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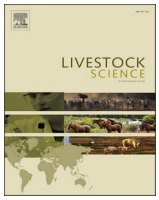

Genome-wide single nucleotide polymorphisms reveal the genetic diversity and population structure of Creole goats from northern Peru

Flor-Anita Corredor [a,1], Deyanira Figueroa [a,1], Richard Estrada [a], William Burgos-Paz [b], Wilian Salazar [a], Wilder Cruz [a], Roiser Lobato [a], Pedro Injante [a], David Godoy [c], Christian Barrantes [c], Jorge Ganoza [c], Juancarlos Cruz [c], Carlos I. Arbizu [a,2,*]

[a] Dirección de Desarrollo Tecnológico Agrario, Instituto Nacional de Innovación Agraria (INIA), Lima 15024, Peru
[b] Corporación Colombiana de Investigación Agropecuaria-AGROSAVIA, Centro de Investigación Turipaná, Km 14 Vía Montería-Cereté, Montería, Colombia
[c] Dirección de Supervisión y Monitoreo en las Estaciones Experimentales Agrarias, Instituto Nacional de Innovación Agraria (INIA), Lima 15024, Peru

HIGHLIGHTS

- This work analyses the Peruvian Creole goat (PCG) with genomic data for the first time.
- PCG possesses high genetic variability and low inbreeding.
- The Peruvian Creole goat is grouped in a single cluster.
- Inter-breed structure demonstrated the PCG corresponds to a different population.

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ABSTRACT

Goat farming constitutes a significant source of income for farmers in northern Peru. There is currently an absence of information about the genetics of Peruvian Creole goats that would enable us to understand their origins and genetic spread. The objective of this study was to estimate the genetic diversity of Creole goats from northern Peru using SNP markers. This study involved the collection of 192 male Creole goats from three key goat production geographical departments in northern Peru. These goat samples were genotyped using the GGPGoat70k SNP panel. To explore the genetic influence of other breeds on Peruvian Creole goats, our dataset was combined with previously published SNP genotypes. External data set includes multiple breeds genotypes sampled from Argentina, Brazil, Spain, and Alpine breed from Italy, France, and Switzerland. After quality control 52,832 autosomal SNPs were used to assess genetic diversity in the Peruvian goats. For the population structure analysis of the merged data 20,513 common SNPs were used. Estimations for expected heterozygosity (H_e), observed heterozygosity (H_o), and inbreeding coefficient (F_{IS}) were computed for the Peruvian groups. AMOVA, principal component analysis and ADMIXTURE were conducted to evaluate the population structure in the two data sets, Peru and merged. The results revealed a considerable genetic diversity, with H_o values ranging from 0.40 to 0.41 for the Peruvian sampling groups, and inbreeding coefficient was notably low for Peruvian goat. The population structure analysis demonstrated a distinction ($p < 0.05$) from other breeds. These findings suggest a level of genetic differentiation of the Peruvian goat population among other breeds, although further research is needed considering samples from other Peruvian areas. We expect this study will contribute to define genetic management strategies to prevent the loss of genetic diversity in Peruvian goat populations and for upcoming advancements in this field.

* Corresponding author.
E-mail address: carlos.arbizu@untrm.edu.pe (C.I. Arbizu).
[1] These authors contributed equally to this work.
[2] Facultad de Ingeniería y Ciencias Agrarias, Universidad Nacional Toribio Rodríguez de Mendoza de Amazonas (UNTRM), Amazonas 01001, Peru.

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1. Introduction

In Peru, goat production was developed in several agroecosystems such as the central coast valleys, the northern coast, and western Andes (Sarria et al., 2014), and today it is mainly focused on milk production for cheese and kid goat's meat. Goats in Peru are primarily sold locally and regionally. Since their arrival on the American continent in 1493, the Spanish colonizers were in charge of propagating the goat species. Over the years, the introduction of many goat breeds, such as Saanen, Alpina, Malagueña, and Anglonubian, influenced the appearance of Creole goats in Peru, representing 80% of the total goat population (Gómez-Urviola et al., 2016). In the northern regions of Peru, goat farming is mainly found in the dry tropical forest, which presents harsh environments such as prolonged droughts and high temperatures (Parra et al., 2015), demonstrating great adaptability to extreme conditions in comparison with other livestock species. Moreover, goat farming in northern Peru is mostly a grazing system with a diet based on crop residue and the usage of natural pastures (Perevolotsky, 1990).

Genetic diversity is crucial in the conservation of genetic resources and constitutes the basis of selection processes and genetic improvement (Coates et al., 2018; DeWoody et al., 2021). The loss of genetic diversity in goats raises the risk of losing specific genes associated with economically valuable traits. Additionally, the loss of diversity hinders the advancement of future breeding (Alderson, 2018), making it harder for organisms to adapt to changing environmental conditions. Numerous studies of genetic diversity were conducted in various livestock species using single nucleotide polymorphism (SNP), becoming the genetic markers of choice for many molecular applications. Some of these studies focus on genetic diversity (Chokoe et al., 2020; Mukhina et al., 2022), while others explore population structure (Berihulay et al., 2019; Monau et al., 2020; Muner et al., 2021), phylogeny (Ciaravino et al., 2021; Mukhina et al., 2022; Xiao et al., 2021), and paternity assessment (Domínguez-Viveros et al., 2020; Talenti et al., 2018). In Latin America, previous studies of genetic and morphological characterization of the Creole goat were conducted in Ecuador (Aguirre-Riofrio et al., 2020; Lucas et al., 2020), Mexico (Domínguez et al., 2018; Silva-Jarquin et al., 2019b, 2019a; Villarreal-Arellano et al., 2020), Venezuela (Arangur-en-Mendez et al., 2013; Muñoz Milano et al., 2014; Pariacote et al., 2004), and Cuba (Chacón et al., 2011, 2010; Guevara-Hernandez et al., 2012). These studies mainly employed microsatellite markers.

Most research on Peruvian Creole goats (PCG) was focused on animal health issues. On the other hand, due to the absence of genetic improvement program proposals on goats, there are few studies on phenotypic characterization, creating a significant knowledge gap to fill. There are few previous studies related to the morphology of the goats in specific locations in Peru (Gómez et al., 2012; Montesinos et al., 2015; Moscol Chung, 2016). For instance, Gómez et al. (2012) studied the morphology of goats from five locations of the Apurimac department (southern Peru). The authors found that the length and width of the head, among other body measurements, were important for differentiating the goats among locations. Moscol Chung (2016) studied the relationship between the chest perimeter and the live weight of goats from the northern region of Peru, finding strong correlations ranging from 0.93 to 0.97. To support these zoometric descriptions and to encourage a closer examination of the genetic development and management of the Creole goats in Peru, genetic studies are urgently required.

Some studies employed microsatellite markers to investigate the genetic diversity and the genetic link between PCG and Spanish breeds (Azor Ortiz et al., 2008; Urviola et al., 2011). According to these findings, the genetic diversity of the Peruvian goats from the Andean region is substantial and is genetically related to Spanish breeds like Murciano-Granadina and Malagueña. SNP marker analysis is now a standard approach for genetic diversity analysis. The availability of SNPs panels enables comprehensive investigation and superior power for examining genetic variation and the relationship across many diverse livestock genomes, which is impossible to achieve with other types of markers (Berihulay et al., 2019). Because of the need for a better understanding of the PCG, SNP-type markers are an adequate tool for determining the genetic structure and diversity of the Peruvian Creole goat populations. To the best of our knowledge, this is the first time a set of samples from northern Peruvian locations for Creole goats was genotyped employing a SNP panel. These findings will benefit the development of a modern national breeding program for the rescue, conservation, and appropriate use of this goat genetic resource.

2. Materials and methods

2.1. Animal sampling, DNA extraction, and SNP genotyping

A total of 192 ear punch tissue samples were collected from goats identified as Creole by a technical assistant and owners. Goats were sampled from three main producing areas of goats in Peru: Tumbes ($n = 35$), Piura ($n = 129$), and Lambayeque ($n = 28$) (Fig. 1). Individuals from different locations were randomly sampled to ensure a representative genetic background of the population. A maximum of five animals from each herd were sampled. The populations included in this study come from similar selection environments of dry tropical forest fields (Parra et al., 2015). Only males were sampled because of their influence over the genetics of the populations. To avoid sampling animals with a degree of relatedness only adult individuals were included as well as the owners' indications about their origin. Genomic DNA was extracted from tissue samples with the Wizard Genomic DNA Purification Kit (Fitchburg, WI, USA) following the manufacturer's instructions. The quality and quantity of genomic DNA were assessed using agarose gel electrophoresis and a Nanodrop spectrophotometer (Model ND2000, Thermo Fisher Scientific, Wilmington, DE, USA) prior to genotyping. DNA samples were genotyped using Illumina GGP Goat 70 K with the help of the commercial genotyping service provider (Neogen, Geneseek, NL, USA).

In addition, 598 genotypes from a publicly available dataset (Colli et al., 2018) were included in this work. This dataset encompasses genotypes from various breeds sourced from different regions, including Argentina (Angora, Creole, Nubian, Saanen, Saanen x Creole), Brazil (Caninde, Moxoto, Saanen x Anglo Nubian), Spain (Bermeya, Mallorquina, Malaguena, Murciano-Granadina, Palmera, Blanca de Rasquera), and Alpine breed from Italy, France, and Switzerland (Supplementary Table 1).

2.2. SNP quality control

SNPs quality control was performed using PLINK v1.9 program (Chang et al., 2015; Purcell and Chang, 2015), and those with missing rate per individual of 10%, missing rate per SNP of 10%, and minor allele frequency (MAF) lower than 0.05 were excluded. SNP filtering based on the Hardy–Weinberg equilibrium was performed using the parameter –hwe (0.00005). Furthermore, SNPs assigned to sex chromosomes and those lacking genomic locations were excluded from the analysis. The final number of SNPs after quality control was 52,832 and were used to assess genetic structure and diversity in the PCG populations.

Furthermore, prior to conducting the population structure analysis on the PCG genotypes, linkage disequilibrium (LD) pruning was implemented using the PLINK parameter –indep 50 5 2, resulting in 24,159 SNPs. The filtering criteria for the external dataset's LD pruning was less stringent, as it was intended to be used as an outgroup (PLINK parameter –indep 50 5 3). Finally, both the Peruvian and external datasets were merged (merged database), comprising 790 animals and 20,513 common SNPs for population structure analysis.

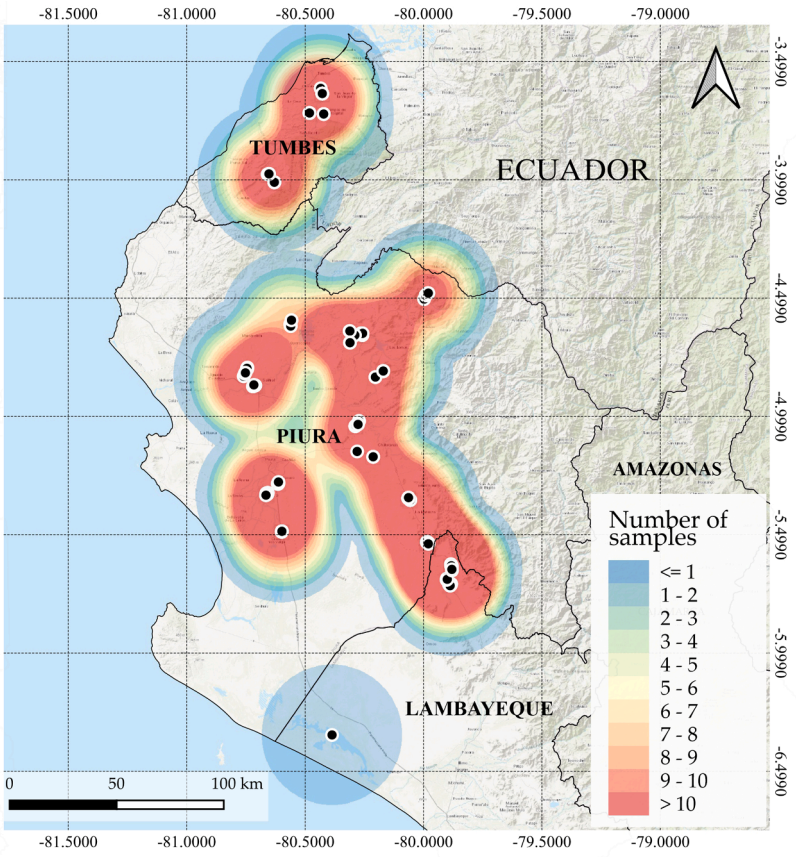

Fig. 1. Geographical localization of Lambayeque, Piura, and Tumbes goat populations in northern Peru.

2.3. Genetic diversity

The within-population genetic diversity, observed heterozygosity (Ho) and expected heterozygosity (He) were estimated using PLINK v1.9 program (Chang et al., 2015; Purcell and Chang, 2015). The inbreeding coefficient (FIS) was assessed with ARLEQUIN v3.5.2 software (Excoffier and Lischer, 2010). The distribution of MAF was determined using PLINK program and was grouped into five different categories based on the frequency of alleles ($0 < MAF \leq 0.1$), ($0.1 < MAF \leq 0.2$), ($0.2 < MAF \leq 0.3$), ($0.3 < MAF \leq 0.4$), and ($0.4 < MAF \leq 0.5$). The allele in minor frequency for each SNP in the Alpine goat population was used as reference allele (Supplementary Figure 1).

2.4. Population structure

Molecular variance, principal components, admixture, and genetic distances alongside neighbor-joining tree analysis were conducted to explore the population structure of the PCG, and merged dataset.

Four analytical strategies were applied to explore the population structure in the PCG, and merged dataset. Initially, the analysis of molecular variance (AMOVA) was performed with ARLEQUIN, with the locus-by-locus option and 1000 permutations. PGDSpider v2.1.1.5 software (Lischer and Excoffier, 2012) was used to convert files between PLINK and Arlequin formats. To perform a principal component analysis (PCA), PLINK, and *cmdscale* function in *stats* R package (R Core Team, 2020) were used to generate eigenvectors and eigenvalues, and the outputs were visualized using the R package *ggplot2* (Wickham, 2016). In addition, ARLEQUIN was employed to assess the pairwise genetic differentiation among breeds using fixation indices (F_{ST}) calculated using 20,000 permutations and a significance level of 0.05.

Genetic relationships among the PCG populations as well as the relationships within the merged dataset were assessed through an admixture analysis. The level of admixture was estimated through a model-based clustering algorithm implemented in the software ADMIXTURE v1.3.0 (Alexander et al., 2009). For the PCG dataset, a 15 cross-validation procedure was executed to estimate prediction errors for each K value (from 2 to 15). For the merged dataset, a fivefold cross-validation procedure was executed to estimate prediction errors for each K value (from 2 to 20, Supplementary Figure 2). The value of K that minimizes the estimated prediction error represented the best predictive accuracy. Individual coefficients of membership to each K cluster produced by ADMIXTURE were visualized using *ggplot2* R package.

A neighbor-joining (NJ) tree was constructed based on pairwise genetic distances using *vcfR* (Knaus and Grünwald, 2017), *adegenet* (Jombart, 2008), *pegas* (Paradis, 2010) and *ape* (Paradis and Schliep, 2019) R packages. Additionally, 1000 bootstrap replicates were conducted.

3. Results

3.1. Genetic diversity analysis

Table 1 summarizes the results of the genetic diversity parameters

Table 1
Genetic diversity for the Peru dataset, showing the name of the population, sample size (N), minor allele frequency (MAF), expected heterozygosity (He), observed heterozygosity (Ho), and inbreeding coefficient (F_{IS}).

Population	N	MAF	He	Ho	F_{IS}
Lambayeque	28	0.33 ± 0.12	0.41 ± <0.01	0.41 ± 0.03	0.01
Piura	129	0.33 ± 0.11	0.42 ± <0.01	0.40 ± 0.02	0.04
Tumbes	35	0.33 ± 0.12	0.41 ± <0.01	0.41 ± 0.02	0.02

calculated for the PCG populations. The mean MAF observed across the population was the same (0.33). Individuals from Piura had the lowest observed heterozygosity (0.40 ± 0.02), while Lambayeque and Tumbes possessed the highest (0.41). For the populations of Lambayeque and Tumbes, the mean H_e was the same as the H_o (0.41). For Piura, H_e was greater than the H_o. The highest F_{IS} was observed in Piura (0.04), while the lowest was in Lambayeque (0.01).

The MAF distribution (Fig. 2) showed a common trend in the three PCG populations, indicating a rise in the count of SNPs with higher MAF value. Around 34% of the SNPs showed a higher MAF ($0.4 < MAF \leq 0.5$). The Tumbes population showed the highest SNP count (2595), while Piura had the lowest (1595) when MAF was ≤ 0.1. For MAF in the range of 0.1 to 0.2, Lambayeque (6886) population had the highest, and Piura (5740) the lowest SNP count. In the 0.2 to 0.3 MAF range, Tumbes (11,074) population possessed the highest, and Lambayeque (9729) the lowest SNP count. Lambayeque (16,112) and Tumbes (15,581) populations had the highest and lowest numbers of SNPs when MAF was in the range of 0.3 to 0.4. The highest and lowest SNP counts were observed for the Piura (19,038) and Tumbes (16,894) populations when MAF was in the range of 0.4 to 0.5.

3.2. Population structure

The AMOVA results (Table 2) demonstrated most of the genetic variation (94.84%) was observed within individuals of the PCG dataset, whereas 0.92% accounts for the differentiation among PCG populations. In the merged dataset, 3.17% of the variance was assigned to the among-groups level, which explained the separation among countries.

Additionally, pairwise F_{ST} and Reynold's distance calculations were performed for the merged dataset. Among the PCG populations, low values (0.01) for both pairwise F_{ST} and Reynold's distances were observed, indicating low genetic differentiation. When comparing pairwise F_{ST} values between PCG populations and the external dataset, the highest pairwise F_{ST} values (ranging from 0.15 to 0.17) were observed between PCG populations and Caninde + Palmera breeds, from Brazil and Spain countries respectively (Supplementary Figure 3).

Table 2
Analysis of molecular variance for Peru dataset and alongside 15 breeds from six different countries (external dataset[1]).

Source of variation	Sums of squares	Variance component	% of variations
Peru dataset			
Among population	43,098.20	104.37	0.92
Among individuals within populations	2200,768.42	477.77	4.23
Within individuals	2052,860.50	10,709.14	94.84
Peru + External dataset			
Among groups	397,914.74	147.76	3.17
Among populations within groups	307,392.81	323.82	6.95
Among individuals within populations	3287,688.78	87.12	1.87
Within individuals	3227,907.50	4103.43	88.02

[1] External dataset comprises 598 goat genotypes (Supplementary Table 1) obtained from a publicly available dataset (Colli et al., 2018).

In contrast, the pairs involving PCG and Nubian breed from Argentina displayed the lowest pairwise F_{ST} values (0.03) (Supplementary Figure 3), suggesting genetic similarity. The pairwise Reynold's distance showed the same pattern as the one obtained with the F_{ST} statistics. The pairs between PCG populations with Caninde and Palmera breeds showed the highest pairwise Reynold's distance values (0.16 - 0.19). The pairs PCG – Nubian showed the lowest pairwise Reynold's distance values (0.03).

Principal component analysis was performed to visualize individual relationships among the three PCG populations. Individuals were labelled according to sampling location. The first and second components accounted for a total of 4.8% and 2.5% of variance explained respectively (Fig. 3A). In addition, a low differentiation among the Lambayeque, Piura, and Tumbes populations was observed, but interestingly some clusters of individuals from the Piura population were present. In Fig. 3B a graphic representation of cluster admixture analysis is depicted. Based on the ΔK value, $K = 4$ was the most optimal number

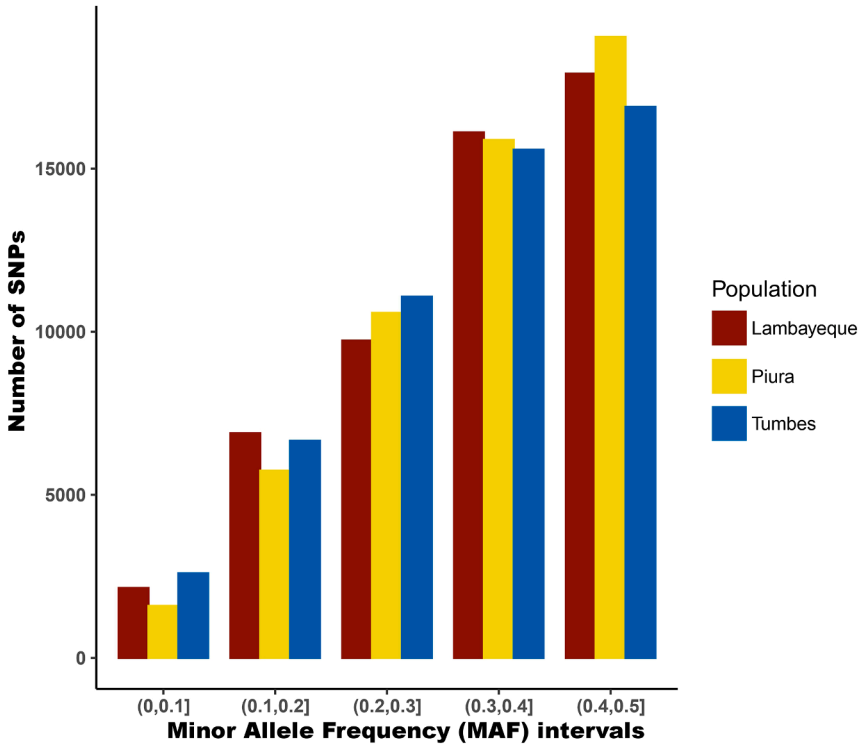

Fig. 2. Number of SNPs within intervals of minor allele frequency for each Peruvian goat population. Each population is represented by a different color.

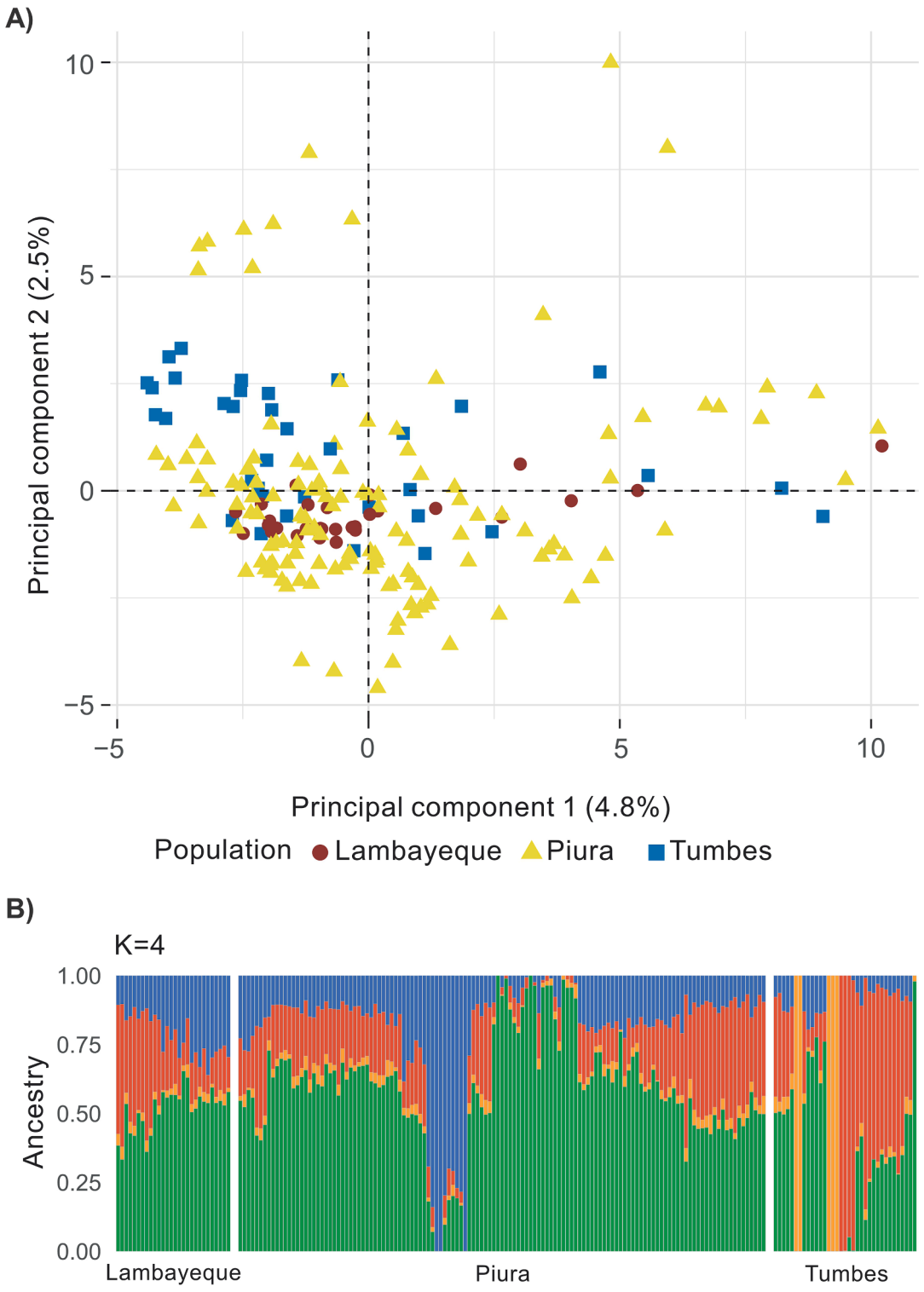

Fig. 3. Principal component analysis and Admixture analysis for the Peru dataset. **A.** For PCA plot, the x- and y-axes are indicated by the first and second components, respectively, and the values in parentheses show the percentages of total variance explained. **B.** Admixture analysis showing the proportions of ancestral populations for $K = 4$, each vertical bar exemplifies an individual.

for the inferred genetic structure of the populations. Clusters 1 (blue) and 4 (green) comprised part of the Piura population ($N = 9$ and $N = 28$ genotypes for each cluster). Cluster 4 comprised part of the Tumbes population ($N = 5$ genotypes), whereas clusters 2 (red) and 3 (yellow) consisted of the Tumbes population ($N = 5$ genotypes for each cluster). The individuals from Lambayeque population do not correspond to any cluster, showing a high level of admixture.

Fig. 4A presents the results of the PCA analysis concerning the individual relationships within the merged dataset, with individuals labelled based on their respective sampling origins. The first and second components contributed to 8% and 4.02% of the variation, respectively. The PCA revealed a distinct differentiation among all populations

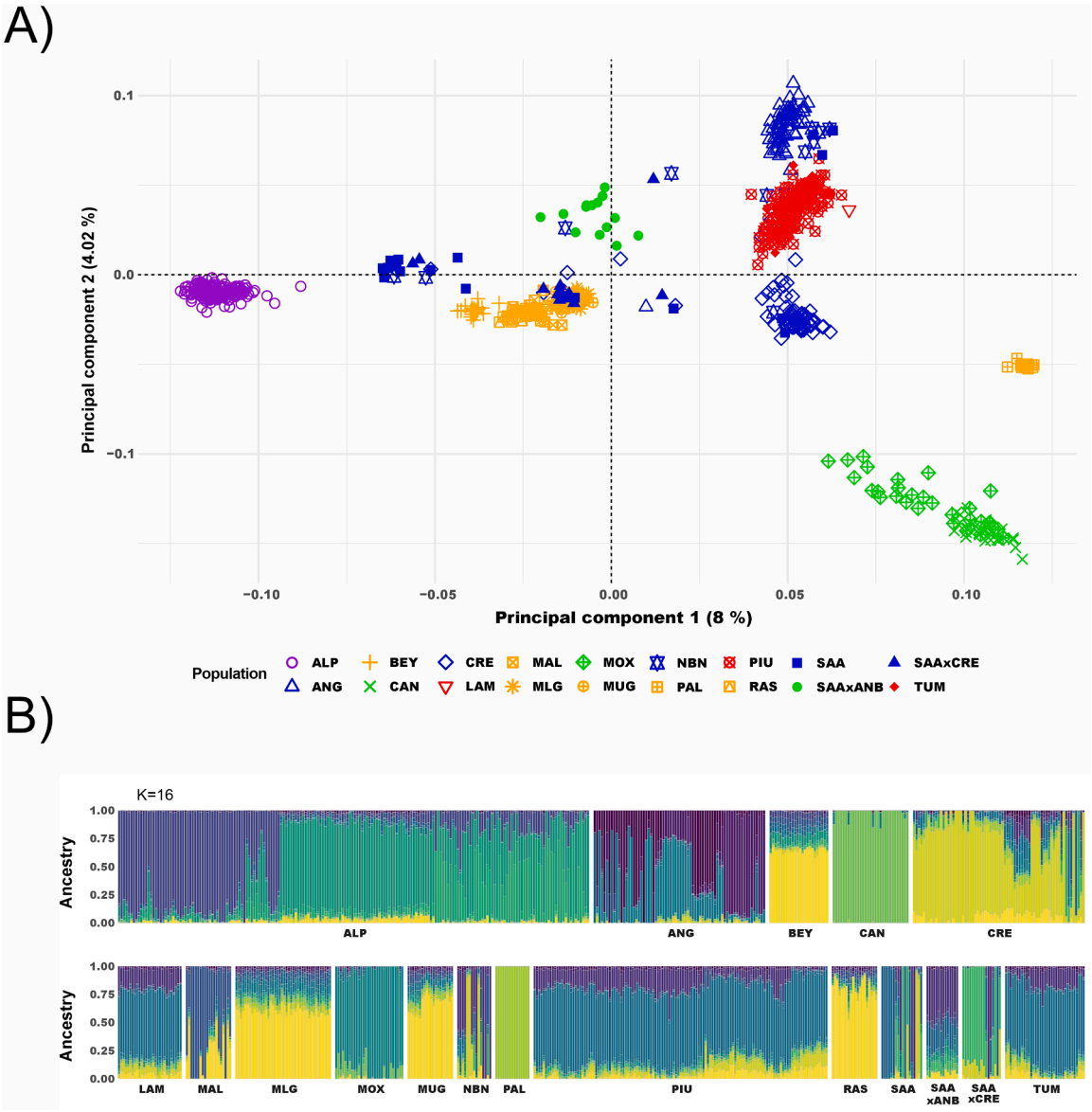

Fig. 4. Principal component and Admixture analysis for Peruvian Creole goat genotypes (LAM=Lambayeque, TUM=Tumbes, PIU=Piura) alongside with 15 breeds from six different countries. **A.** For PCA plot, the x- and y-axes are indicated by the first and second components, respectively, and the values in parentheses show the percentages of total variance explained. The population sample dots are colored according to their sampling origin as follows: red = Peru, blue = Argentina (ANG=Angora, CRE=Creole, NBN=Nubian, SAA=Saanen, SAAxCRE=Saanen x Creole), green = Brazil (CAN=Caninde, MOX=Moxoto, SAAxANB=Saanen x Anglo Nubian), orange=Spain (BER=Bermeya, MAL=Mallorquina, MLG=Malaguena, MUR=Murciano-Granadina, PAL=Palmera, RAS=Blanca de Rasquera), purple = Alpine breed (ALP) from Italy, France, and Switzerland. **B.** Admixture analysis showing the proportions of ancestral populations for $k = 16$, each vertical bar exemplifies an individual.

included in the study. The optimal K value for inferring the genetic structure of these populations was 16 (Fig. 4B).

Our neighbor-joining tree exhibited a bootstrap confidence level exceeding 90% (Fig. 5). Goats from the three Peruvian populations formed a single group. Similar to our PCA (Fig. 4), a closeness is distinguished between the Peruvian and the Argentinean populations. In examining populations from Peru, five distinct groups (G) were identified. (G1) The first group includes 17 individuals from Piura, supported by a bootstrap value of 100. (G2) The second group consists of 20 individuals from Tumbes along with two from Piura. (G3) The third group is divided into two subgroups: (i) one with 14 individuals from Piura and one from Tumbes, (ii) and another with 17 individuals from Piura and one from Tumbes. (G4) The fourth group is made up of three subgroups: (i) the first comprising 11 individuals from Piura, (ii) the second including 13 from Tumbes and 2 from Piura, (iii) and the third containing 26 individuals exclusively from Piura. (G5) The fifth group is organized into four subgroups: (i) the first features 19 individuals from Piura and one from Lambayeque, (ii) the second includes 15 from Lambayeque, (iii) the third comprises 12 from Lambayeque, (iv) and the fourth contains 21 from Piura.

4. Discussion

The current study employed SNP data for the first time to assess the genetic variability and population structure of goat populations from three locations in northern Peru, which is recognized as this species' primary distribution area. Additionally, this work constitutes the first effort to elucidate the relationship of the PCG with other breeds from other countries.

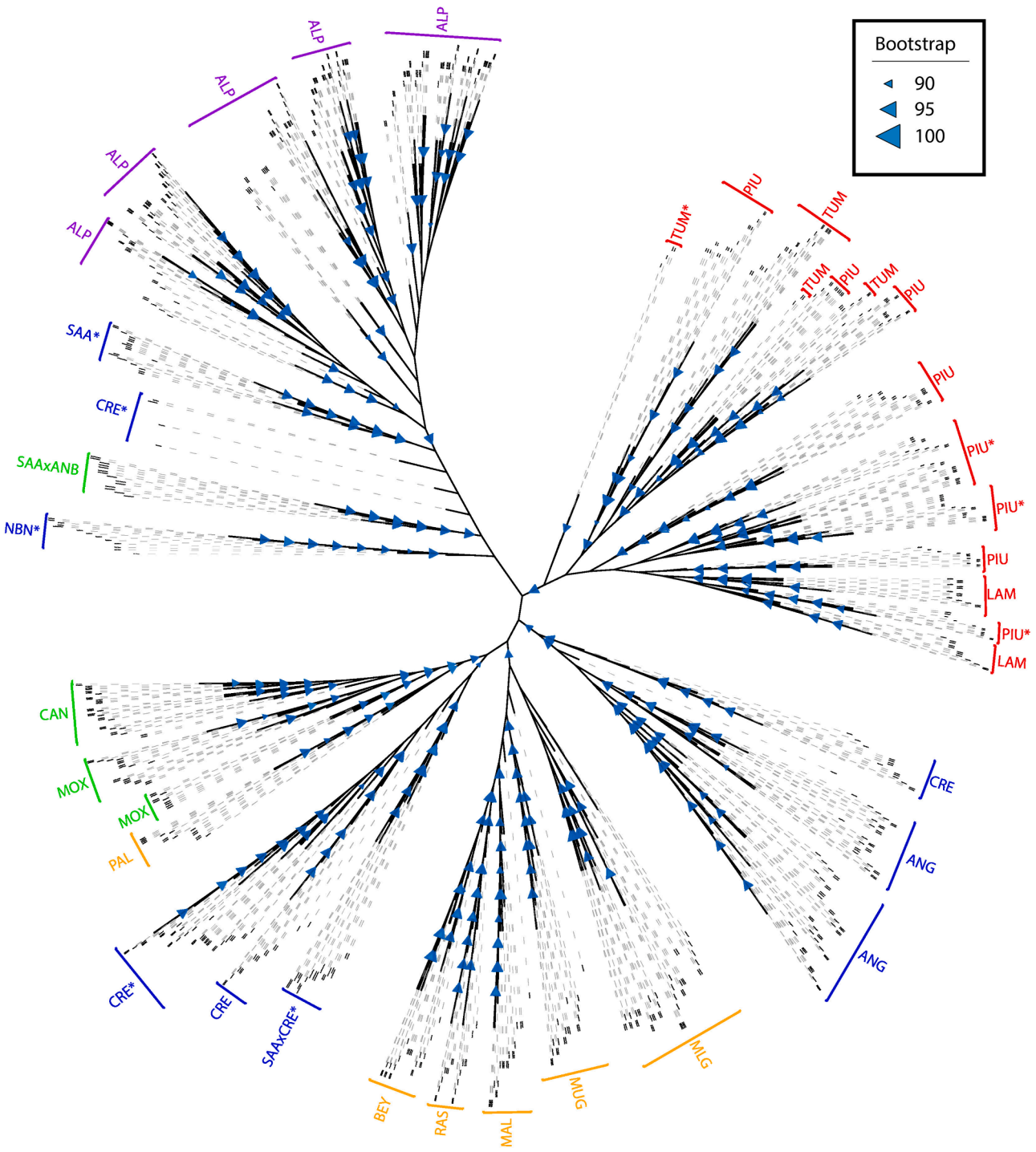

Fig. 5. Dendrogram based on pairwise F_{ST} distance between goat breeds and the NJ clustering algorithm method using 20,513 SNP markers. Symbols above the branches represent bootstrap values, with only values greater than 90% shown. Asterisks indicate clusters with goat individuals from different breeds/populations. The population acronyms are colored according to their sampling origin as follows: red = Peru (LAM=Lambayeque, TUM=Tumbes, PIU=Piura), blue = Argentina (ANG=Angora, CRE=Creole, NBN=Nubian, SAA=Saanen, SAAxCRE=Saanen x Creole), green = Brazil (CAN=Caninde, MOX=Moxoto, SAAxANB=Saanen x Anglo Nubian), orange=Spain (BER=Bermeya, MAL=Mallorquina, MLG=Malaguena, MUR=Murciano-Granadina, PAL=Palmera, RAS=Blanca de Rasquera), purple = Alpine breed (ALP) from Italy, France, and Switzerland.

4.1. Comparison with other populations

In our initial analysis, we observed significant genetic diversity and low genetic differentiation among the PCG populations of Lambayeque, Piura, and Tumbes, based on 192 goats individuals using a 70 K SNP panel. Ginja et al. (2017) indicated that the levels of genetic diversity in American Creole goats, representing 24 breeds from 10 countries, were not high when compared to breeds from other regions, such as Alpine, Anglo-Nubian and Saanen from Brazil. However, it should be noted that they employed 21 microsatellites. Given the limited availability of genetic studies focusing on PCG populations, the insights gained from the work of Ginja et al. (2017) serve as valuable point of reference. When we examined the PCA of Ginja et al. (2017), specifically the first and second components, we found that PCG share commonalities with other Creole

populations from South America, including those from Venezuela, Bolivia, and Ecuador.

In our study, we conducted a comparative analysis of PCG genotypes alongside 15 breeds from six different countries (Supplementary Table 1). When we contrasted the PCG population with the external populations, our analyses revealed a clear differentiation among the PCG versus imported breeds. That is, the PCG from the northern Peruvian ecosystem is not crossbreeding with other breeds. This result suggests that PCG should be considered as a different population. Similar to the Peruvian Creole cattle (Arbizu et al., 2022), Peruvian farmers have been selectively choosing goats that align with their commercial requirements and adapt well to the northern Peruvian ecosystem. Therefore, the PCG is a valuable genetic resource whose conservation and use in modern breeding programs have to be conducted in the near future in Peru.

The results derived from the computation of Reynolds' genetic distance indicated that the Creole, Nubian, and Saanen breeds from Argentina exhibited a close genetic affinity with the PCG population (ranging from 0.03 to 0.05). Notably, the Nubian breed emerges as having the most immediate genetic proximity to the Peruvian population, with a genetic distance of 0.03. This result provides strong evidence that the PCG originated from Nubian breed, as also depicted by Gómez-Urviola et al. (2016). Furthermore, there are noticeable physical resemblances between these two groups. The PCG is characterized by a convex facial profile and long pendulous ears. Features include variations in coat colors, encompassing both solid and patterned shapes. Furthermore, their coats are short and fine. These physical characteristics align with the phenotype of Nubian breed, as described by the ADGA (American Dairy Goat Association, 2020).

The genetic diversity of the Peruvian Creole goat is high in terms of observed heterozygosity, with values ranging from 0.40 to 0.41 for the Lambayeque, Piura, and Tumbes groups. A previous study (Colli et al., 2018) used SNP panels to study worldwide goat populations. Similar values were observed in Saanen goats from Italy (H_o=0.415) and higher than others observed in South America (Colli et al., 2018). A work conducted by Tefiel et al. (2018) employed 18 microsatellite markers and reported mean observed and expected heterozygosity values of 0.84 and 0.94 in four Algerian goat breeds. Ginja et al. (2017) discovered that the genetic diversity of Creole populations (mean number of alleles = 5.82 ± 1.14, observed heterozygosity = 0.585 ± 0.074) was moderate and slightly lower than that found in other studies with breeds from other regions.

Ginja et al. (2017) also reported a F_{IS} value of 0.13 for a Peruvian Creole goat sample. F_{IS} values for all the other breeds were positive, from 0.01 (Neuquina from Argentina) through 0.14 (San Clemente goat from the USA). Compared to our study, this difference may be explained due to our samples are widespread in the Peru's northern region. Also, we possess a higher sample size (192) compared to Ginja et al. (2017) study (61 samples). Our results showed that F_{IS} estimates were small and positive which can infer low levels of inbreeding. Also, some level of connection among the populations was demonstrated. This may be explained due to the very common practice in Peru to sell or share the male goats from one population to another to mate with female goats from other herds from nearby localities.

Previous studies in goats and sheep indicated that production performance can decrease as a result of inbreeding (Illa et al., 2020; Kiya et al., 2019; Paiva et al., 2020; Wang et al., 2021). A study on Inner Mongolia White Cashmere goats demonstrated the effect of inbreeding on the live body weight and other fiber-related traits (Wang et al., 2021). They concluded that when the inbreeding coefficient exceeded 6.25%, according to multiple comparison analyses, the live body weight clearly demonstrated a decreasing trend. Based on our findings, goat individuals from Lambayeque, Piura, and Tumbes have experienced random mating. However, to accurately manage this crucial parameter when creating breeding programs, it is essential to have a robust and comprehensive official pedigree in place.

The NJ tree allowed us to visualize that the genetic distances between Lambayeque, Piura, and Tumbes populations are low, that is, they are in agreement with our results of F_{ST} and PCA, and are in agreement to the results of Urviola et al. (2011). Also, there is a very close genetic connection between some Lambayeque and Piura populations, similarly in Tumbes and Piura populations. This lack of differentiation represents a high level of genetic resemblance and low divergence, which may be a result of gene flow among these Peruvian populations, and also may be attributed to the adjacent regions of the populations. Similar results were reported by Mukhina et al. (2022) and Waineina et al. (2021). Our dendrogram also revealed that the Peruvian populations form a single group, and are closely related to the Creole and Angora populations from Argentina.

Despite that four genetic groups ($K = 4$) were estimated within PCG, this genetic composition is shared mostly among individuals across sampling location. However, because of the origin and demography of goat Creole populations, introgression and admixture events have been widely observed in different populations and countries (Sevane et al., 2018). Some individuals within Piura and Tumbes populations constitutes differentiated groups, and those individuals could potentially contribute to the genetic diversity of the PCG population. Further research is needed to determine the potential benefits in terms of milk and meat production of the PCG.

4.2. Description of Peruvian goat management

The goat-rearing system in northern Peru is mainly an extensive production system (grazing). The goats are bred extensively in this area, with a heavy reliance on natural resources in the vast scrub plains. These are systems whereby animals spend, all or a substantial part, of each day outdoors and obtain most of their nutrients from pasture. In these breeding types, it is common for herds to gather in grazing areas when they are geographically close. This practice may have had a depth impact on the genetic differentiation (F_{ST} = 0.01 - 0.02) between the three populations. In fact, considering the high levels of H_o in the populations, pastoralism practices have promoted introgression and high gene flow, similarly to other goat populations (Colli et al., 2018). A very close relationship between these practices and limited access to sires with better genetic performance led to the use of "better animals" phenotypically selecting the best animals without genetic information about their performance

Moreover, there have been private and government efforts to spread imported goat breeds among these local populations in northern Peru. These initiatives have aimed to improve response to Creole goats' productive performance through crossbreeding with specialized breeds. However, these imported breeds and their hybrids have not thrived due to harsh climatic conditions such as protracted drought and high temperatures. This situation more likely affected the Piura population, where the individual dispersion observed across first principal component (Fig 3A) and the conformation of populations or genetic groups in admixture analysis (individuals labelled in blue, Fig 3B).

The results of this study showed the populations' actual geographic proximity to one another. Therefore, the connection by geographic proximity has played an important role in shaping the genetic differentiation between Peruvian goat populations. A similar study was conducted in multiple breeds of Chinese goats using SNP markers (Berihulay et al., 2019) and microsatellite markers (Wei et al., 2014). When the physical distance between populations was modest, genetic divergence was minimal, but as the geographic distance between populations increased, so did genetic differentiation (Berihulay et al., 2019).

4.3. Impact of genetic diversity on production performance

The understanding Peruvian Creole goat populations' genetic diversity and population structure has significant implications for their conservation and management. Genetic diversity is essential for the

adaptation and resilience of populations to environmental changes, such as climate change and disease outbreaks. Additionally, genetic variability provides a valuable resource for selective breeding programs aimed at improving productivity and disease resistance in goat populations. Furthermore, goat populations in Peru and other countries often have cultural and economic significance, particularly for small-scale farmers and indigenous communities. Therefore, the information obtained from genetic studies such as the current one can inform policies and conservation strategies aimed at promoting the sustainable management of goat populations and supporting the livelihoods of local communities.

Currently, INIA is conducting a national public project named PROCAP, aiming to promote and improve goat livestock through research and development of new technologies. In addition, researchers of PROCAP are currently collecting additional samples from other areas of goat production in Peru to elucidate also the genetic composition of the individuals that inhabit in other ecosystems. This project will employ the information of our work to establish a conservation and modern breeding program in Peru.

5. Conclusion

The current study provides valuable insights into the genetic structure and diversity of Creole goat populations from three large producing areas in Peru using SNP molecular markers. The high diversity and low genetic differentiation between populations in northern Peru suggest a lack of genetic structure, which could be attributed to common ancestry. These findings are consistent with previous studies that have used microsatellite markers to assess the genetic variability of goat breeds in other regions. The informative panel of markers used in this study highlights the potential for the development of efficient breeding strategies that promote genetic diversity in goat populations. Future studies should focus on expanding the sample size and incorporating additional populations from other geographical areas of Peru to further enhance our understanding of the genetic parameters of these Creole goat populations.

Ethics statement

The sample collection from goat specimens was conducted in accordance with the Peruvian National Law No. 30407: “Animal Protection and Welfare”.

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CRediT authorship contribution statement

Flor-Anita Corredor: Conceptualization, Data curation, Formal analysis, Investigation, Writing – original draft, Writing – review & editing. **Deyanira Figueroa:** Data curation, Formal analysis. **Richard Estrada:** Formal analysis, Writing – review & editing. **William Burgos-Paz:** Formal analysis, Investigation, Writing – review & editing. **Wilian Salazar:** Funding acquisition, Project administration, Resources, Supervision, Writing – review & editing. **Wilder Cruz:** Investigation, Resources. **Roiser Lobato:** Funding acquisition, Resources, Supervision. **Pedro Injante:** Funding acquisition, Resources, Supervision. **David Godoy:** Conceptualization, Investigation, Writing – review & editing. **Christian Barrantes:** Conceptualization, Investigation, Supervision. **Jorge Ganoza:** Funding acquisition, Project administration, Resources. **Juancarlos Cruz:** Conceptualization, Funding acquisition, Project administration, Supervision. **Carlos I. Arbizu:** Conceptualization, Funding acquisition, Investigation, Project administration, Resources, Supervision, Writing – review & editing.

Declaration of competing interest

None.

Data availability

The data that support the findings of this study are openly available in Dryad at https://datadryad.org/stash/share/cqDmcB6Phs-2JmNXVORq-abaoMx3c-Yq6Hr-e2ztPPA

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Supplementary materials

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