:

$$\Delta F = (F_n - F_{n-1})/(1 - F_{n-1})$$

where F_n and F_{n-1} are the average inbreeding coefficients of offspring and parents, respectively (Falconer and Mackay, 1996).

Alternatively, N_e was estimated by calculating the inbreeding rate for each individual (ΔF_i), according to the equation:

$$\Delta F_i = 1 - \sqrt[t_i-1]{1 - F_i}$$

where F_i is the individual i inbreeding coefficient (González-Recio et al., 2007), and t is calculated as the sum of all known ancestors using the term $(1/2)^n$, where n is the number of generations separating the individual from each known ancestor (Boichard et al., 1997; Gutiérrez et al., 2008).

By averaging ΔF_i values, $\overline{\Delta F}$ was obtained for the reference population. The corresponding effective population size N_e was then estimated as $\overline{N_e}\ \overline{\Delta F} = 1/(2\overline{\Delta F})$ (Cervantes et al., 2008).

Effective number of founders, ancestors, and founding genomes

The effective number of founders (f_e) represents the number of equally contributing founders that would produce the same genetic diversity as observed in the studied population (Lacy, 1989). It was calculated as the reciprocal of the probability that two randomly sampled alleles originated from the same founder. Thus, $f_e = 1/\sum_{k=1}^{f} q_k^2$, where q_k is the probability of genetic origin from ancestor k. When founders contribute unequally, the effective number of founders is lower than the actual number. However, Boichard et al. (1997) demonstrated that the this method does not account for population bottlenecks, which are one of the main causes of gene loss in bovine populations.

Therefore, they proposed the effective number of ancestors (f_a), which is the minimum number of ancestors, founders or not, necessary to explain the complete genetic diversity of the population, calculated as $f_a = 1/\sum_{j=1}^{a} q_j^2$. In this case, q_j is the marginal contribution of ancestor , representing the genetic contribution made by an ancestor not explained by previously chosen ancestors.

The effective number of founding genomes (f_g) is defined as the number of founders that would produce the genetic diversity present in the population if all founders were equally represented and no allele loss had occurred (Ballou and Lacy, 1995). It was calculated according to Caballero and Toro (2000) by twice the inverse of the mean coancestry of the individuals included in the population.

For the estimation of genetic parameters, the software PEDIG (Boichard, 2002), ENDOG version 4.6 (Gutiérrez and Goyache, 2005), and POPREP (Groeneveld et al., 2009) were used.

RESULTS

Population censuses and effective population size

The genealogical database comprised records for 8,164 animals (3,796 males and 4,368 females). Validation of genealogical relationships prior to 1980 was conducted through the review of herd recording cards available in the historical archives of AGROSAVIA. This was done to ensure the accuracy of digital records and to identify either individuals with unknown parents or discrepancies in animal identification patterns.

As expected, the population census showed a clear increase over the years (Fig. 2), both for the total population and for sires and dams.

The animal inventory maintained at Turipaná Research Center increased by up to fivefold during the 1970s (Fig. 2). Moreover, the establishment of a CCC selection nucleus in 2012 led to a 40% increase in the herd over the period 2018 - 2022, mainly in breeding females. In fact, the ratio of dams per bull ranged from 5 to 7, reflecting the limited use of artificial insemination.

The effective population size, estimated from the number of parents through random mating, followed a trend similar to the proportion of bulls in the herd and their extensive utilization (Fig. 2). In 2023, the effective population size was 253, indicating that the population is not currently at risk of extinction.

Pedigree completeness and generation intervals

The pedigree completeness of the CCC population was analyzed considering from first to sixth generations. At first generation, average completeness reached 100%. Although completeness decreased in earlier generations, it remained above 80% even up to the sixth generation (Fig. 3).

In addition to efforts to recover historical genealogical information, the productive recording carried out in the 1990s strengthened the genealogy of CCC and supported the consolidation of the animal improvement program (Fig. 3).

Generation interval influences both the rate of genetic progress and the genetic structure of
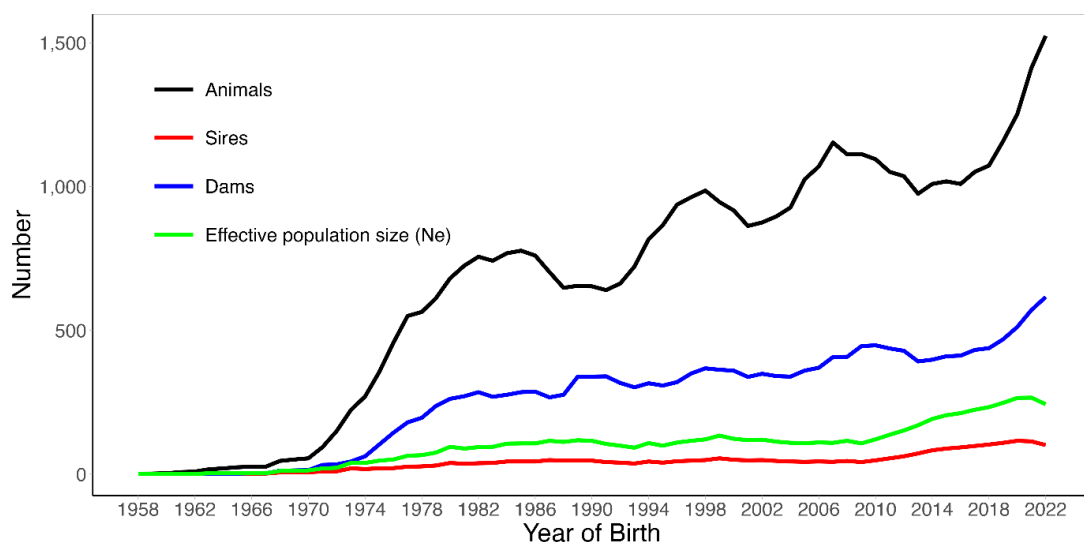

Fig. 2. Population census and effective population size (N_e) based on the number of parents of the Costeño con Cuernos breed.
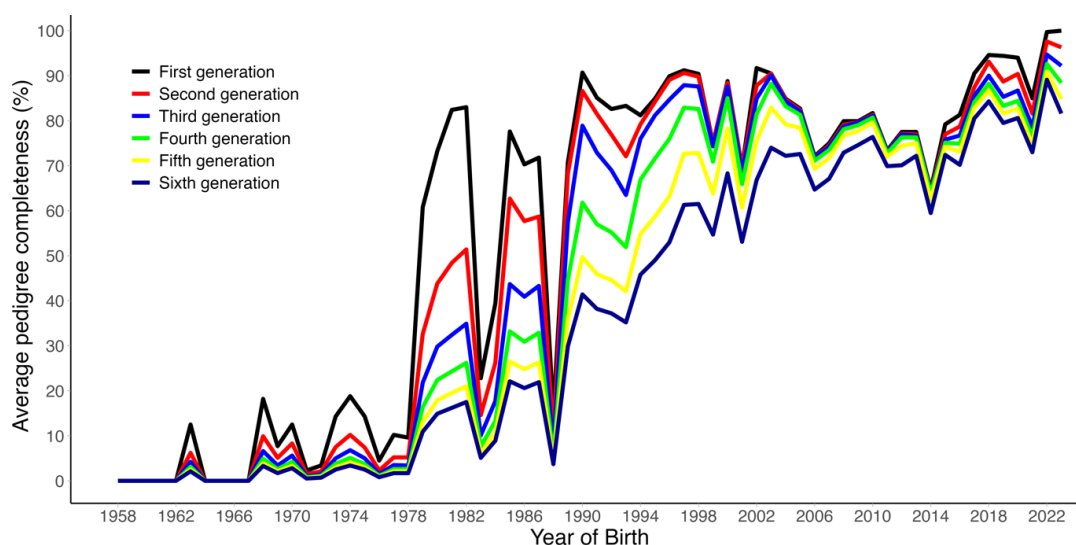
Fig. 3. **Evolution of average pedigree completeness estimated from 1 to 6 generations in the Costeño con Cuernos breed.**

a population. Shorter generation intervals result in a faster genetic change. In this study, sires showed a lower average generation interval (5.6 years) compared to dams (6.5 years), suggesting a higher replacement rate (Table 1).

Inbreeding coefficient and coancestry

The average inbreeding coefficient increased over time, driven by the small population size and the high level of completeness of genealogical records. By 2020, the average inbreeding coefficient for the entire population and for inbred animals was 3.34 and 3.93%, respectively (Table 2). Notably, approximately 85% of animals born in 2020 exhibited some degree of inbreeding.

High standard errors (SE) were observed in the estimates for all animals, including inbred individuals (Table 2). This variability is primarily attributable to the wide range of inbreeding estimates, which ranged from 0% to 25%. The inbreeding coefficients may be underestimated due to incomplete pedigree information.

The variation in average inbreeding (F) and coancestry (f) values over the entire evaluation period is shown in Fig. 4. The F and f increased from the 1990s onward, stabilizing in the most recent decade, with slight increases that reached a maximum of approximately 4%.

The average inbreeding increase per generation was $\Delta F = 0.0047$ according to the slope of the adjusted regression, resulting in a coancestry coefficient increase per generation of $\Delta f = 0.0060$ (Fig. 4).

Effective population size

Three methods were used to estimate the effective population size in the 2018-2023 period (Table 3). Estimates based on $\overline{N_e}$ $\overline{\Delta F}$ were considerably lower than those obtained using the $\overline{N_e}$Census method, suggesting that the CCC breed does not conform to the assumptions of an idealized population with random mating among bulls and cows. Moreover, $N_e \Delta F$ estimates exhibited high variability due to fluctuations in inbreeding over the years. Negative inbreeding rates may produce negative effective sizes, as observed in 2018 and 2019 (Table 3), highlighting the potential for errors when averages over several years are not considered. The average effective population sizes of CCC based on F and f were 83 and 106, respectively.

Effective number of founders, ancestors, and founder genomes

Of the analyzed population (n=8,164), 2,206 individuals had unknown sires, and 852 were classified as founders with both parents unknown. Additionally, 505 individuals were identified as ancestors. The effective number of founders for the entire population was 69.6, accounting for 8.2% of the total number of founders. Notably, only 26 founders accounted for 50% of the genetic variability within the population.

DISCUSSION

The CCC nucleus was established in 1937, following the identification of 110 animals from different herds in the Caribbean region

Table 1. Generation intervals in the four classic pathways and average age for sires, dams, and the entire population, estimated every five years for the Costeño con Cuernos breed.

Year	Father - son	Father - daughter	Mother - son	Mother - daughter	Sires	Dams	Entire population
1980	4.7	4.8	7.3	6.8	4.8	6.9	6.0
1985	4.3	5.0	9.1	6.9	5.0	7.0	6.0
1990	3.8	3.9	4.1	5.0	3.9	4.9	4.5
1995	4.3	4.2	7.8	7.4	4.2	7.5	5.9
2000	3.2	3.2	6.0	6.5	3.2	6.4	4.8
2005	4.0	4.2	4.9	5.8	4.2	5.6	4.9
2010	6.4	5.3	8.0	5.9	5.3	6.0	5.6
2015	8.2	5.1	6.5	7.7	5.6	7.5	6.7
2020	5.9	4.6	6.5	7.2	5.2	6.9	6.1
Total	**5.5**	**5.7**	**6.4**	**6.6**	**5.6**	**6.5**	**6.1**

Table 2. Average inbreeding coefficients of the entire population and of inbreed animals born in each five-year period in the Costeño con Cuernos breed.

| Year	Entire population			Inbreed animals	
	Animals	Maximum F	Average F (SE)	Animals (%)	Average F (SE)
1980	138	0.000	0.000 (0.000)	0 (0.0)	0.000 (0.0000)
1985	134	0.250	0.005 (0.033)	4 (2.9)	0.172 (0.094)
1990	97	0.156	0.025 (0.046)	29 (29.9)	0.085 (0.046)
1995	179	0.266	0.027 (0.050)	75 (41.9)	0.065 (0.059)
2000	152	0.143	0.036 (0.027)	132 (86.8)	0.042 (0.024)
2005	202	0.145	0.030 (0.021)	166 (82.2)	0.037 (0.016)
2010	180	0.069	0.031 (0.018)	146 (81.1)	0.038 (0.012)
2015	178	0.288	0.038 (0.043)	129 (72.5)	0.053 (0.043)
2020	267	0.273	0.033 (0.026)	227 (85.0)	0.039 (0.024)
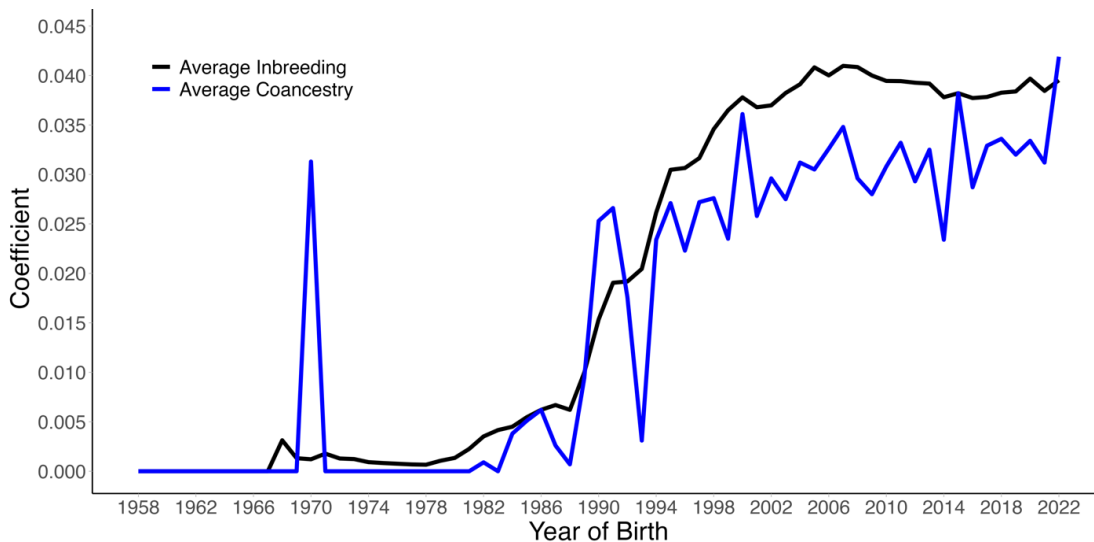
Fig. 4. Evolution of Average Inbreeding and Coancestry during the evaluation period in the Costeño con Cuernos breed.

Table 3. Effective population size of Costeño con Cuernos breed from 2018 to 2023.

Year	$\overline{N_e}$ Census	$N_e \, \Delta F$	$\overline{N_e} \, \overline{\Delta F}$
2023	253	230	89
2022	243	265	89
2021	266	14,818	92
2020	265	481	88
2019	248	-319	91
2018	233	-228	89

of Colombia (Ossa et al., 2011). The animals were kept in herds within facilities owned by government entities, and it was not until 1962 that they were definitively relocated to the Turipaná Research Center in the Caribbean region of Colombia, where the Germplasm Bank is currently located.

Several efforts have been made to preserve the CCC population, which represents a valuable genetic resource for Colombia. Therefore, all available historical information was evaluated and verified to achieve the most accurate description of its current demographic status. Furthermore, the selection program is based not only on genetic values but also on the use of animals with lowest genealogical relatedness and reduced inbreeding (Cañas-Álvarez et al., 2020).

Similar to other creole breeds in Colombia, maintaining the conservation nuclei has involved increasing population size and preserving genetic variability (Cañas-Alvarez et al., 2023). Continuous monitoring has ensured effective management for the conservation of genetic diversity. Additionally, family-based management practices and cyclic mating schemes favored the use of multiple bulls, thereby supporting population viability and minimizing inbreeding (Widing and Kall, 2008). These practices do not shorten the generation interval compared to populations that use artificial insemination, where the exchange rate is usually higher. Compared with other Colombian creole breeds, the average generation interval calculated for the CCC breed is similar to that reported for the Sanmartinero Criollo breed (5.35 years; Ocampo-Gallego et al., 2021); higher than that reported for Blanco Orejinegro Criollo breed (4.59 years; Ocampo-Gallego et al., 2020); and lower than that previously reported for Costeño con Cuernos (5.4 years; Martínez et al., 2008).

Pedigree recording has become an important advantage for the management of creole breeds in Colombia. According to Boichard et al. (1997), pedigree completeness level can also be assessed based on the maximum number of known generations, the number of complete generations, and the number of equivalent generations, which in this study were 7.43, 1.95, and 3.51, respectively. The genealogical information available to date allows obtaining reliable data up to approximately 3.5 generations back.

The estimation of an individual's inbreeding coefficient depends on the completeness of its ancestry. A high proportion of unknown parents leads to a significant underestimation of inbreeding levels. Conversely, the more complete the knowledge of an individual's ancestry, the more reliable the estimation of the inbreeding coefficient relative to a defined base population (Li et al., 2011).

The inbreeding values observed in CCC were lower than those reported for other Colombian Criollo breeds (Cañas-Álvarez et al., 2023), Japanese breeds (Nishio et al., 2023), and fighting bulls (Domínguez et al., 2010). Limitations in herd size and inventory have resulted in an increasing number of animals being born with some degree of relatedness. Integrating pedigree records with genomic data will be crucial to identify animals that reduce inbreeding while contributing to genetic diversity (Alemu et al., 2021). However, with reliable genealogical information available since 1953, these estimates are likely to closely reflect reality.

Inbreeding per generation has increased by approximately 0.60%, which is below the 1% maximum recommended by the FAO (2013). A slow increase in inbreeding allows selection to remove harmful alleles without compromising population viability. Additionally, high levels of inbreeding can cause inbreeding depression, leading to the expression of harmful traits in the population and a decrease in the performance of traits influenced by the non-additive action of genes (Ollivier 1981), which are generally associated with reproduction (Pirchner, 1985).

Regarding effective population size, the N_e-Census method provided estimates based on the total number of sires and dams; the $N_e \, \Delta F$ method was based on inbreeding rates; whereas

the $\overline{N_e}$ $\overline{\Delta F}$ method considered the inbreeding rate for each individual and the average sum of all known ancestors (Cervantes et al., 2008). These values were higher than those reported for Colombian creole cattle like Romosinuano (66.1) and Sanmartinero (27.1) breeds (Martínez et al., 2008), or for Romosinuano in Mexico, where Δf =45 and ΔF =48 (Nuñez-Domínguez et al., 2020). Overall, the effective population size exceeded the minimum of 50 animals recommended by the FAO (2013) to maintain maximum genetic variability across generations.

Moreover, the marginal contribution of ancestors showed that only 26 animals accounted for 50% of the variability of the population. Under different conservation scenarios or economic factors in commercial breeds, population diversity can be explained by a small number of individuals (Ramírez-Valverde et al., 2018). Consequently, it is crucial to identify additional individuals that could enhance the genetic diversity of the CCC through genomic characterization (Kristensen et al., 2015), allowing validation of allele frequencies, ancestry, and phenotypic similarity. Achieving this will require collaboration with breeders to effectively promote both the conservation and sustainable use of these animals (Biscarini et al., 2015).

Both individual and population-level identification can strengthen decision-making in two ways. First, accounting for country-level genetic diversity in the CCC breed allows better estimates of variability and effective population (Simianer, 2005). Second, promoting the establishment of data standards and interoperability among breeders (Baldin et al., 2021) facilitates the expansion of animal inventories and enhances the identification of individuals with higher performance and better environmental adaptation.

Efforts to recover pedigree and productive records will enhance genetic management in CCC and other creole breeds, given the pivotal role of well-adapted breeds in improving cattle productivity and sustainability (Spiegel et al., 202). This is particularly relevant for environmental adaptation, a factor that has limited the success of specialized commercial breeds in tropical regions (Marchioretto et al., 2023). Colombian creole cattle breeds, especially those adapted to persistently high temperatures and humidity in the Caribbean region, represent a valuable genetic resource for livestock systems, enhancing their sustainability in face of ongoing climatic conditions.

CONCLUSIONS

Efforts to maintain conservation nuclei focused on increasing population size and preserving variability. The effective population size for 2023 was 253, indicating that the population is currently at a very low risk of extinction. Inbreeding per generation increased by approximately 0.6% and 85% on the animals born showed some degree of relatedness. Therefore, it is crucial to identify new individuals that could contribute to the genetic background of the breed, based on both genomic characterizations and phenotypic similarity.

Conflict of interest

The authors declare no conflicts of interest, financial or otherwise, with any individuals or organizations related to the material discussed in the manuscript.

Author contributions

Active participation in literature review: Jhon Cañas-Alvarez, Enoc Paternina, David Quintero, William Burgos-Paz, Edison Julian Ramirez Toro, active participation in methodology development: Jhon Cañas-Alvarez, Jorge Garcés-Blanquiceth, Enoc Paternina, Diego Bejarano, William Burgos-Paz, Edison Julian Ramirez Toro; active participation in the discussion of results: Jhon Cañas-Alvarez, Diego Bejarano, David Quintero, William Burgos-Paz, Edison Julian Ramirez Toro. All authors reviewed and approved the last version of the manuscript.

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