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Genetic diversity and population structure of a Creole sheep flock from Uruguay

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Abstract: Since 2020, the National Agricultural Research Institute (INIA) has conserved a Creole sheep flock at INIA Las Brujas. This study genetically characterised this population and compared it with six others: San Miguel National Park Creoles, commercial farms Creoles, Brazilian Creoles, Corriedale, Merilin and Soay sheep. The analysis included 628 individuals and 31 392 autosomal SNPs. Soay and San Miguel National Park Creoles exhibited the lowest genetic diversity (Ho = 0.266 and 0.279) and highest inbreeding (F_{HOM}: 0.283 and 0.249; F_{ROH}: 0.199 and 0.202). Merilin and Corriedale showed the highest genetic diversity (Ho = 0.351 and 0.364), while Brazilian Creoles had the highest Ho (0.327) among Creoles. Short runs of homozygosity (ROH) segments (≤4 Mb) predominated, with San Miguel National Park and INIA Las Brujas Creoles exhibiting the highest numbers of ROH (22 773 and 16 762, respectively). Fixation index (Fst) and Reynolds distances highlighted INIA Las Brujas Creoles and Soay as the most distinct (0.318 and 0.321, respectively). INIA Las Brujas Creoles also showed notable differentiation from San Miguel National Park Creoles (Fst = 0.269; Reynolds = 0.272). Principal component analysis (PCA) revealed clear clustering, with Corriedale and Merilin closely related (Fst = 0.060; Reynolds = 0.068). Admixture analysis indicated distinct ancestries for Soay, Corriedale and San Miguel National Park Creoles, while commercial and Brazilian Creoles showed significant admixture. INIA Las Brujas Creoles exhibited a distinct ancestry with traces of Corriedale. Phylogenetic analysis confirmed the divergence between Creole and Corriedale/Merilin populations. Results suggest the historical genetic exchange among INIA Las Brujas Creoles, Corriedale, and commercial farms Creoles, while high differentiation of San Miguel National Park Creoles reflects their closed status since 1929.

Keywords: inbreeding coefficient; local sheep breed; model-based clustering; observed heterozygosity; phylogenetic tree

Management of animal genetic resources (AnGR) is essential for sustainable livestock contributions to global food security (Ajmone-Marsan et al. 2023). Recent efforts have emphasised the importance

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of accurate characterisation of AnGR, including the development of molecular and genomic approaches (Ajmone-Marsan et al. 2023). Uruguayan Creole sheep, locally adapted AnGR, are listed as "at risk" in the Domestic Animal Diversity Information System (http://www.fao.org/dad-is/en). In 2010, the population was estimated at 1 500 individuals, mainly located at San Miguel National Park (300) and on commercial farms in Lavalleja (500). Traditionally used for rustic fabrics and meat (Armstrong and Postiglioni 2010), these sheep descend from Spanish autochthonous breeds (Churra, Manchega, Rasa, Canaria) introduced in the 18th century during the colonisation of the Americas (Pedraza et al. 1992). Initially undervalued, Creole sheep gained economic importance in the 19th century with rising wool demand during the US Civil War, leading to crossbreeding with Merino (Fernandez 2000). In 1975, breeders founded the Uruguayan Creole Sheep Breeders Association, and by 1985, it included six general flocks and two stud flocks ("San Pedro del Timote" and "Marmarajá") which likely exchanged genetic material (Fernandez et al. 2009), resulting in sheep with a phenotypically similar, all-white coat.

Morphological and phaneroptic characterisation of Creole sheep in Uruguay began in 1999 (Mernies et al. 2007) and the first genetic characterisation in 2013 (Pieruccioni Banchero 2018).

This study aimed to genetically characterise the INIA Las Brujas Creole sheep and compare it with six local and global populations.

MATERIAL AND METHODS

Ethics declaration statement

Animal handling and blood collection procedures were approved by the INIA Animal Ethics Committee (Approval No. INIA_2018.2) following Uruguayan Law 18611 (cnea.gub.uy) and complying with the ARRIVE guidelines.

Animals and sampling method

A total of 495 animals were sampled from five Uruguayan sheep populations (Figure 1): Creole sheep from INIA Las Brujas (CLB, *n* = 139), San

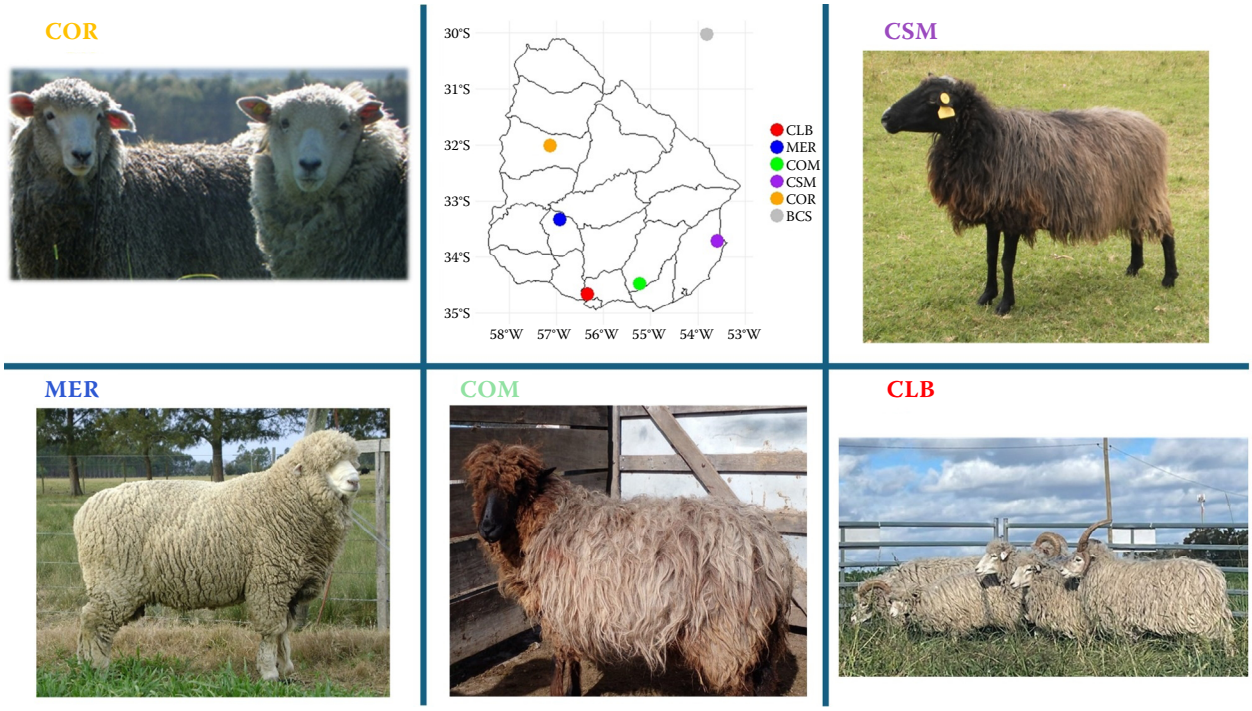

Figure 1. Sheep populations evaluated in this study
SOA population, used as an outgroup, is not displayed
BCS = Brazilian Creoles (–30.006, –53.803); CLB = INIA Las Brujas Creoles (–34.670, –56.341); COM = commercial farms Creoles (–34.480, –55.231); COR = Corriedale (–32.006, –57.134); CSM = San Miguel National Park Creoles (–33.724, –53.579); MER = Merilin (–33.325, –56.928)

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Miguel National Park (CSM, *n* = 139), and commercial farms (COM, *n* = 35); Corriedale sheep from INIA Tacuarembó (COR, *n* = 139) and Merilin sheep from commercial farms (MER, *n* = 43). Creole samples from commercial farms included individuals from the "San Pedro del Timote" stud flock, while the INIA Las Brujas flock traces back to the "Marmarajá" stud. Corriedale and Merilin are dual-purpose breeds (wool and meat), with Corriedale originating in New Zealand from crossing Lincoln rams with Merino females, and Merilin developing in Uruguay from crossing Merino Rambouillet rams with Lincoln females. Blood samples were collected by jugular venipuncture, transported in cooler bags, and stored at 4 °C at the INIA Las Brujas Animal DNA Bank until DNA extraction.

Additionally, 23 Brazilian Creole (BCS) and 110 Soay (SOA) sheep samples were incorporated from the WIDDE database (http://widde.toulouse.inra.fr/widde/; accessed on January 16, 2025). The Brazilian Creole sheep are mainly raised in Rio Grande do Sul and Santa Catarina states (Moreira 2022), while the Soay sheep from St. Kilda, Scotland, were included as an outgroup for comparative analysis. Further details are provided in Electronics Supplementary Materials (ESM) Table S1.

DNA extraction, SNP genotyping, and quality control

Genomic DNA was extracted (Medrano et al. 1990) and afterwards DNA concentration and quality were assessed using a NanoDrop™ 8000 spectrophotometer (Thermo Fisher Scientific, Waltham, MA, US). DNA integrity was checked with a 1% agarose gel with a 0.5X TBE buffer (Tris-Borate-EDTA; Sigma-Aldrich, St. Luis, MO, USA) during 25 min at 100 V. Finally, DNA samples were stored at –80 °C.

SNP genotyping was performed on two platforms, CSM population with the Ovine Infinium® HD SNP BeadChip (606,006 loci; Illumina, San Diego, CA, USA) and CLB, COM, COR and MER with the Applied Biosystems™ Axiom™ Ovine Genotyping Array 50K (Thermo Fisher Scientific, Waltham, MA, US). In COR, individuals with relatedness >0.354 were discarded based on KING estimates (Manichaikul et al. 2010) using PLINK v2.0 (—make-king-table) (Chang et al. 2015). For COM, CLB, and MER populations, all available genotypes were used. To match sample sizes, 139 CSM genotypes with the highest call rates were selected from 170 available. Data were merged with WIDDE genotypes using PLINK (—merge-list), and SNPs were mapped to the Oar_v4.0 assembly. Genomic quality control (QC) performed in PLINK v2.0 included the removal of unmapped and sex chromosome SNPs, SNPs with call rates <90% or MAF <1%, and individuals with call rates <90%. After QC, 31 392 SNPs remained for further analysis.

Assessment of genomic variation within populations

Genetic variability within each population was assessed using observed heterozygosity (Ho), expected heterozygosity (He), and the inbreeding coefficient (F_{HOM}), which compares observed and expected homozygosity. Population inbreeding was calculated as the mean individual F_{HOM}, all estimated with PLINK v2.0 (—het command). Effective population size (Ne) was estimated using SNeP v1.1 (Barbato et al. 2015), based on LD information and the Sved and Feldman recombination rate modifier. To capture both recent and distant Ne estimates, values from 13 generations (Ne_{13}) and 45 generations (Ne_{45}) ago were selected, following Ceccobelli et al. (2023).

ROH were identified using a sliding window method in detectRUNS (Biscarini et al. 2018) with the following parameters: minimum 20 consecutive SNPs, minimum ROH length of 250 kb, SNP density ≥1 SNP/100 kb, maximum gap of 250 kb, sliding window size of 20 SNPs, window threshold of 0.05, and allowance of one missing and one heterozygous SNP per ROH. Subsequently, ROHs were categorised into five size classes: 0–2 Mb, 2–4 Mb, 4–8 Mb, 8–16 Mb, and >16 Mb. Mean ROH sums per breed were calculated by summing ROH lengths per animal and averaging across populations.

The inbreeding coefficient based on ROH (F_{ROH}) was estimated as the sum of ROH lengths divided by the total autosomal SNP coverage (2 445.13 Mb) (McQuillan et al. 2008).

Assessment of population structure and genomic variation between populations

Population structure was assessed using three approaches. The first one, Principal Component

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Analysis (PCA) with PLINK v2.0 (—pca) and plotted using ggplot2 (R Core Team 2022). The second approach, model-based clustering with Admixture v1.3 (Alexander et al. 2009), testing K values from 1 to 10 and selecting the K minimising 5-fold cross-validation error. Admixture results were plotted using the membercoeff.circos function from the Bite v2 package (Milanesi et al. 2017). The third one, a Neighbour-Joining (NJ) phylogenetic tree (Saitou and Nei 1987) based on Reynolds distances, computed with hapFLK (Fariello et al. 2013), using the SOA population as outgroup and visualised using FigTree v1.4.4 (http://tree.bio.ed.ac.uk/software/fgtree/).

Genetic variability between populations was assessed by estimating pairwise Fst (Weir and Cockerham 1984) using the stamppFst function (StAMPP package; 100 bootstraps) (Pembleton et al. 2013); and Reynolds distances using hapFLK (—reynolds).

RESULTS

Genomic variation within populations

Average Ho values were higher for domestic sheep (COR and MER) at 0.364 and 0.351, respectively, compared to the Creole populations, which ranged from 0.279 to 0.327 (Table 1). Among the Creole populations, CSM had the lowest Ho (0.279), while BCS exhibited the highest (0.327).

Inbreeding coefficient estimates (F_{HOM}) ranged from 0.020 in COR population to 0.283 in SOA population, with CSM displaying the second highest value (0.249).

These results align with inbreeding estimates based on runs of homozygosity (F_{ROH}), which revealed a minimum of 0.054 in COR population and a maximum of 0.202 in CSM population, closely followed by SOA (F_{ROH} = 0.199) (Table 1). Although BCS, CLB, and COM populations exhibited significant variability (Figure 2), their mean values aligned with the overall mean F_{HOM} pattern.

Recent effective population size values (Ne_{13}) were lower for Uruguayan Creole populations, with a similar trend for Ne_{45} values. The lowest Ne_{13} values were observed in CLB (49) and CSM populations (55), while COR population had the highest Ne_{13} (225) and Ne_{45} (432) estimates. All populations exhibited a declining trend from Ne_{45} to Ne_{13}, with a slightly steeper decline observed in BCS and COM populations (Table 1).

A total of 79 083 ROH were detected across the genome for all populations. The number of ROH per population ranged from 2 140 in BCS to 22 773 in CSM (Figure 3, ESM Table S2). SOA (21 679) and CLB populations (16 762) also exhibited high ROH counts.

CSM population had the highest values for both F_{ROH} (0.202) and total ROH detected (22 773). The analysis of ROH distribution by size revealed that most ROH across all populations were shorter than 4 Mb, with few falling within the 8–16 Mb class and almost none exceeding 16 Mb. All Creole populations exhibited a higher frequency of ROH in the 8–16 Mb size class compared to domestic breeds (ESM Figure S1).

Table 1. Genetic diversity indices for the seven sheep populations

Population	*n*	Ne_{13}	Ne_{45}	Ho	He	F_{HOM}	F_{ROH}
CSM	139	55	97	0.279	0.371	0.249	0.202
CLB	139	49	108	0.287	0.371	0.226	0.138
COM	35	62	169	0.287	0.372	0.227	0.194
COR	139	225	432	0.364	0.372	0.020	0.054
MER	43	113	256	0.351	0.371	0.056	0.075
BCS	23	79	227	0.327	0.372	0.118	0.124
SOA	110	130	172	0.266	0.371	0.283	0.199

Number of individuals (*n*), effective population sizes 13 and 45 generations ago (Ne_{13} and Ne_{45}, respectively); average observed heterozygosity (Ho); average expected heterozygosity (He), and average inbreeding coefficients (F_{HOM} and F_{ROH}) for each population

BCS = Brazilian Creoles; CLB = INIA Las Brujas Creoles; COM = commercial farms Creoles; COR = Corriedale; CSM = San Miguel National Park Creoles; MER = Merilin; SOA = Soay

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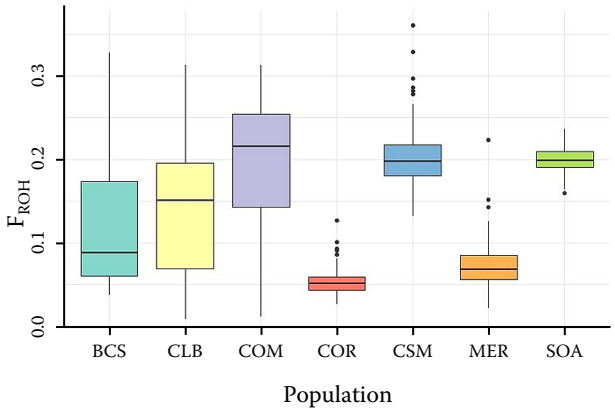

Figure 2. Inbreeding levels (F_{ROH}) based on individual runs of homozygosity (ROH) for the seven sheep populations

BCS = Brazilian Creoles; CLB = INIA Las Brujas Creoles; COM = commercial farms Creoles; COR = Corriedale; CSM = San Miguel National Park Creoles; MER = Merilin; SOA = Soay

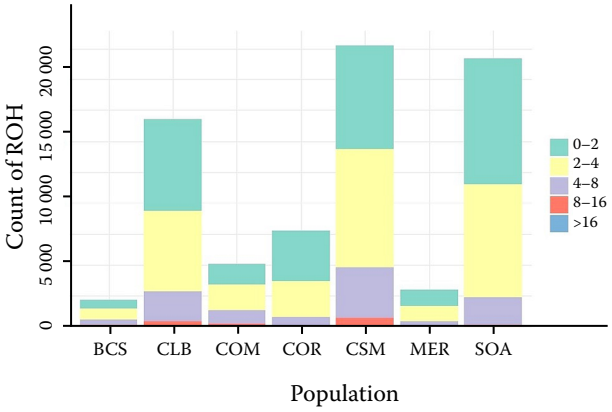

Figure 3. Number of runs of homozygosity (ROH) detected per size class (length of ROH in Mb) for the seven sheep populations

BCS = Brazilian Creoles; CLB = INIA Las Brujas Creoles; COM = commercial farms Creoles; COR = Corriedale; CSM = San Miguel National Park Creoles; MER = Merilin; SOA = Soay

Population structure

PCA was able to separate the seven sheep populations with some overlap between COR and MER (Figure 4). The first principal component (PC1), which accounted for 27.94% of total genetic variance, separated the SOA population from all others. Most Creole populations (CSM, CLB, and COM) clustered together, while COR, MER, and BCS populations formed a distinct group. The second principal component (PC2), explaining 24.66% of the total variance, separated CSM from CLB and identified certain individuals within the COM population as distinct. However, PC2 did not differentiate between COR, MER, BCS, some COM individuals, and SOA, which all clustered together.

When the SOA population was excluded from the analysis (Figure 5), PC1 (32.2%) clearly differentiated CSM from CLB and some COM individuals, but it did not distinguish MER, COR, BCS, and the remaining COM individuals, which all clustered together. PC2 (24.17%) differentiated all the Creole populations from the commercial breeds (COR and MER). The cross-validation error plot from admixture analysis (Figure 6A) showed a steady decrease as K increased, with the rate of decrease slowing after K = 4. Beyond K = 5, the error reduction became much smaller, suggesting that K = 4 or K = 5 is the most probable number of clusters

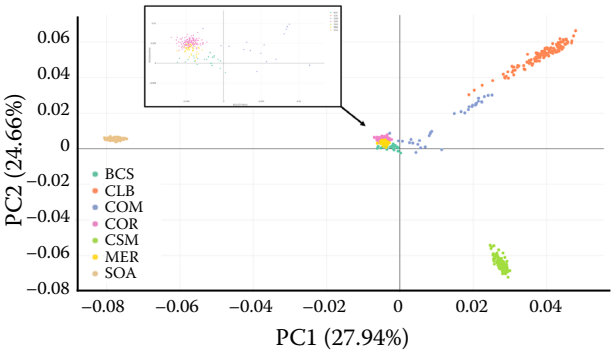

Figure 4. Principal component analysis (PCA) plot for the seven sheep populations

BCS = Brazilian Creoles; CLB = INIA Las Brujas Creoles; COM = commercial farms Creoles; COR = Corriedale; CSM = San Miguel National Park Creoles; MER = Merilin; SOA = Soay

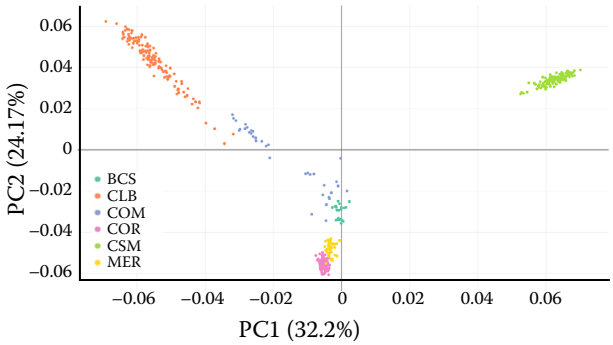

Figure 5. Principal component analysis (PCA) plot for all populations excluding Soay

BCS = Brazilian Creoles; CLB = INIA Las Brujas Creoles; COM = commercial farms Creoles; COR = Corriedale; CSM = San Miguel National Park Creoles; MER = Merilin

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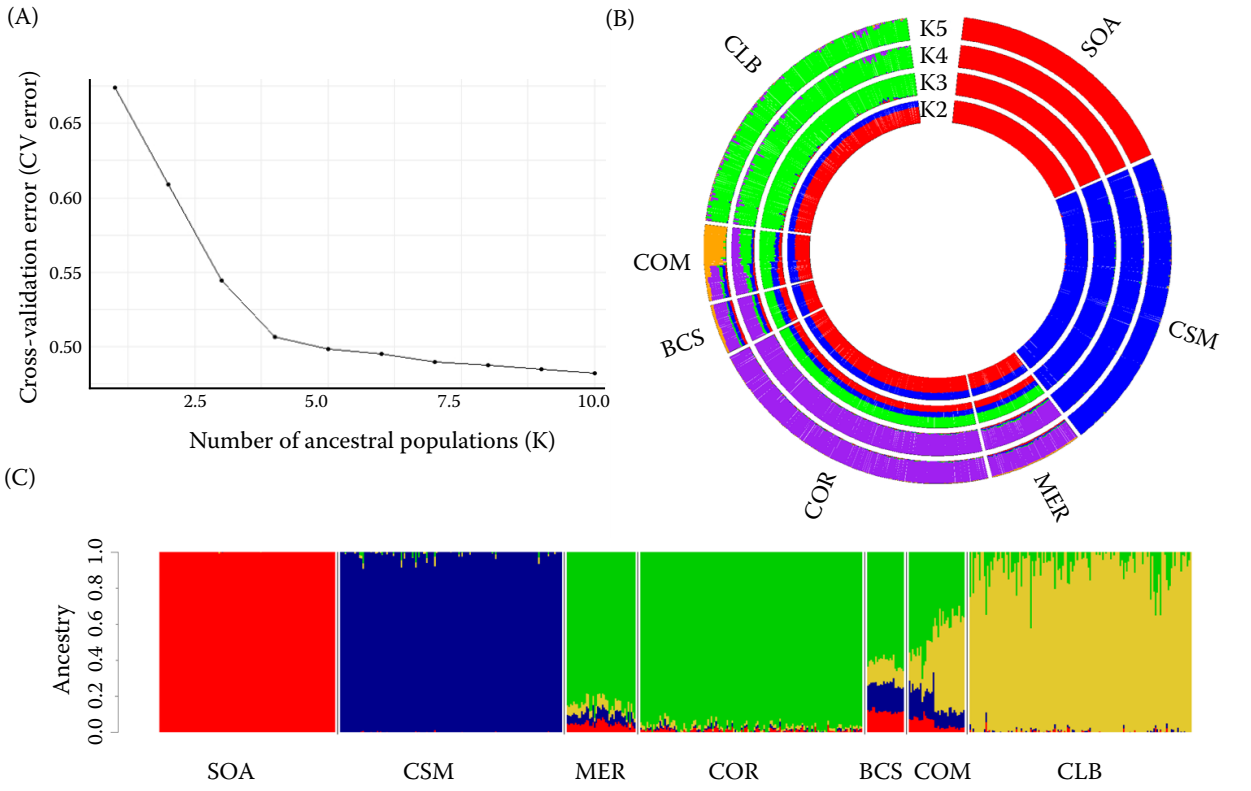

Figure 6. Model-based clustering analysis

(A) Prediction error plot; (B) Circle plot from K = 2 to K = 5; (C) Bar plot from K = 4

BCS = Brazilian Creoles; CLB = INIA Las Brujas Creoles; COM = commercial farms Creoles; COR = Corriedale; CSM = San Miguel National Park Creoles; MER = Merilin; SOA = Soay

explaining the variation. At K = 2, SOA and CSM exhibited distinct genetic backgrounds, while the remaining populations showed admixed ancestry (Figure 6B). At K = 3, CLB population was separated (highlighted in green), and at K = 4, COR and MER populations were differentiated (marked in purple). At K = 5, a subcluster emerged within COM population, highlighting the genetic variability present in this group and beginning to differentiate the different farms. These findings suggest that K = 4 is the optimal number of populations, as it clearly differentiates SOA, CSM, and CLB, each exhibiting unique genetic clustering patterns (Figure 6C). MER and COR share a similar ancestry, distinct from the others, while BCS and COM exhibit admixed ancestry. BCS displayed a significant proportion of Corriedale ancestry, while COM showed a high proportion of ancestry from both Corriedale and CLB. This aligns with PCA results, which reveal a COM subcluster positioned near the CLB population and another subcluster closer to MER, COR and BCS populations.

To further investigate the genetic relationships among the studied populations, a rooted NJ tree was constructed based on Reynolds distances, with the Soay breed serving as the outgroup (Figure 7).

The tree topography revealed that COM and CLB populations branched together but separated

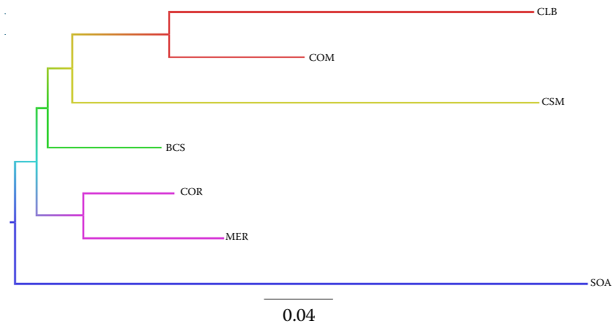

Figure 7. Neighbour-joining tree for the seven sheep populations

BCS = Brazilian Creoles; CLB = INIA Las Brujas Creoles; COM = commercial farms Creoles; COR = Corriedale; CSM = San Miguel National Park Creoles; MER = Merilin; SOA = Soay

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Table 2. Matrix of pairwise estimates of Fst statistics (below the diagonal) and Reynolds distances (above the diagonal) between populations

Population	BCS	CLB	COM	COR	CSM	MER	SOA
BCS	0.000	0.177	0.109	0.078	0.176	0.092	0.209
CLB	0.182	0.000	0.146	0.181	0.272	0.197	0.321
COM	0.092	0.145	0.000	0.114	0.204	0.131	0.255
COR	0.067	0.180	0.103	0.000	0.190	0.068	0.214
CSM	0.182	0.269	0.206	0.187	0.000	0.203	0.320
MER	0.076	0.201	0.118	0.060	0.208	0.000	0.228
SOA	0.218	0.318	0.259	0.208	0.316	0.234	0.000

BCS = Brazilian Creoles; CLB = INIA Las Brujas Creoles; COM = commercial farms Creoles; COR = Corriedale; CSM = San Miguel National Park Creoles; MER = Merilin; SOA = Soay

from CSM, which is consistent with PCA analysis that showed CLB population closer to COM than to CSM (Figure 5). Additionally, the four Creole populations (CLB, COM, CSM and BCS) branched together and separated from Corriedale and Merilin populations that branched together as well. BCS population was positioned closer to COR and MER, consistently with PCA analysis.

A longer branch for CSM population indicates higher inbreeding, while a shorter branch for COR population represents lower inbreeding, in accordance with estimated F_{HOM} and F_{ROH} values.

Genomic variation between populations

Genetic distances between CLB and the other six populations ranged from 0.145 to 0.318 and 0.146 to 0.321 for Fst estimates and Reynolds distances, respectively (Table 2). CLB population showed the lowest differentiation from COM (Fst = 0.145 and Reynolds = 0.146), followed by COR population (Fst = 0.180 and Reynolds = 0.181) and BCS population (Fst = 0.182 and Reynolds = 0.177) and the highest differentiation from SOA (Fst = 0.318 and Reynolds = 0.321) and CSM (Fst = 0.269 and Reynolds = 0.272). The shortest distances among all populations were observed between COR and MER (Fst = 0.060, Reynolds = 0.068), followed by COR and BCS (Fst = 0.067, Reynolds = 0.078).

DISCUSSION

This study investigated within and between breed diversity and population structure of INIA Las Brujas Creoles, in relation to other Uruguayan Creoles, two commercial breeds (Corriedale and Merilin), and two global populations (Brazilian Creoles and Soay).

Observed heterozygosity estimates and inbreeding coefficients (F_{HOM} and F_{ROH}) demonstrated low genetic diversity and high inbreeding in CLB population. Unsurprisingly, COR population (Ho = 0.364) and Merilin population (Ho = 0.351) were more diverse than Creole populations, with CSM exhibiting the lowest Ho (0.279). COR diversity reflects its large national population and well-managed breeding program, including imported rams from Australia. Merilin, though fewer samples were available, also benefits from a well-managed breeding program. In a previous study, a lower observed heterozygosity was found in the Corriedale breed (0.355) and a slightly higher observed heterozygosity for the San Miguel National Park Creole population (0.285) (Grasso et al. 2014). Compared to Creoles from Argentina (Ho = 0.642–0.708) (Pena et al. 2017), Brazil (Ho = 0.295–0.350) (Paim et al. 2021), and Colombia (Ho = 0.31–0.37) (Revelo et al. 2022), Uruguayan Creoles showed much lower diversity. F_{HOM} values observed in our study (0.118–0.249) were notably higher than reported Fis values in other Latin American studies (Pena et al. 2017; Revelo et al. 2022). Moreover, the presence of positive F_{HOM} values in the three Uruguayan Creole populations could be attributed to the limited number of individuals within each population, which favours inbreeding, added to the lack of selective breeding, mostly in CSM population.

A previous study in Uruguay in the same CSM population (Pieruccioni Banchero 2018) reported

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F_{ROH} values of 0.27 (using a 50K chip) and 0.24 (using a 606K chip), both slightly higher than the 0.202 value observed in our study. They also analysed a Corriedale population (different from the one in our study, belonging to a single farm selected for resistance and susceptibility to gastrointestinal parasites) and reported a F_{ROH} value of 0.08 (using a 50K chip), also higher than our estimate of 0.054. Consistently with our findings, most ROH in both populations were shorter than 6 Mb, with CSM showing a higher ROH count than COR, approximately 15 500 and 3 700, respectively, compared to 22 773 for CSM and 7 711 for COR in our study. Another study examining inbreeding and runs of homozygosity in Creole sheep breeds from Africa, Barbados, Brazil, Colombia, Ecuador, and Spain (Ramirez-Diaz et al. 2024) reported average F_{ROH} values below 0.26 for Colombian (Ethiopian, Peliguey, Sudan, and Wayúu breeds) and Ecuadorian Creole populations. These findings are consistent with the F_{ROH} values observed in our study, which did not exceed 0.202. Another study on Colombian Creole wool sheep (Revelo et al. 2022) reported average F_{ROH} values of 0.094 for Wool Creole Boyacá and 0.045 for Wool Creole Nariño, which are considerably lower than those observed in our study for Creole populations. The predominance of short ROH across all breeds in our study suggests ancient inbreeding events (McQuillan et al. 2008), while a slight increase in longer ROH (8–16 Mb) among Creoles may indicate more recent inbreeding.

PCA analysis (excluding Soay) revealed a clustering pattern that clearly separated CSM, CLB, and some individuals from COM population, but clustered together the COR and MER populations. This close genetic relationship could be explained by the fact that both breeds developed from crossing Lincoln with Merino. PC1 did not differentiate BCS, some individuals from COM, COR and MER, which clustered together and closer to CLB, which agrees with the medium differentiation found between CLB and COM (0.145 and 0.146), CLB and COR (0.180 and 0.181), CLB and BCS (0.182 and 0.177), and CLB and MER (0.201 and 0.197), according to Fst and Reynolds distances, respectively. On the other hand, PCA analysis yielded two different and clearly separated clusters for CLB and CSM, congruent with the very high Fst and Reynolds distance found between these two populations (0.269 and 0.272, respectively). The PCA plot also shows that the populations that are closer together are COR and MER, in agreement with the low Fst and Reynolds distance observed between them (0.060 and 0.068, respectively).

Admixture analysis revealed distinct ancestral populations in SOA, COR and CSM while COM population showed diversity and admixture, with a high degree of Corriedale breed ancestry and some CLB ancestry. This is consistent with PCA analysis that showed tighter clusters in COR and CSM in contrast to COM, which showed a broader distribution, with two subclusters, one closer to CLB and the other closer to COR, MER, and BCS. In the case of CLB, a discernible ancestral population was evident, albeit with detectable Corriedale ancestry.

Results obtained from the phylogenetic tree support both PCA and admixture analysis reinforcing the clustering of populations. The tree clearly distinguishes the Creole populations from both the Corriedale and Merilin populations, as well as demonstrating a distinct separation of the CLB population.

In line with these findings, the Brazilian Creole population exhibited lower inbreeding (as indicated by both F_{HOM} and F_{ROH}), higher observed heterozygosity, and larger effective population sizes (Ne_{13} and Ne_{45}) compared to our Creole populations. This may be attributed to the population growth over the past century, driven by the conservation efforts initiated by the Brazilian Agriculture Research Corporation (EMBRAPA) in 1982 and the establishment of the Brazilian Association of Creole Sheep Breeders (ABCOC) in 1999, which helped expand the population to 112 Creole flocks and 8 844 reproductive ewes, as reported in a recent farmer survey (Moreira 2022). Admixture and PCA analysis indicate a strong similarity between the Brazilian Creole population and the Uruguayan Creoles from commercial farms, particularly the subcluster closely aligned with BCS, suggesting a shared origin. The other COM subcluster, which is closer to INIA Las Brujas Creoles, corresponds to the farm that originated from the "San Pedro del Timote" stud flock. As previously mentioned, both this stud flock and the one from which the CLB farm originated were selectively bred for an all-white coat and they likely exchanged genetic material in the past, a finding now confirmed by our results. In contrast to the other Creole sheep from commercial farms which exhibit a variety of coat colours, including black, brown and white ones.

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To conduct a more detailed genetic study of these populations from commercial farms, it will be necessary to sample at least 20 animals from each farm.

Overall results show a close genetic relationship between CLB, COR and COM, which could be explained by the fact that Creoles were the genetic base when Corriedale breed was introduced into Uruguay and ever since these breeds have been managed jointly within farms, which could explain gene exchange among them. On the other hand, the medium to high differentiation observed between these three populations with CSM is explained because the latter has been a closed population since its foundation in 1929 (Fernandez et al. 2009).

CONCLUSION

In this study, we conducted a genetic characterisation of the Creole population from INIA Las Brujas. Unfortunately, historical information supporting the original genetics of this population is not available.

Our results revealed a distinct population, markedly different from the larger San Miguel National Park Creole population, exhibiting low genetic variability, low effective population size, and high levels of inbreeding.

Our findings provide valuable information, particularly given that this population is managed within the Extensive Livestock Production System at INIA, contributing essential data for research. The results presented here could be integrated into breeding programs to control reproduction and avoid the negative effects of inbreeding, preserving the genetic pool of this locally adapted sheep population.

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Conflict of interest

The authors declare no conflict of interest.

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