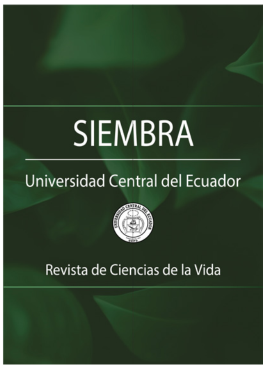
Population structure and genetic diversity of a small population of Montbéliarde dairy cattle in Ecuador

Estructura poblacional y diversidad genética de una pequeña población de ganado lechero de raza Montbéliarde en Ecuador



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Abstract

In Ecuador, the Montbéliarde Association has been using absorption crossbreeding methods to obtain purebred cattle offspring, due to the difficulties of importing embryos, and the high costs of other options. This study aimed to analyze the genetic diversity and structure of the registered population. We used data from the Montbéliarde Association, consisting of 1,794 animals (210 bulls and 1,584 cows). The database was divided into historical, current, and reference groups. Genetic structure and diversity parameters were analyzed, complemented by a gene origin probability analysis. The calculations were carried out using the ENDOG program. The genetic structure and diversity of the Montbéliarde population showed adequate values to develop a genetic improvement plan, which would have a promising future if more comprehensive breeding policies were implemented.

Keywords: historical analysis; inbreeding; small population genetics; Montbéliarde; pedigree.

Resumen

En Ecuador, la Asociación Montbéliarde ha utilizado el método de cruzamiento por absorción, para la obtención de crías puras debido a las dificultades y costos elevados de otras opciones. El objetivo de este estudio fue analizar la diversidad genética y la estructura de la población registrada, para esto se consideraron los datos de la Asociación Montbéliarde constituida por 210 toros y 1584 vacas. La base datos fue dividida en tres grupos uno histórico, uno actual y uno de referencia. Se estimaron parámetros de estructura y diversidad genética complementados con un análisis de probabilidad de origen de genes. Para los cálculos se utilizó el programa ENDOG. La estructura y diversidad genética de la población Montbéliarde presentó valores adecuados para el desarrollo de un plan de mejora genética y tendría un futuro prometedor si se implementara políticas más integrales en la cría.

Palabras clave: análisis de históricos, consanguinidad, genética de poblaciones pequeñas, Montbéliarde, pedigrí.

1. Introduction

The Montbéliarde breed, originally from France, is characterized by good milk quality, adaptation to dry forages, muscular quality, resistance to wide temperature fluctuations, as well as fertility and longevity (Barbat et al., 2010; Boichard et al., 2012; Mihai et al., 2020). This breed was introduced to Ecuador in the 1990s with the aim of exploiting hybrid vigor, mainly through crosses with the Holstein Friesian breed. Its introduction was carried out using frozen semen due to the difficulty of importing animals and embryos from its country of origin. Subsequently, the management of the herd book between the Montbéliarde and Holstein Friesian Association of Ecuador was initiated, a process that continues to this day.

One of the fundamental pillars of genetic improvement programs is to conserve and maintain the genetic diversity of populations. This diversity can be evaluated through genealogical information (Gicquel et al., 2020), which allows estimation of parameters related to the structure and genetic diversity of populations, such as inbreeding (Wright, 1922), generation interval (James, 1977), effective population size (Cervantes et al., 2011), among others. Currently, the development of molecular genetics has provided new tools to estimate these parameters with greater precision, based on genomic information (Oldenbroek, 2017). Additionally, various free software programs have been created for the analysis of genealogical information, such as Endog (Gutiérrez & Goyache, 2005), CFC (Sargolzaei et al., 2006), POPREP (Groeneveld et al., 2009), among others.

Worldwide, both in specialized and conservation cattle breeds, a significant loss of genetic diversity over time has been evidenced, despite the presence of robust genetic improvement programs (Ablondi et al., 2023; Cartuche-Macas et al., 2024a; Tenhunen et al., 2024). This phenomenon has intensified particularly in the last decade due to the implementation of genomic selection (Lozada-Soto et al., 2021; Luštrek et al., 2021; Scott et al., 2021). In Ecuador, studies in this area are still limited. For example, Cartuche et al. (2014) estimated inbreeding in the Jersey and Brown Swiss populations. However, more comprehensive research has been conducted in recent years on the Charolais breed (Cartuche-Macas et al., 2024b; Lozada et al., 2023).

In this context, since the Montbéliarde breed in Ecuador does not have a genetic improvement plan, it is likely that kinship between animals is not considered during mating, which can lead to a loss of genetic diversity and an increase in inbreeding at both the individual and population levels, causing negative effects in the future (Falconer & Mackay, 1996). The objective of this study was to analyze the genetic diversity and population structure of the registered Montbéliarde breed in Ecuador, using parameters such as the inbreeding coefficient, generation interval, coancestry, average kinship, and gene origin probabilities.

2. Materials y Methods

2.1. Genealogical Information

The genealogical data were provided by the Montbéliarde Breed Breeders Association of Ecuador. A total of 1,794 registered animals were used, including 210 bulls and 1,584 cows, born between November 1969 and December 2021 (including animals imported via semen). For the analysis, three populations were considered: a historical population (born between 1969 and 2021), a current population (born between 2011 and 2021) which included 896 animals (38 bulls and 858 cows), and a reference population that included animals with known parents from the current population, consisting of 472 animals (38 bulls and 434 cows). The populations were defined because calculations related to genetic diversity, gene origin probabilities, and founder analyses can only be performed considering animals with both known parents, or by comparing them with historical and current datasets, as suggested by Casanovas Arias et al. (2020) and Navas et al. (2017).

The software ENDOG (v4.8) was used to carry out demographic and genetic analyses to quantify and trace genealogial diversity back to the ancestors (Gutiérrez et al., 2005).

2.2. Population Structure

The number of births was calculated to determine the maximum and average number of offspring per bull or cow. The total cow-to-bull ratio and the mated cow-to-bull ratio were also calculated by dividing the total number of cows by the total number of bulls, and the number of breeding cows by the number of breeding bulls, respectively. Additionally, the Pedigree Completeness Index (PCI) was calculated following the premises of

Navas et al. (2017) from the first to the fifth generation, along with the maximum number of generations, the number of complete generations, and the number of equivalent generations in the three populations under study.

The generation interval (GI) was calculated for the four gametic pathways: from sire and dam to son and daughter, respectively, using the recorded birth dates of each animal along with those of their parents (James, 1977). At the same time, gene flow between herds was evaluated according to the contribution of bulls to the population (Vassallo et al., 1986). Herds were grouped into four types: a) nucleus, if breeders only use their own bulls, which can also be sent to other herds; b) multiplier, when breeders use bulls from other herds and provide bulls to other herds; c) commercial, if breeders use bulls from other herds but do not provide bulls; and d) isolated, when breeders only use their own bulls and do not provide them to other herds.

2.3. Inbreeding and coancestry

Inbreeding (F) is defined as the probability that two alleles randomly taken are identical by descent (IBD); whereas coancestry (C) between two individuals is the probability that genes randomly taken from each of the individuals in question are identical by descent (Lindgren et al., 1996). Consequently, the coancestry (C) between two individuals corresponds to the inbreeding (F) of their potential offspring. Individual inbreeding (F) was calculated using the methods described by Meuwissen and Luo (1992).

The average relatedness coefficient (AR) of each individual was calculated as described by Gutiérrez et al. (2005) and refers to the probability that two related individuals have inherited a particular allele at a single locus/gene from their common ancestor (this allele is known as IBD).

The individual inbreeding rate [$\overline{\Delta F}$] for each generation was calculated according to Gutiérrez et al. (2009) as shown in equation [1], where t_b is the number of equivalent complete generations and F_b is the F of individual b.

$$\Delta F_b = 1 - \sqrt[t_b - 1]{1 - F_b} \qquad [1]$$

The individual coancestry rate [$\overline{\Delta F}$]] for each generation was calculated following the methods described by Cervantes et al. (2011), using equation [2], where t_b and t_a are the number of equivalent complete generations, and C_{ba} is the C between individuals b and a.

$$C_{ba} = 1 - \sqrt[\frac{t_b + t_a}{2}]{1 - C_{ba}} \qquad [2]$$

2.4. Ancestral Contributions and Gene Origin Probabilities

The effective number of founders [f_e] was calculated using equation [3], where q_k is the gene origin probability of the kth founder and f is the actual number of founders (Lacy, 1989).

$$f_e = \frac{1}{\sum_{k=1}^{f} q_k^2} \qquad [3]$$

The effective number of ancestors [f_a] was determined using equation [4], where p_k is the marginal contribution of the kth ancestor (Boichard et al., 1997). The effective number of founder genomes [f_g] was calculated as the inverse of twice the average coancestry (C), as reported by Caballero and Toro (2000). The marginal contribution of each major ancestor j was calculated according to Boichard et al. (1997).

$$f_a = \frac{1}{\sum_{k=1}^{f} p_k^2}, \qquad [4]$$

The software CFC version 1.0 was used to calculate ancestral contributions and gene origin probabilities (Sargolzaei et al., 2006).

3. Results and Discussion

3.1. Demographic Statistics

The average number of herds decreased from 50 to 41 in the current population. The average herd size also declined from 35.88 to 21.85 animals per herd in the same population datasets, respectively. This reduction was possibly due to decreased breeder interest in using this breed. While historically, bulls and cows represented 11.71% and 88.29% of the total population, respectively, these percentages changed to 4.24% for bulls and 95.76% for cows in the current population. The average number of calves per mated bull increased from 8.33 to 12.05 from the historical to the current population, while the average number of calves per mated cow remained relatively constant at 1.38 and 1.58. The cow-to-bull mating ratio increased from 3.27/1 to 3.43/1. Male selection intensity rose from 22.61% to 62.50% from the historical to the current population, while female selection intensity was halved in the current population compared to historical values (86.21% to 46.15%). The maximum progeny per bull (107) and per cow (5) in the historical population decreased significantly in the current population to 13 calves per mated bull and slightly to 3 calves per mated cow, respectively, as shown in Table 1.

Table 1. Summary of demographic statistics.

Parameters	**Population**	
	Historical	**Current**
	1794	**(896)**
Total number of herds	50	41
Total number of provinces	5	5
Average herd size	35.88	21.85
% of bulls in total	11.71	4.24
Average number of calves per bull, n	7.61	2.63
Maximum number of female calves per mated bull, n (excluding animals with unknown sire)	107	13
Average number of female calves per mated bull, n (excluding animals with unknown sire)	8.33	12.05
% of cows in total	88.29	95.76
Average number of calves per cow, n	0.55	0.26
Maximum number of female calves per mated cow, n (excluding animals with unknown dam)	5	3
Average number of female calves per mated cow, n (excluding animals with unknown dam)	1.38	1.58
Cow-to-bull ratio	7.541	30.64/1
Mated cow-to-bull ratio	3.27/1	3.43/1
Progeny of bulls selected for breeding, %	91.43	96.63
Progeny of cows selected for breeding, %	39.71	45.85

The population census analysis considered animals born from 1995 onwards, the year in which the Montbéliarde Association of Ecuador was founded; earlier records refer to the genealogical information of ancestors. From 1995, there was steady growth until 2012, after which a sharp decline occurred, reaching only 19 animals registered in 2021. This effect is likely due to the crisis faced by dairy producers in Ecuador in recent years, particularly regarding high production costs, fixed (but uncontrolled) support prices, low per capita consumption, the use of whey, and cattle rustling (Bonilla Jurado, 2020; ESPAE Graduate School of Management, 2016; Ministerio de Agricultura, Ganadería, Acuacultura y Pesca [MAGAP], 2016; Pais Chanfrau et al., 2017; Superintendencia de control del poder de mercado, 2015). In addition, there was a considerable reduction in the proportion of bulls and a slight increase in the proportion of cows, which respectively affected the number of calves per mated bull and cow. This was possibly due to the exclusive and limited use of imported bulls through semen doses, and in the case of cows, to improvements in reproductive practices, as well as producers' interest in retaining more females for replacement. An opposite effect was reported for the Braford breed used for beef production, where there is greater interest in males (González et al., 2022).

Table 2 shows the pedigree completeness of the populations under study. Pedigree completeness in the first generation of the historical population was 68.81%, increasing to 75.11% in the current population. In the second and third generations, it was 44.82%–26.19% in the historical population and 67.77%–57.76% in the current population, respectively (Figure 1). In subsequent generations, there was a progressive decline, reaching 3.63% and 22.98% in the fifth generation for the historical and current populations, respectively.

Table 2. Pedigree completeness statistics.

Parameter	Population	
	Historical	Current
Population size	1794	896
Maximum number of generations, n	10	10
Pedigree completeness in 1st generation (parents known)	68.81	75.11
Pedigree completeness in 2nd generation (grandparents known)	44.82	67.77
Pedigree completeness in 3rd generation (great-grandparents known)	26.19	57.76
Pedigree completeness in 4th generation (great-great-grandparents known)	13.03	37.88
Pedigree completeness in 5th generation (great-great-great-grandparents known)	3.63	22.98
Maximum number of generations (mean ± SD)	4.35±2.10	5.53±1.63
Number of complete generations (mean ± SD)	0.70±0.85	0.86±0.95
Number of equivalent generations (mean ± SD)	2.15±1.19	2.71±1.10

The number of generations traced for this breed is quite large compared to the beginning of its establishment in Ecuador (1995–2000). This is because the association commonly records genealogical certificate information (usually 3 generations of ancestors). This effect can also be seen in Figure 1, where known paternal ancestors in the current population range between 69.87% and 96.76%, while known maternal ancestors are below 50%. Similarly, both analyzed populations showed a progressive decline in pedigree completeness up to the fifth generation, reaching values of 3.63% and 22.98% for the historical and current populations, respectively. This effect has also been observed in other dairy breeds such as Holstein (Sieklicki et al., 2020).

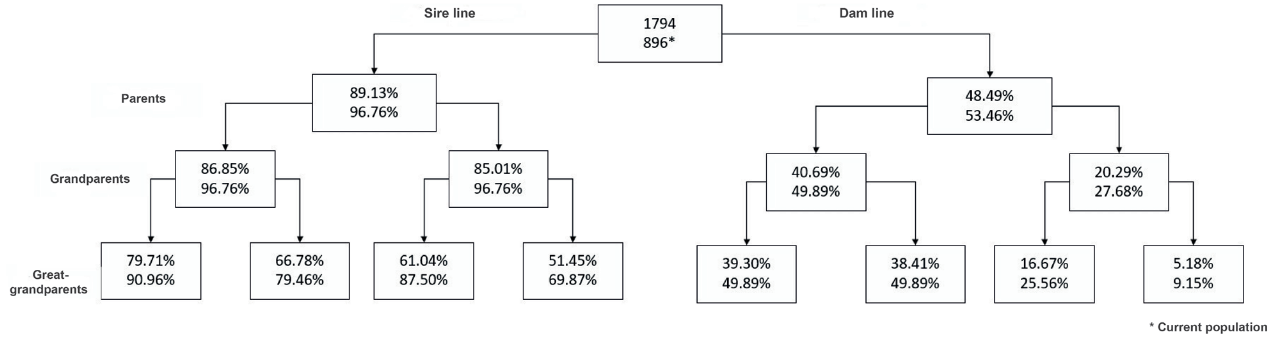

Figure 1. Total number of animals in the pedigree with the percentage of known ancestors in the historical and current population.

The accuracy and reliability of population structure analysis depend on pedigree completeness and the amount of genealogical information available across generations (Vásquez-Loaiza et al., 2021). Additionally, MacCluer et al. (1983) consider that a pedigree completeness value above 0.6 produces reliable inbreeding estimates, whereas lower values lead to imprecise estimates. In the case of the Montbéliarde breed, only the first and second generations of the current population showed pedigree completeness values above 0.6 (Table 2). Similar values have been found in developing breeds such as Braford in Argentina (Macor, 2013), Holstein in southeastern Brazil (Sieklicki et al., 2020), and beef breeds such as Brahman in Costa Rica (Vásquez-Loaiza et al., 2021). Furthermore, the effect of low pedigree completeness can be offset by methodologies that consider family size as a variable with a discrete bivariate distribution, as reported in the Brangus breed in Argentina

(Ron Garrido et al., 2008). Likewise, the increase in equivalent complete generations (from 2.15 to 2.71) and the average number of known parents in the historical and current populations reflects an improvement in pedigree quality, although not at the pace of other breeds such as Brown Swiss (Hagger, 2005) or Japanese Black (Honda et al., 2004). This is possibly due to the use of an open herd book for this breed and the registration of animals with unknown sire(s).

Table 3 presents descriptive statistics of the GI (in years) for the four gametic pathways in the Montbéliarde dairy cattle breed. The average GI for the historical population was 7.41 years, while the current population had an average of 3.92 years. The GI for the Montbéliarde breed was 7.17 and 7.9 years for the historical and current populations, respectively, which are higher values than those found for the same breed in France: 6.2 years in 2012 (Danchin-Burge et al., 2012) and 5.3 years for 2021–2023 (Institut de l'Élevage [IDELE], 2021, 2023). Regarding the sire-to-son/daughter pathway, a slight reduction was observed. When comparing the GI via sire to son/daughter in the historical population (7.41–8.19 years, respectively) with the GI via dam to son/daughter in the historical population (8.76–4.18 years, respectively), the former was longer. This trend was similar in some breeds such as Simmental in Mexico and Colombia (8.5–6.5 years via sire to offspring; 5.9–5.4 years via dam to offspring) (Ríos Utrera et al., 2018); Shorthorn in Japan (7.5–9.4 years via sire to offspring; 6.6–6.6 years via dam to offspring) (Uemoto et al., 2021); and Holstein in Brazil (7.0–8.5 years via sire to offspring; 5.6–4.1 years via dam to offspring) (Sieklicki et al., 2020).

Table 3. Generation interval (years) of the four gametic pathways in the Montbéliarde breed in Ecuador.

Population	Gametic Pathway*	Sire to Son	Dam to Son	Sire to Daughter	Dam to Daughter	Total
Historical (n=1794)	N	167	159	514	275	1115
	Average	7.41	8.76	8.19	4.18	7.17
	SD	3.28	3.86	4.68	2.05	4.23
	MSE	±0.254	±0.306	±0.206	±0.124	±0.127
Current (n=896)	n	32	32	153	100	317
	Average	3.92	6.37	11.43	4.27	7.90
	SD	2.14	2.51	4.30	2.18	4.85
	MSE	±0.38	±0.44	±0.76	±0.39	±0.27

* SD = Standard deviation; MSE = Medium standard error.

A long GI via the sire pathway indicates that in the Montbéliarde breed in Ecuador, genetic material from older sires is being used. For example, for animals born in 2018, sires born between 2002 and 2007 were observed (data not shown), imported through semen doses from France. The reasons for using older sires may include higher reliability of genetic tests (due to a greater number of daughters in the genetic evaluation), the sires maintaining superior genetic evaluations within the breed, or the cost that producers are willing to pay. This issue generally occurs in countries where semen from proven sires is almost exclusively imported for genetic improvement of their populations, meaning that the sires have undergone progeny testing and have been widely used both nationally and internationally (e.g., evaluated in INTERBULL) (Sieklicki et al., 2020).

Parallel to the introduction of genomic evaluations for this breed in Ecuador (2014–2015), a considerable decrease in the generation interval (GI) of the current population was observed via the sire-to-son pathway (3.92 years) and the dam-to-son pathway (6.37 years). Additionally, an analysis of animals born in 2021 within the database revealed sires born in 2018 (data not shown), which justifies this reduction. On the other hand, the dam-to-daughter pathway in the historical population showed the lowest GI (4.18 years), with a slight increase in the current population (4.27 years). Similar values have been reported for Holstein breeds in Brazil, Spain, and the USA (4.1, 3.77, and 3.5 years, respectively) (García-Ruiz et al., 2016; Rodríguez-Ramilo et al., 2015; Sieklicki et al., 2020). These values indicate that breeders might be managing a high replacement rate of females within herds, which can affect the productive life and overall profitability of the herd (García-Ruiz et al., 2016).

Table 4 shows the classification of herds according to the origin of sire usage. In this case, no herds were found to function as nucleus herds; only one herd could be considered a multiplier, and most herds were commercial because they use imported semen.

Table 4. Classification of herds according to the origin and use of Montbéliarde sires.

Herd type	Semen used from sires born in another herd	Semen used from sires born within the herd	Bulls sold as breeders	Number of herds
Nucleus	No	Yes	Yes	0
Multiplier	Yes	Yes	Yes	1
Multiplier	Yes	No	Yes	0
Commercial	Yes	Yes	No	0
Commercial	Yes	No	No	21
Isolated	No	Yes	No	0

In Ecuador, since the Montbéliarde breed lacks a genetic improvement program and uses imported genetic material via the paternal line, it was confirmed that only commercial herds exist (Table 4). These results were like those observed in the Romosinuano breed introduced in Mexico (except for a higher number of multipliers, indicating that this breed is growing) and the Holstein Friesian breed introduced in Brazil (Magalhães Araújo da Silva et al., 2016; Núñez-Domínguez et al., 2020).

3.2. Inbreeding

Table 5 presents the results for average F, ΔF, maximum F, percentage of highly inbred animals, C, ΔR, and GCI. The average F was low (0.43% in the historical population and 0.53% of the current population), with only a small percentage of highly inbred animals present (maximum F of 25%). The percentage of inbred animals was 0.23% and 0.11%, and the average coancestry was 1.31% and 1.46% (Table 5). The average F reached a maximum of 2.5% in 1984 and 1987, while the maximum average coancestry of 1.79% was reached in 2015. Mating between highly related animals occurred, with 1 (0.06%) mating between full siblings and 4 (0.22%) matings between half-siblings. The Genetic Conservation Index increased from 3.09 in the historical population to 3.65 in the current population.

Table 5. Summary of pedigree analysis statistics.

Parameter	Población	
	Historical (n=1794)	Current (n=896)
Inbreeding coefficient (F, %) (mean ± SD)	0.43±1.60	0.53±0.011
Average individual increase in inbreeding (ΔF, %) (mean ± SD)	0.14±0.76	0.14±0.003
Maximum inbreeding coefficient (%)	25	12.50
Inbred animals (%)	19.50	35.27
Highly inbred animals (%)	0.23	0.11
Average coancestry coefficient (C, %) (mean ± SD)	1.31±0.67	1.46±0.60
Average relatedness coefficient (ΔR, %) (mean ± SD)	2.63±1.35	2.91±0.012
Genetic Conservation Index (GCI) (mean ± SD)	3.09±2.29	3.65±2.62

Figure 2 shows the trend of inbreeding since the formation of the Montbéliarde Association of Ecuador, with several peaks starting in 1999 that could be attributed to the registration of animals resulting from crosses between animals of the base population, as well as the limited number of bulls used during these periods. This effect was also found in the Holstein breed in southeastern Brazil (Sieklicki et al., 2020). The current average inbreeding of the breed is 0.53%, with an increase rate of 0.14%, values relatively higher than those of the Charolais breed in Ecuador (0.14% and 0.044%, respectively) (Lozada et al., 2023). This is possibly because the Charolais breed is more recently established and structured compared to the Montbéliarde breed. When compared to other specialized dairy breeds in other countries, the values obtained are low, as this breed in Ecuador has not undergone an objective genetic improvement process, despite being present since 1995. For example, the Montbéliarde breed in its country of origin, France, has had an average inbreeding of 5.5% over the last 10 years (IDELE, 2023). In other breeds such as Holstein, Jersey, and Brown Swiss, the values are also higher (Sieklicki et al., 2020; Tenhunen et al., 2024). Similarly, in local or conservation breeds such as Guzerat, tropical creole dairy, and Gyr, among others (Peixoto et al., 2021; Rosendo Ponce et al., 2018; Wang, 2015). This effect could also be due to the low pedigree completeness currently present in the maternal line.

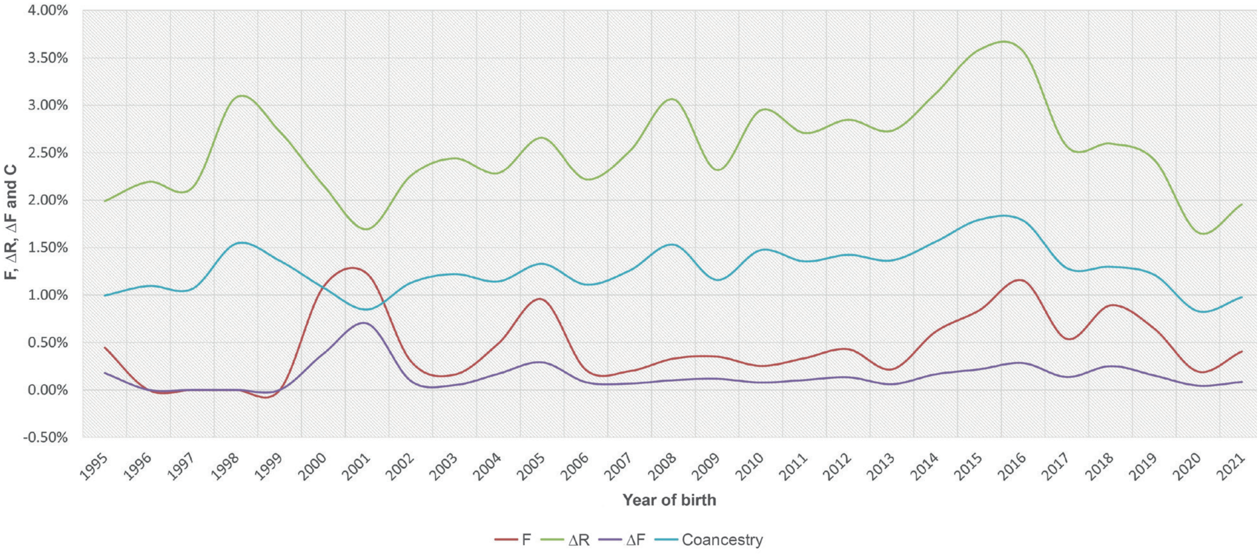

Figure 2. Evolution of inbreeding, average relatedness, inbreeding rate, and co-ancestry of the Montbéliarde breed in Ecuador.

3.3. Gene Origin Probability and Ancestral Contributions

The results for the analysis of gene origin probability and ancestral contributions are shown in Tables 6 and 7. Regarding gene origin probability, the ratios *fe/fa* and *fg/fe* showed values of 3.79 and 0.24, respectively. The *fe/fa* value indicates that the population has remained stable when considering the animals that effectively contribute to the population. Meanwhile, the number of ancestors explaining between 25%–50% and 75% of the genetic origin were 4–10 and 38, respectively.

Table 6. Probabilities of gene origin and founder analysis.

Parameter	**Reference population (both parents known) (n=472)**
Historical population	1794
Current population	896
Base population (one or more parents unknown)	937
Current base population (one unknown parent = half-founder)	559.5
Number of founders contributing to the reference population, n	329
Number of ancestors contributing to the reference population, n	246
Effective number of non-founders (*Nef*)	37.36
Number of equivalent founders (f_e)	113.99
Effective number of ancestors (f_a)	30
Equivalent founder genomes (f_g)	28.14
Ratio f_e/f_a	3.79
Ratio f_g/f_e	0.24
Ancestors explaining 25% of genetic diversity (n)	4
Ancestors explaining 50% of genetic diversity (n)	10
Ancestors explaining 75% of genetic diversity (n)	38

Table 7. Description of the ten main ancestors that have contributed the most to the historical population and the current population of Montbéliarde breed in Ecuador.

Name	Year of birth	Sex	Number of off-spring	CG (%)	CGA (%)
			Historical Population		
MARTIEN	1976	Male	8	8.05	8.05
FAUCON	1990	Male	16	7.70	15.74
GARDIAN	1991	Male	15	6.50	22.25
EZOZO	1989	Male	17	5.18	27.43
MICMAC	1996	Male	19	4.13	31.56
ISANGRIN	1993	Male	6	3.69	35.25
LAURINE	1990	Female	1	3.00	38.26
TELLA	1976	Female	2	2.92	41.17
LECUYER	1995	Male	13	2.55	43.73
INEUSION	1991	Female	1	2.22	45.95
			Current Population		
GARDIAN	1991	Male	15	6.35	6.35
FAUCON	1990	Male	16	5.99	12.33
MICMAC	1996	Male	19	5.95	18.28
EZOZO	1989	Male	17	4.02	22.31
LECUYER	1995	Male	13	4.02	26.32
BOIS LE VIN	1979	Male	21	3.81	30.13
ISANGRIN	1993	Male	6	3.47	33.60
SATURNE	2001	Male	54	2.76	36.35
INEUSION	1991	Female	1	2.35	38.71
VALFIN JB	2004	Male	54	2.04	40.75

Considering the accumulated marginal genetic contribution, the top 10 ancestors explain 45.95% of the genetic diversity in the historical population, while in the current population they explain 40.75%. On the other hand, the individual genetic contribution of a single ancestor, Martien, explained 8.05% of the genetic diversity in the historical population, whereas in the reference population the bull Gardian explained 6.35%, as shown in Table 7.

The estimated *fe*/*fa* ratio in the current Montbéliarde population of Ecuador is similar to that of the population in France (3.79 vs. 3.82) (IDELE, 2023), which could be due to the fact that the majority of the Ecuadorian population has ancestors of French origin. Additionally, the contribution of the main ancestor is 8.05%, and 10 ancestors explain 50% of the genetic diversity compared to the population in France, where it was 15.1% and 6 ancestors explained the same genetic diversity (IDELE, 2023). This occurs because the pedigree depth is greater in the French population compared to the Ecuadorian one, as well as the number of descendants. Regarding the ancestors contributing genetically to the population, they are consistent: Gardian with 6.35% (1st), Faucon with 5.99% (2nd), Micmac with 5.95% (3rd), compared to France, where they ranked 8th with 3.4%, 7th with 4.2%, and 6th with 4.5%, respectively.

Overall, these results will allow the establishment of strategies to prevent the loss of genetic diversity and ensure the sustainability of this population in the country.

4. Conclusions

The analysis of the genealogical information of the Montbéliarde population showed adequate values of genetic diversity and population structure. On the other hand, inbreeding and its increase showed a progressive rise in the current population, but remained below the levels recommended by the FAO. However, it is recommended to implement strategies that maximize diversity and genetic progress within a genetic improvement program.

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Contributor roles

- Oscar Jhonathan Guaman Ilvay: investigation, methodology, resources.
- Luis Favian Cartuche-Macas: conceptualization, investigation, software, writing – original draft.
- Edilberto Chacón Marcheco: validation, writing – review & editing.
- Rafael Alfonso Garzón Jarrín: validation, writing – review & editing.
- Clímaco Campuzano Carriel: validation, writing – review & editing.
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Ethical Implications

Ethics approval not applicable.

Conflict of Interest

The authors declare that they have no affiliation with any organization with a direct or indirect financial interest that could have appeared to influence the work reported.

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