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A comprehensive genome-wide analysis for signatures of selection in goat (genus *Capra*) revealed new candidate genes for environmental adaptation and productive traits

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Abstract

Background The species *Capra hircus* encompasses numerous breeds that exhibit a high level of phenotypic and genetic variability, resulting from environmental adaptation and artificial selection for meat, milk, and fiber production. Today, the global domestic goat population is steadily increasing, primarily due to their ability to adapt to harsh environments. Their worldwide distribution offers the opportunity to study how different environmental conditions and farming systems have shaped the goat genome. In this work, 194 whole-genome sequencing data sets from wild, feral, and domestic goats have been used to detect Runs of Homozygosity (ROH) and study Extended Haplotype Homozygosity (EHH) to identify the so-called 'Signatures of Selection' that uniquely characterize each goat population.

Results Common signals of selection have been identified in *CCSER1* and *ADAMTSL3*, two genes associated with body development, which were under selection in feral and wild goats, and in Angora and Boer breeds, respectively. Similarly, both feral and cashmere breeds exhibited selection signals in *PCDH15*, a gene linked to environmental adaptation. Selection in wild and feral goats was primarily observed at loci related to environmental adaptation and immune response. Moreover, selection signals related to productive traits such as milk and meat production were still detectable in feral populations. The Angora goat genome showed selective pressure mainly targeting efficient reproduction and body development, with relatively low pressure related to environmental adaptation. The four cashmere breeds studied displayed selection signals predominantly in genes involved in environmental adaptation, immune response, and hair follicle biology. Several signatures of selection related to environmental adaptation were also observed in both meat- and milk-producing goats, as well as in genes associated with reproduction, milk, and meat production.

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Conclusion These findings suggest that, despite long-term domestication, natural and environmental selection have shaped the goat genome more than artificial selection. Identifying genes linked to adaptation and fitness is vital for future livestock production amid climate change. Our study highlights genetic loci related to environmental adaptation and disease resistance, offering a foundation for targeted breeding and conservation strategies to enhance resilience and sustainability in goat populations.

Keywords Signature of selection, Goat, Environmental adaptation, Runs of homozygosity, Extended haplotype homozygosity

Background

The global domestic goat population is steadily increasing, primarily due to their remarkable resilience and adaptability to harsh environments, including extreme temperatures, poor pasture quality, high altitudes, and exposure to pathogens [1]

Today, the species *Capra hircus* encompasses numerous breeds that exhibit a high level of phenotypic and genetic variability, resulting from environmental adaptation and artificial selection for meat, milk, and fiber production. In this regard, Alpine, Saanen, and Poitevine breeds, initially selected in Europe, are among the most widely distributed dairy breeds [2]. Meanwhile, the Creole and Boer goats, developed in Guadeloupe and South Africa, respectively, are two popular breeds primarily raised for meat production [3]. Centuries of selective breeding for fiber production have resulted in the development of two primary types of goats: Angora and Cashmere. The Angora goat, originally from the Ankara district in Turkey, is bred for mohair production and has since spread to Europe, the Americas, and Australasia [4]. The Chinese Cashmere goat population, on the other hand, includes various breeds, such as the widely common Liaoning Cashmere breed from Liaoning Province [5], as well as local breeds in Inner Mongolia, including the Alashan Cashmere goat [6], Aerbasi Cashmere goat [7], and Erlangshan Cashmere goat [8].

In the face of climate change, identifying genetic loci related to environmental adaptation and selecting variants that enhance animal fitness are essential for the future of livestock production. Indeed, the rise in temperatures harms animal production, impacting body growth, fiber, meat, and milk yield and quality, as well as reproductive performance, metabolic health, and immune response. Additionally, desertification is reducing the carrying capacity of rangelands and the resilience of pastoral systems [9]. Furthermore, new infectious diseases are likely to continue emerging, with concerns that climate change accelerates this trend, posing additional risks to public health, food security, and livelihoods [10].

The identification of loci associated with an individual's ability to cope with environmental changes and stressors, as well as those linked to productive traits, can be achieved through various methodological approaches. In this regard, analyses such as detecting Runs of Homozygosity (ROH) [11, 12], or studying Extended Haplotype Homozygosity (EHH) [13], enable the identification of so-called 'Signatures of Selection' (SOS) - genomic regions characterized by reduced diversity around naturally or artificially selected loci. In a population, beneficial haplotype variants can increase in frequency over time. They may eventually become fixed, resulting in all individuals carrying the advantageous allele [14], which can be detected as an SOS.

In this context, goats serve as an excellent model for studying how both human-driven and natural selection have shaped the animal genome, owing to the species' unique characteristics. The worldwide distribution of goats provides an opportunity to study the diverse environmental selective pressures on domestic populations, which are subjected to a range of environmental conditions and farming systems. Moreover, several breeds have been selected, allowing for the study of human selective pressure on the main productive traits, i.e., milk, meat, fibre, and skin. In this regard, cashmere goat breeds are extraordinary populations reared under extensive and extremely harsh conditions in which natural selection may play the leading role in shaping the genome. Besides, the presence of nine ancestral wild species of the genus *Capra* distributed in scattered locations across Eurasia and North Africa [1] allows us to study the genome of the goat population, where the environment should be the sole selective force driving the shaping of the genome. Similarly, the presence of feral populations, such as the European Montecristo and Old Irish feral goats [15, 16] or the Australian Rangeland feral goats [17], offers an animal model in which both artificial and natural selection may have played a role in shaping the goat genome.

Building on this, the present work aims to provide novel insights through a comprehensive genome-wide analysis of domestic, feral, and wild goats, focusing on loci associated with adaptive and productive traits. We identified signatures of selection (SOS) that are population-specific across 12 distinct goat groups, as well as cross-population signatures of divergent selection through six pairwise comparisons. The findings offer valuable information as a foundation for developing a resilient goat breeding system.

Methods

Sample collection

A total of 221 Whole Genome Sequencing (WGS) datasets were used for the study. All the samples were generated by previous projects (PRJEB37122, PRJEB4371, PRJNA310684, PRJNA338022, PRJNA378894, PRJNA387635, PRJNA399234) and were retrieved from the NCBI Sequence Read Archive (SRA) (Supplementary Table 1A). The SRA files were downloaded to our server and converted to FASTQ files.

WGS quality control, variant calling and sample relatedness check

The quality of the FASTQ files was checked using FastQC [18], and adapter trimming was performed with Trimmomatic [19]. Read pairs were mapped to the goat reference genome ARS1.2 using Burrows-Wheeler Alignment MEM (BWA-MEM) [20]. The X chromosome and the unplaced-scaffold sequences were removed from the reference genome FASTA file before performing the alignment.

BAM files were processed using the Genome Analysis Toolkit (GATK) [21], performing base recalibration using the set described in Denoyelle et al. [22]. The HaplotypeCaller method was then used for variant calling. The resulting VCF containing the genomic variant calling was converted to PLINK file using VCFtool [23].

All the samples were checked for missingness, and three samples were removed due to a high level of missingness (ranging from 31% to 58%). To obtain independent samples, remove potentially duplicate samples, and reduce the underlying population structure that could bias the estimation of ancestry and ROHs, pairs with Identity-By-Descent (IBD) PI-HAT≥0.5 were identified using PLINK 1.9; 24 samples were removed due to PI-HAT values ranging from 0.5 to 1. All the variants with minor allele frequency (MAF) <1% and genotyping rate <95% were removed. Missing genotypes of the remaining 194 samples were imputed using Beagle (v5.0) [24] with the default parameters as suggested by Yang [25]. The final dataset used for the study included 194 goats with PI-HAT values ≤ 0.5 and a total of 6,376,154 variants.

The final breed-specific dataset included 23 Liaoning cashmere, 19 Erlangshan cashmere, 16 Alashan cashmere, 15 Aerbasi cashmere, 19 Saanen, 18 Alpine, 17 Angora, 15 Creole, 13 Boer, 12 Poitevine, 11 Feral goats, 16 Wild goats (Supplementary Table 1B). The WGS sample description and exclusion criteria are reported in the Supplementary Table 1A.

Population structure analysis

To perform population structure analysis, we removed from the joint called variant file all the variants with a minor allele frequency (MAF) <5% and we pruned the remaining variants by Linkage Disequilibrium (LD) using the PLINK command "--indep-pairwise 1,500 150 0.1". A total of 190,909 variants and 194 samples were used to run the Principal Component Analysis (PCA) and admixture analyses. PCA was performed using PLINK 1.9. The results were plotted using the ggplot R package [26]. Population structure analysis was performed using ADMIXTURE (v. 1.23) with K values ranging from 3 to 12. The correct value for K was determined according to ADMIXTURE's cross-validation procedure [27], and the results were plotted using STRUCTURLY [28].

Runs of homozygosity (ROHs) detection and genomic inbreeding (F_{ROH}) estimation

To detect ROHs, the dataset was not pruned for low MAF (< 0.5%) or high LD (r2 >0.9), as suggested by Meyermans [29], and we used the following PLINK parameters: "--homozyg-kb 100 (or 500, 2000, 3000, 4000 and 8000) --homozyg-snp 20 --homozyg-gap 500 --homozyg-window-missing 1 --homozyg-window-het 3". Different minimum lengths of a ROH were evaluated by setting the option --homozyg-kb to 100, 500, 1000, 2000, 4000 and 8000 kb as suggested by Signer-Hasler [30]. The lower level of length was chosen according to Silva [31] and Signer-Hasler [30]. The "--homozyg-window-het" was selected according to the information provided by Quinodoz [32] and Silva [31]. As 100-kb segments allow to trace back common ancestors 500 generations ago, whereas a 1-Mb ROH-segments indicate that the homozygosity originated from a common ancestor 50 generations ago [33], all the ROHs detected were divided into six groups according to segments length i.e. 100 to 500 kb, 500 to 1,000 kb, 1,000 to 2,000 kb, 2,000 to 4,000 kb, 4,000 to 8,000 kb and finally >8,000 kb.

For the identification of overlapping ROHs and all the subsequent analyses, feral and wild goat samples (three breeds and five species, respectively) were grouped together into two groups named "Feral" (FER) and "Wild" (WIL) as reported in Table 1. We kept ROHs overlapping in at least 70% of the sample, according to each breed/group, starting from a minimum ROH length of 100 kb.

Six different inbreeding coefficients based on ROHs length (F_{ROH}) were computed for each group by applying the formula proposed by McQuillan [34]:

$$F_{ROH} = \frac{L_{ROH}}{L_{aut}}$$

where L_{ROH} is the total length of all ROHs in the individual's genome, and L_{aut} is the length of the autosomal genome.

ANalysis Of Variance (ANOVA) was used in IBM SPSS Statistics 21 software to test for significant differences in the number of ROHs as well as for the F_{ROH} values

Table 1 Genes annotated and those identified as under selection across the 12 groups analyzed

Breed/Group	Number of annotated genes	Number of genes considered under selection[a]
Erlangshan	2,487	10
Aerbasi	2,018	7
Alashan	1,958	12
Liaoning	845	10
Wild	776	9
Feral	314	9
Boer	135	10
Poitevine	97	21
Angora	81	10
Creole	80	8
Saanen	48	5
Alpine	34	6

[a]variants within the top 0.1% of the SNPs distribution

between the 12 groups, setting a statistical significance threshold of $P < 0.05$.

Extended haplotype homozygosity (EHH), genome-wide fixation index and nucleotide diversity

The EHH analysis, which includes both the Integrated Haplotype Score (iHs) and the cross-population XP-EHH analysis, was performed using the software Selscan [35] with default parameters, considering only the SNPs with a MAF>5%.

Genome-wide fixation index (Fst, i.e. Weir and Cockerham's estimator), and nucleotide diversity (θπ ratios) were computed using VCFtools [23] by applying the following parameters proposed by Wang et al. [36]:

Fst: --fst-window-size 50,000 --fst-window-step 20,000 --maf 0.05 --max-missing 0.90

Θπ: --window-pi 50,000 --window-pi-step 20,000 --maf 0.05 --max-missing 0.90

For the cross-population analysis (i.e.: XP-EHH, Fst and θπ ratios), the sample was divided into six goat groups: fibre-producing (n = 90), milk-producing (n = 49), meat-producing (n = 28), domestic (n = 167), wild (n = 16), and feral (n = 11) (Supplementary Table 1C).

Identification of signatures of selection

Genomic intersections between overlapping ROHs present in at least 70% of the samples and the outlier windows with the top 5% of extreme iHs values were identified as specific selection signals within each breed/group. The resulting file was converted into VCF format, and the variants were annotated using VEP [37]. We then calculated the distribution of total SNPs across all genomic intersections identified for each breed/group, considering genes under putative selection if they contained annotated variants within the top 0.1% of the SNPs distribution (Supplementary Table S2).

In the cross-population analysis, we adopted a similar approach, considering the genomic intersection between the top 5% extreme XP-EHH values and the top 2.5% of extreme Fst and Θπ values.

Gene-based enrichment analysis

Gene enrichment analysis was performed using the genes encompassing the selection signals with the web-based tool ShinyGO [38].

A comprehensive flowchart of the steps applied to the full dataset is reported as Fig. 1.

Results

Population structure and admixture

PCA was used to visualize the relationships between the groups of goats considered in the analysis. The plot showed the presence of three main clusters, with the first two components explaining 15.78% of the total variability (Figure 2). A more detailed PCA plot, considering each breed/species (not grouped by production attitude), is provided as Supplementary Figure 1. The cross-validation (CV) error test was performed for each K value to determine the most probable number of clusters. The CV errors ranged from 0.542 to 0.602 for K=3 to K=12, respectively, suggesting that K=3 was the most probable value. The admixture plot for K=3 is shown in Figure 3. A more detailed admixture plot with the SRA ID reported for each sample is provided in the Supplementary Figure 2.

Runs of homozygosity (ROHs) and genomic inbreeding values (F_{ROH})

Descriptive statistics for ROHs and F_{ROH} values are reported in Supplementary Table 3. ANOVA showed significant differences in the F_{ROH} values among all the groups.

The four cashmere breeds showed the highest level of F_{ROH} (100–500 kb) with values of 0.37, 0.34, 0.33, and 0.31 for Liaoning (LIA), Erlangshan (ERL), Aerbasi (AER), and Alashan (ALA), respectively. WIL goats, Creole (CRE), and FER showed levels of F_{ROH} (100–500 kb) of 0.27, 0.22, and 0.20, respectively. Finally, Saanen (SAA), Alpine (ALP), Boer (BOE), Angora (ANG), and Poitevine (POI) showed a level of F_{ROH} (100–500 kb) of 0.17, 0.16, 0.16, 0.16, and 0.15, respectively.

A similar situation was observed for F_{ROH} (500-1,000 kb), for which the highest levels of inbreeding were observed for the four cashmere breeds (range 0.20 to 0.14), followed by WIL (0.08).

The remaining breeds showed the lowest level of F_{ROH} (500-1,000 kb) values ranging from 0.04 to 0.01.

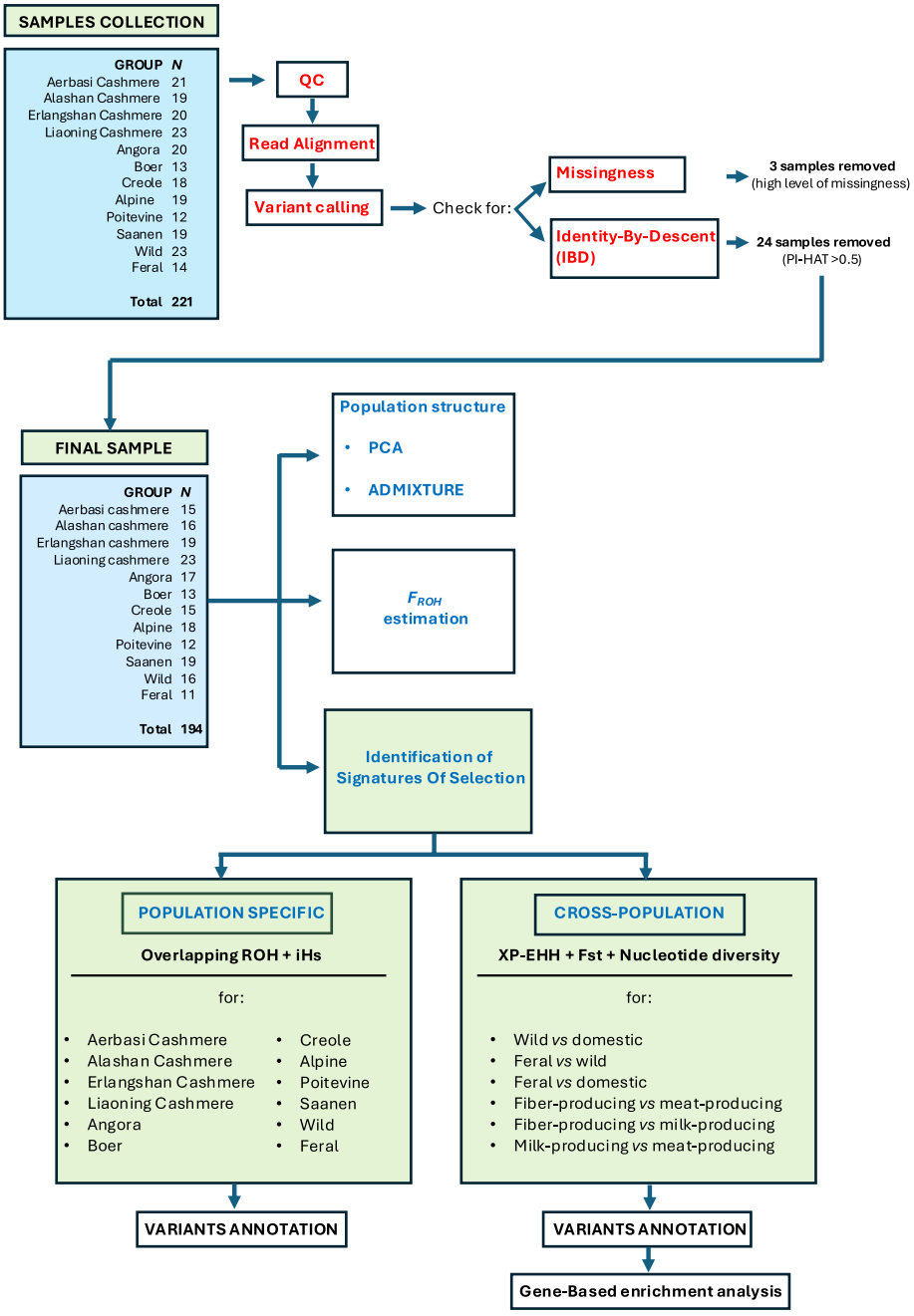


Fig. 1 Flow-chart of the workflow adopted in the data processing of the full dataset QC = Quality control

The highest values of F_{ROH} (1,000–2,000 kb) were found for the four cashmere breeds (range 0.17 to 0.10) and WIL (0.07). The F_{ROH} (1,000–2,000 kb) values for the remaining breeds ranged from 0.04 to 0.01. F_{ROH} (2,000–4,000 kb) values showed the highest level for ALA, AER, and ERL (range 0.13 to 0.10), followed by WIL, FER, LIA, BOE, ANG, and POI (0.06 to 0.03). Finally, SAA, CRE, and ALP showed the lowest level of F_{ROH} (2,000–4,000 kb) (0.01). ALA and WIL goat showed the highest level of F_{ROH} (4,000–8,000 kb) with values of 0.06 and 0.05, respectively. AER, FER, BOE, and ANG showed a comparable level of inbreeding with F_{ROH} (4,000–8,000 kb) value of 0.04. POI and ERL showed a F_{ROH} (4,000–8,000 kb) value of 0.03, followed by LIA (0.02). Finally, a F_{ROH} (4,000–8,000 kb) value of 0.01 was found for ALP, SAA, and CRE.

The highest F_{ROH} (>8,000 kb) values were observed for wild goats (0.1), followed by AER and BOE with values of 0.04 and 0.03, respectively. A F_{ROH} (>8,000 kb) value of 0.02 was observed for POI, FER, ANG, LIA, and ALA.

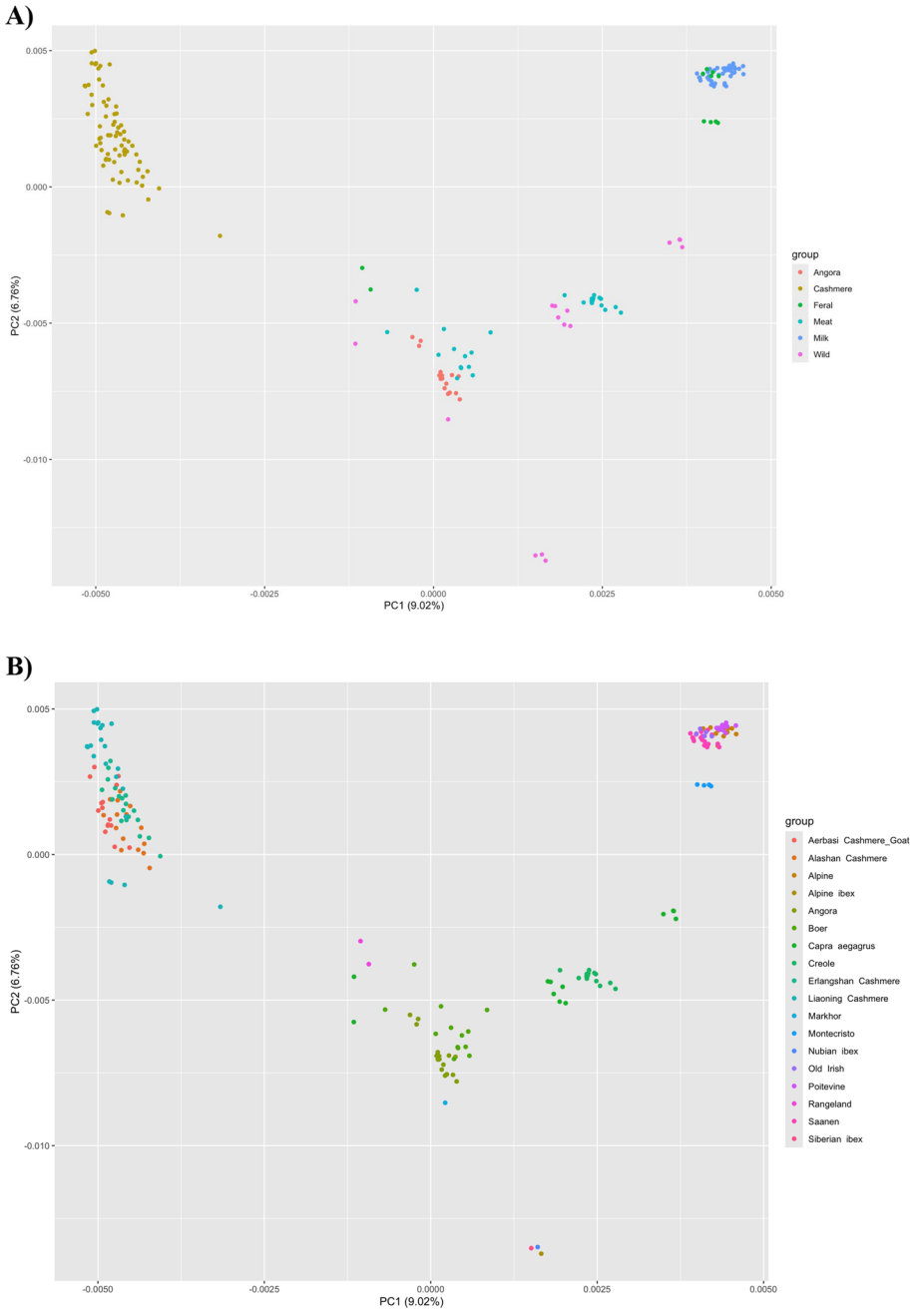


Fig. 2 **A** PCA plot for the first two dimensions, illustrating the relationships between goat populations grouped by production attitude. **B** PCA plot for the first two dimensions, considering each individual breed/species. Each dot represents an individual sample. The x-axis displays the first principal component (PC1), while the y-axis represents the second principal component (PC2). The percentage of total variation explained by each axis is indicated in parentheses

Hard detectable F_{ROH} (>8,000 kb) values were observed for CRE, ALP, ERL, and SAA, for which the values ranged from 0.008 to 0.006.

Overlapping ROHs

Cashmere goat breeds showed the highest number of overlapping ROHs: 48,746, 35,011, 34,859, and 33,830 overlapping ROHs were found for ERL, LIA, AER, and ALA cashmere goat, respectively. WIL and FER showed 14,414 and 5,426 overlapping ROHs, respectively. A lower number of overlapping ROHs was found for the other breeds; in fact, the number of overlapping ROHs detected for BOE, CRE, POI, ANG, SAA, and ALP was 2,439, 1,838, 1,778, 1,635, 1,025, and 680, respectively (Supplementary Figure 1).

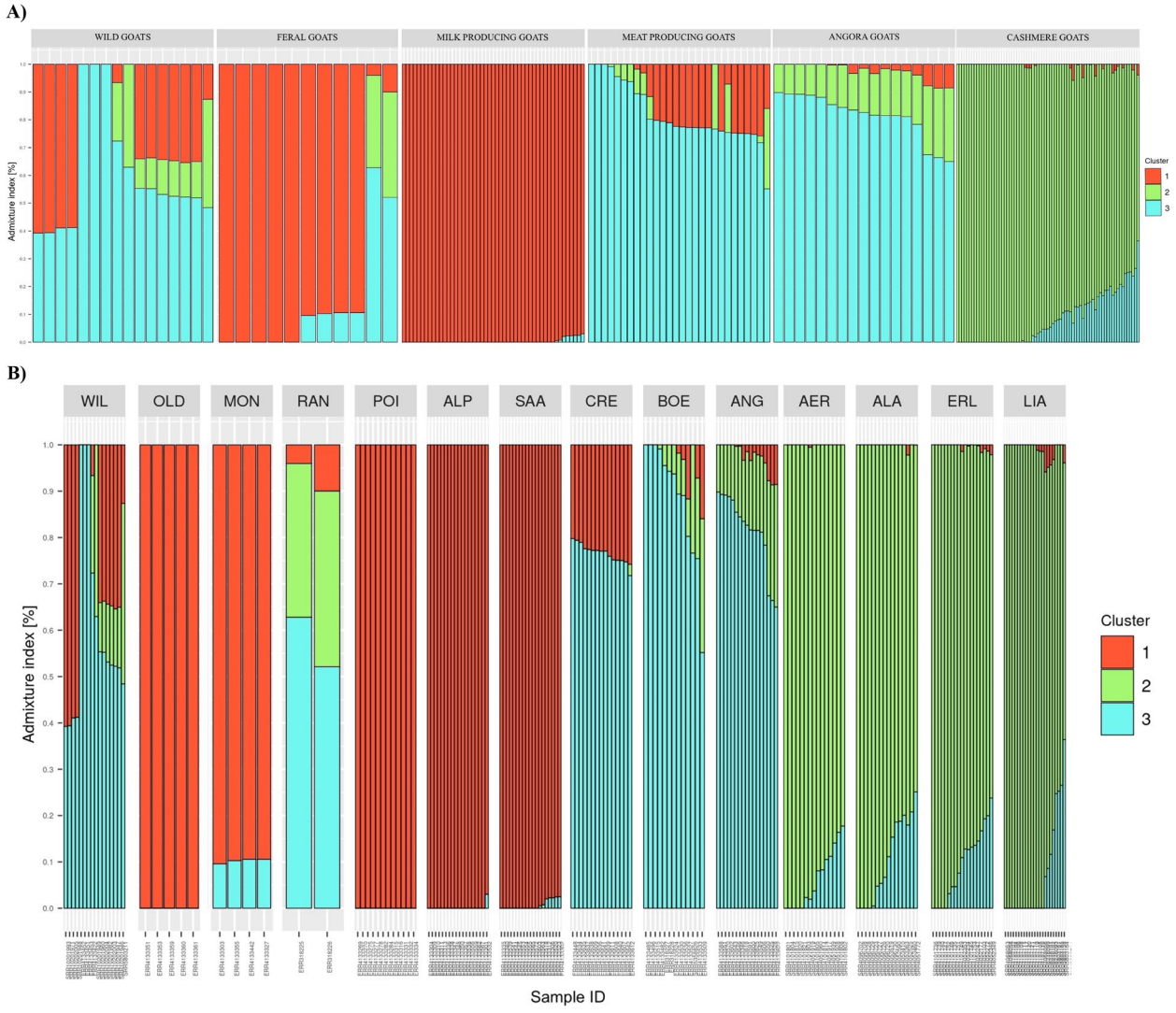


Fig. 3 **A** Admixture analysis plot displaying population assignments for K = 3, with samples grouped by production attitude. **B** Admixture analysis plot showing population assignments for K = 3, considering each individual breed/species (the SRA ID for each sample is indicated on the x-axis). A distinct color represents each cluster, and each individual is represented by a vertical line divided into K colored segments, with heights proportional to their genotype membership in the clusters. WIL = wild goats; OLD = Old Irish feral goats; MON = Montecristo feral goats; RAN = Rangeland feral goats; POI = Poitevine goats; ALP = Alpine goats; SAA = Saanen goats; CRE = Creole goats; BOE = Boer goats; ANG = Angora goats; AER = Aerbasi cashmere goats; ALA = Alashan cashmere goats; ERL = Erlangshan cashmere goats; LIA = Liaoning cashmere goats

Signatures of selection

The filtered variants located on the overlapping ROHs and outlier windows with top 5% of extreme iHs values (Supplementary Figure 2) were 24,020 for Erlangshan, 23,382for Alashan, 23,063 for Aerbasi, 7,647 for Liaoning, 7,195 for wild goats, 3,187 for feral goats, 1,060 for Boer, 788 for Angora, 689 for Creole, 647 for Poitevine, 449for Alpine and 443 for Saanen. The variants were annotated on a total of 5,347 genes (Supplementary Table 4A-M). As reported in Table 1, 2,487, 2,018, 1,958, and 845 genes were annotated for ERL, AER, ALA, and LIA, while 776, 314, and 135 genes were annotated for WIL, FER, and BOE. Finally, 97, 81, 80, 48, and 34 loci were annotated for POI, ANG, CRE, SAA, and ALP.

After filtering each population for the genes showing a number of annotated variants corresponding to the top 0.1% of the extreme SNP value distribution, the number of loci detected under selection was 21 for POI, 12 for ALA, 10 for ANG, LIA, ERL, and BOE, respectively, 9 for WIL and FER, respectively, 8 for CRE, 7 for AER, 6 for ALP, and 5 for SAA (Table 1).

Cross-population signatures of selection

We conducted pairwise analyses between the selected groups to identify potential signals of divergent selection.

Cross-population analysis between WIL and domestic goats (fibre, meat and milk producing breeds) showed 1,339 significant SNPs located on 205 genes

Table 2 Genes related to environmental adaptation, immune response, body and growth traits that show signatures of selection

Environmental/climatic adaptation		Immune response		Body and growth traits	
Gene	**Group/breed[a]**	**Gene**	**Group/breed[a]**	**Gene**	**Group/breed[a]**
TRMT44	WIL	*RNF213*	WIL	*ADAM12*	WIL
RUND-C3B		*BCHE*	FER	*CCSER1*	WIL-FER
ENAH		*TUBGCP5*	ANG	*CCSER1*	FER
CNGA4		*SEMA5A*	LIA	*MCM3AP*	ANG
CSMD3		*BPI*	AER	*POP1*	
RBM45		*NEDD4L*	ALA	*ADAMTSL3*	ANG-BOE
FAM83B	FER	*MYO5B*		*CDH18*	LIA
PCDH15		*IDO1*	CRE	*TNS3*	
GRIN2B	AER	*FCHSD2*	BOE	*NALCN*	
ATRNL1	ERL	*TNFAIP8L3*	ALP	*SNX29*	LIA-ERL
PDE11A		*ZDHHC13*		*SORCS1*	
PHF14		*SELL*		*EIF5B*	CRE
CDK14		*PSD3*	POI	*DKK3*	
DISC1		*UQCC1*		*TMEM132C*	BOE
ANO2	ALA	*RPF2*		*NR2E1*	
TENM4		*MGAT5*		*DIAPH3*	ALP
KLHL29		*UGGT2*	SAA	*NLN*	POI
GRIK4				*FAM135A*	
THSD7B	ALA-LIA			*NFS1*	
PCDH15					
REV1	CRE				
OLA1					
TNKS	BOE				
ZFHX4					
GRXCR2					
PRMT8					
KLHL3	POI				
PPA2					
AGAP3					
EXOC6					
XPO4	SAA				
MICU2					
PNPT1	POI-SAA				

WIL Wild goats, *FER* Feral goats, *AER* Aerbasi cashmere goats, *ALA* Alashan cashmere goats, *ERL* Erlangshan cashmere goats, *LIA* Liaoning cashmere goats, *ANG* Angora goats, *CRE* Creole goats, *BOE* Boer goats, *ALP* Alpine goats, *SAA* Saanen goats, *POI* Poitevine goats

[a]Group/breed showing significative selection signals

(Supplementary Table 5). Moreover, 20 significantly enriched pathways have been found (Supplementary Table 5).

Cross-population analysis between FER and domestic goats showed 354 significant SNPs located on 71 genes, with no significantly enriched pathway found (Supplementary Table 6). Similarly, FER and WIL identified 98 significant SNPs located in 22 genes, but no significantly enriched pathways were found (Supplementary Table 7). A low number of SNPs (2 to 1) were found in the 22 annotated genes.

Analysis between fiber-producing (cashmere and ANG) and meat-producing goats showed 23 significant SNPs located on seven genes, where four significantly enriched pathways were observed (Supplementary Table 8).

Fiber-producing (Cashmere and ANG) and milk-producing goats showed 27 significant SNPs under divergent selection, located on 13 genes primarily associated with adaptation and productive traits (Supplementary Table 9), though no pathways were significantly enriched. Similarly, the comparison between milk- and meat-producing goats revealed 58 significant SNPs across 17 genes mainly linked to productive traits (Supplementary Table 10), with no pathways found to be significantly enriched.

Manhattan plots for XP-EHH, Fst, and nucleotide diversity analyses are provided in the Supplementary Figures 3–5.

Discussion

Population structure and F_{ROH}

PCA analysis revealed the presence of three distinct and separated clusters. The four cashmere goat breeds clustered together, clearly differing from the rest of the goat population. Similarly, feral and milk-producing goat breeds are grouped, suggesting a low level of genetic differentiation between the two groups, whereas ANG, meat-producing goats, and WIL tend to form a larger cluster.

Admixture analysis identified three main clusters within the goat populations, each clearly distributed based on their productive purpose (i.e., milk, meat, and fibre). However, the WIL group was an exception, being the most heterogeneous and showing the highest level of co-ancestry with both domestic goats and FER. FER showed a high level of genetic admixture with the dairy goat breeds, particularly evident when considering Old Irish and Montecristo goats (Supplementary Figure S2), suggesting a gene pool selected for milk production. Strong admixture with a meat-producing breed was observed for Rangeland feral goats, suggesting a selection more prone to meat production (Supplementary Figure S2).

Among the fibre-producing breeds, ANG showed a high level of genetic admixture with meat-producing breeds. In contrast, the four Cashmere goat breeds formed a distinct cluster with very low admixture with other breeds/groups. However, a low level of co-ancestry with meat-producing breeds can be observed for some cashmere goats. It is essential to note that, unlike the transboundary dairy and meat-producing goat breeds, the analyzed cashmere breeds are exclusively raised

in China and are therefore less susceptible to genomic introgression from other populations.

Results from F_{ROH} computation showed that the four cashmere goat breeds studied were characterized by the highest levels of both ancient and recent inbreeding (computed on a range of ROH lengths from 100 to 4,000 kb), suggesting higher selective pressures on these populations compared to the other goat groups studied. High F_{ROH} values, comparable to those observed for cashmere breeds, were observed for WIL, which also showed the highest level of recent inbreeding (F_{ROH} >8,000 kb) due to a potential bottleneck in the wild population. Conversely, all the F_{ROH} values observed for the remaining groups were low, decreasing to values < 0.1 when the computation of F_{ROH} started from a minimum ROH length of 500 kb. This outcome suggests lower selective pressures in these breeds, resulting in a higher level of genetic variability.

Moreover, it is worth noting that such transboundary and widespread breeds are less susceptible to genetic erosion caused by potential population bottlenecks.

Distribution of signatures of selection among the goat populations

SOS uniquely characterizes each goat population as the result of both natural and artificial selective pressures in the different environments, farming systems, and breeding goals to which each population is subjected. The identified selected genes can be classified according to their function in loci related to environmental/climatic adaptation, immune response, body and growth traits, reproduction, milk traits, hair follicle biology, feed intake and efficiency, general metabolism, and temperament. As reported in the Figure 4A, B, the highest number of genes under selection were related to environmental adaptation traits, body traits, and immune response, while a lower number of genes were associated with the other traits.

Some considerations can be made on the general distribution of the SOS in the goat populations studied. Unsurprisingly, the highest number of selected SNPs in WIL were found in loci primarily associated with environmental adaptation (*TRMT44, RUNDC3B, ENAH, CNGA4, CSMD3* and *RBM45*) and immune response (*RNF213*), indicating that natural selective pressure is the main force shaping the genome in the wild harsh environments (Supplementary Table 11).

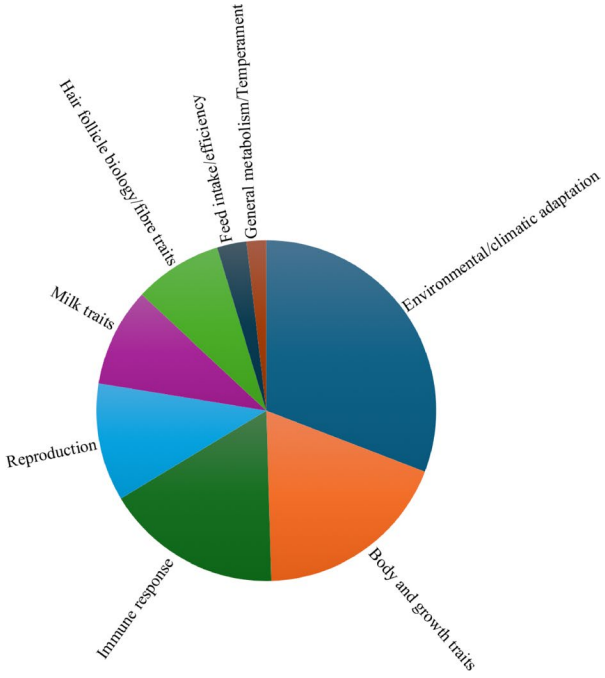
As expected, environmental selective pressure played some roles in shaping the FER genome, leading to the selection of genes involved in environmental adaptation (*FAM83B, GOT1,* and *PCDH15*) as well as immune response (*BCHE*). Moreover, selection signals were still detectable in this population for genes involved in productive traits such as milk (*TMEM165* and *NOA1*) and meat production (*CCSER1*) (Supplementary Table 12). The ANG genome exhibited selective pressure primarily directed toward efficient reproduction (signatures of selection in genes such as *KDM1A, SMC1B, ADAMTSL1* and *TEX46*) and body development (selection signals in *MCM3AP, ADAMTSL3* and *POP1*), with low environmental selective pressure detected for this breed. Notably, none of the genes under selection in our sample were associated with fiber production (Supplementary Table 13). The four cashmere goat breeds studied showed SOS mainly on genes related to environmental adaptation (*ATRNL1, GRIN2B, PDE11A, PHF14, CDK14, DISC1, ANO2, TENM4, KLHL29, GRIK4, THSD7B* and *PCDH15),* immune response and hair follicle biology (*SV2B, PKHD1, FER, FGF12, ASTN2* and *GPR158*) reflecting an extensive goat farming system addressed to fibre production where the extreme environmental conditions strongly influenced the selection of the animals (Supplementary Table 14). In this regard, it is essential to note that most genes selected for environmental adaptation have been identified in the three Inner Mongolian breeds: ALA, ERL, and AER. In contrast, only two loci have been detected under selection in the LIA breed, suggesting that environmental pressures have played a lesser role in its selection. Conversely, the highest number of genes under selection in LIA were related to body traits (*CDH18, RIMS1, TNS3, NALCN, SNX29,* and *SORCS1*), which are putative results of a selection also aimed at improving meat production [39]. Similar to what has been observed in cashmere goat breeds, the distribution of SOS in meat-producing goats indicates a livestock production system where selection, primarily focused on meat production (selection signals on genes such as *EIF5B, DKK3, TMEM132C, NR2E1* and *ADAMTSL3*), is significantly influenced by environmental and climatic selective pressures (signatures of selection detected in the genes *REV1, OLA1, TNKS, ZFHX4, GRXCR2* and *PRMT8*) (Supplementary Table 15). Finally, a high number of genes related to environmental adaptation (*KLHL3, PPA2, AGAP3, EXOC6, XPO4* and *MICU2*) and immune response (*PSD3, UGGT2, TNFAIP8L3, UQCC1, RPF2, ZDHHC13, SELL* and *MGAT5*) were also found to be under selection in milk-producing breeds, alongside loci involved in reproduction (*CEP250, CAMK1D, LMTK2, THAP11, STIM1* and *TMC1*), milk production (*TFDP2, SLC18A2* and *COX15*), and meat production (*DIAPH3, NLN, FAM135A* and *NFS1*). Regarding the genes under selection for productive traits, the highest number of genes under selection has been found in POI, while very few loci showed SOS in ALP and SAA (Supplementary Table 16).

Signatures of selection for environmental adaptation

As shown in Table 2, the highest number of loci under selection for environmental adaptation was detected in

A

Suggested functional classification	*n* of genes	%
Environmental/climatic adaptation	33	31,1
Body and growth traits	20	18,9
Immune response	17	16,0
Reproduction	12	11,3
Milk traits	10	9,4
Hair follicle biology/fibre traits	9	8,5
Feed intake/efficiency	3	2,8
General metabolism/Temperament	2	1,9



B

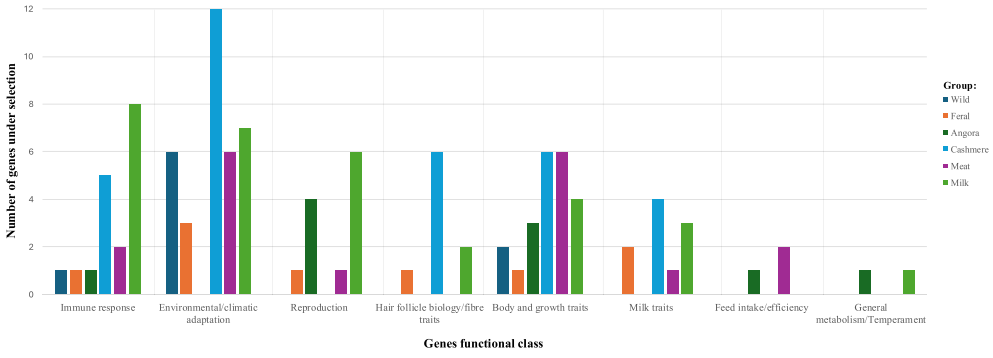


Fig. 4 **A** Number of genes showing selective sweeps according to their functional classification. **B** Distribution of genes under selection across the goat group, categorized by their functional classification. The x-axis displays the functional classes of genes, while the y-axis represents the number of genes under selection

cashmere goat breeds, where 12 genes exhibited selection signals. This was followed by milk-producing goats, which showed signals of selection in seven genes, while meat-producing goat breeds and WIL each revealed six genes under selection. Finally, three genes showed selection signals in FER while none have been detected in ANG and ALP, suggesting a low environmental selective pressure for these two breeds.

Among the genes related to environmental adaptation selected in the four studied cashmere goat breeds**,** ALA exhibited selection signals in *ANO2*, *TENM4*, *KLHL29*, and *GRIK4*. These genes are known to be involved in high-altitude adaptation to hypoxic environments, as well as in responses to high-dose ultraviolet radiation and heat stress in various species [5, 40–44]. ERL exhibited SOS in *PDE11A*, *CDK14*, and *ATRNL1*, which are associated with adaptation to desert environments and thermotolerance to environmental heat stress [45–47]. *DISC1* and *PHF14* are both involved in the mechanisms that enable hypoxia adaptation to high altitudes in various species [48, 49]. Similarly, AER showed selection signals for *GRIN2B*, a gene involved in high-altitude adaptation and the regulation of circadian rhythms [50, 51]. Finally, two loci, *PCDH15* and *THSD7B*, were identified as being under selection in both AER and LIA. The *THSD7B* gene may be associated with adaptation to high-altitude and harsh environments, as it has been detected under selection in species such as cattle raised in an extensive alpine farming system [52] and in the Chinese Moupin pika, which is confined to Chinese alpine habitats and

highly sensitive to environmental changes [53]. Notably, *PCDH15*, a gene essential for maintaining normal retinal and cochlear function, showed selection signals in AER, LIA, and FER [54, 55]. This locus plays various roles in adaptation; it has been identified as under positive selection for vision and hearing in Arctic wolves, playing a crucial role in adaptation to the wild environment [56]. Additionally, it has been reported as a signal of directed selection for local adaptation to harsh environments in indigenous populations of Siberia [57]. Moreover, *PCDH15* appears to be involved in resistance against endoparasite infections (*Dictyocaulus* and *Fasciola*) in cattle [58] and in the regulation of body temperature in mice [59]. Concerning the milk-producing goat breeds**,** seven environmental adaptation-related genes were under selection in POI and SAA, while none were observed in ALP. POI showed SOS in *KLHL3*, *PPA2*, *AGAP3,* and *EXOC6* reported as related to high-altitude adaptation, heat stress response, and thermotolerance in different species [60–63], while two genes under selection in SAA, *XPO4* and *MICU2,* were already involved in local adaptation and stress tolerance in local goat breeds [64, 65]. Both POI and SAA showed selection signals in *PNPT1*, a gene involved in cellular adaptation to hypoxia, which is described as important for adaptation in goat [64]. Different loci related to environmental adaptation were identified under selection in meat-producing breeds. Specifically, BOE showed selection on *TNKS, ZFHX4, GRXCR2,* and *PRMT8,* whereas *REV1* and *OLA1* were identified under selection in CRE. *TNKS* has been suggested as a gene involved in adaptation to variations in local environmental conditions, including feed availability and quality, in Russian cattle breeds [66]. Both *ZFHX4* and *GRXCR2* were reported as selection signatures for climate adaptation in Chinese local cattle [67, 68]. Moreover, *ZFHX4* is differentially expressed in sheep cardiac tissue in response to chronic hypoxia and altitude adaptation [69], similarly to *PRMT8,* which modulates mitochondrial bioenergetics and neuroinflammation in the central nervous system after hypoxic stress [70] and is suggested as a gene related to environmental adaptation in South African cattle breeds [71]. Finally, *REV1* is a gene related to the response to UV radiation and adaptation to high altitudes in local sheep breeds from Russia, as well as in wild boar [72]. In contrast, *OLA1* has been described as important in the thermal adaptation to the tropics, West Africa, and Indian cattle. Such a gene is essential for regulating cellular stress responses, such as oxidative stress, and improving thermal resistance in mammalian cells [73, 74]. Six genes involved in environmental adaptation were under selection in WIL. Among these genes, *TRMT44* has been suggested to enhance climatic adaptation and resistance to pneumonia in sheep [75]. Additionally, methylation of this gene has been observed in fish reared in two contrasting environments [76]. Similarly, *RUNDC3B* has been associated with hypoxic survival and adaptation to high altitudes in Ethiopian goats [77]. *CSMD3*, on the other hand, confers resistance to cold and harsh environments; traces of positive selection for this gene have been observed in mammoths, polar bears [78], and yaks [79], all species adapted to thermal stress in extremely cold Arctic or Antarctic environments. WIL showed strong SOS in *ENAH*, a gene involved in cardiac development and muscle structure. Such a locus has been recently described as an exercise-related gene under selection in Mongolian horses with excellent stress resistance and adaptation to the cold and harsh plateau conditions [80]. SOS in WIL has been observed in *CNGA4*, an olfactory channel which plays a central role in the transduction of odorant signals and subsequent adaptation. Rapid olfactory adaptation enables an animal to continually assess changes in the odor environment and intensity that are essential for following odor plumes and trails [81]. Moreover, *CNGA4* has been suggested as a candidate gene that drove adaptations during goat domestication, enhancing immunity and defense against external adverse factors [82]. Finally, SOS has been detected in WIL for *RBM45,* a highly conserved gene among metazoans that plays functions in a breadth of neural/sensory systems [83]. FER genome showed SOS detected in *FAM83B* and *GOT1*, two genes related to improved adaptive heart functions in high-altitude environment and heat stress tolerance [84, 85], as well as in *PCDH15* discussed above for its selection signals in the cashmere breeds population.

Signatures of selection for immune response

As shown in Table 2, genes involved in immune response and disease resistance exhibited SOS across all groups considered, suggesting that pathogens exerted significant selective pressure on all studied populations. The highest number of immune-related genes under selection was detected in milk-producing breeds, followed by cashmere goat breeds. Conversely, pathogens' selective pressure appeared to play a minor role in the other goat populations studied, as indicated by the low number of immune-related genes detected under selection in meat-producing goats, as well as in the WIL, FER, and ANG populations. Eight genes related to immune response have been found under selection in milk-producing breeds**.** POI showed SOS in *PSD3, RPF2, MGAT5,* and *UQCC1,* which are genes associated with resistance to paratuberculosis [86], peste des petits ruminants virus [87], mastitis [88], and sole ulcer, respectively [89]. Similarly, ALP revealed selection signals for *TNFAIP8L3, ZDHHC13,* and *SELL*, three loci known to be involved in tick resistance [90], and immune response to mastitis [91]. Finally, *UGGT2*, an immune-related gene associated

with resistance to intestinal parasite, was under selection in SAA [92]. Some loci involved in the immune response to a variety of ruminant pathogens have been found under selection in the four cashmere goat breeds. LIA showed selection signals in *SEMA5A,* a gene associated with mastitis resistance [93, 94]. AER showed selection for *BPI* that is related to *Salmonella* [95], and pneumonia resistance in goats [96]. *NEDD4L,* involved in peste des petits ruminant virus immune response [47], and *MYO5B*, an ATP-dependent gene related to adaptive immune response in West African Cattle [97], were under selection in ALA. Two immune-related genes, *IDO1* and *FCHSD2,* have been found under selection in meat-producing breeds. CRE showed selection on *IDO1*, a gene involved in the immune response to different bacteria such as *Brucella* [98] and *Mycobacterium* in cattle [99]. In contrast, *FCHSD2,* under selection in BOE, has been associated with resistance to gastrointestinal nematodes in sheep [100].

Finally, WIL, FER, and ANG showed SOS in *RNF213, BCHE,* and *TUBGCP5* genes, respectively. *RNF213* contributes to resistance to Rift Valley fever, a viral disease that primarily affects ruminants and humans [101]. Moreover, *RNF213* is a potent executioner of ubiquitylation-driven antiparasitic host defense against *Toxoplasma gondii* [102], and has been described as involved in the resistance to *Salmonella* infection [103]. Similarly, *BCHE* is a locus involved in ruminants' immune response to bacteria [104] and parasites [105], stress response [106], and detoxification [107], while *TUBGCP5* is related to resistance to gastrointestinal parasites [108].

Signatures of selection for body and growth traits

All the goat populations studied showed selection signals on loci involved in body development and growth traits. Some of them have been reported as associated with carcass traits in different species (Table 2). It is worth noting that the highest number of such body and growth-related genes were under selection in LIA, which showed SOS on *CDH18* and *NALCN,* recently reported to be associated with body weight and size in sheep [109, 110], and *RIMS1* suggested as related to backfat thickness in pigs [111]. A selection signal in this breed has also been identified for *TNS3*, a gene associated with the pin length in dromedary [112]. Finally, two loci, *SNX29* and *SORCS1*, potentially related to meat production traits, have been found under selection in LIA as well as in ERL. *SNX29*, is a gene related to growth traits in goat [113], while *SORCS1* has been reported for different species as associated with rump fat thickness [114], fat deposition [115].

Genes associated with carcass traits have been detected under selection in both meat- and milk-producing breeds. CRE showed selection signals in *EIF5B* and *DKK3*, which are linked to meat color traits in cattle [116], and backfat deposition in pigs [117]. Meanwhile, *TMEM132C* and *NR2E1*, which are associated with carcass and meat quality in Zebu [118] and cattle [119], were found to be under selection in BOE. Selection for meat production is also suggested by the SOS detected for *ADAMTSL3*, a gene involved in growth and body size selected in both BOE and ANG [120]. *DIAPH3*, a gene associated with meat yield in cattle, has been found under selection in ALP [121], while *NLN, NFS1,* and *FAM135A,* which are genes related to body weight and back fat thickness, have been found under selection in POI [122–124]. Some genes involved in carcass traits under selection in ANG may reflect admixture with meat-producing breeds, as seen in the case of *ADAMTSL3*, which is also under selection in BOE, as discussed above. Similarly, *POP1* and *MCM3AP*, under selection in ANG, are associated with skeletal muscle development, regeneration [125], and backfat thickness [126]. Finally, WIL showed selection signals on *ADAM12* and *CCSER1*, two genes related to body development that may confer some advantage in coping with the wild environment. *ADAM12*, is a gene involved in myogenesis, adipogenesis, and regulation of body growth during the juvenile stage [127], while *CCSER1,* under selection in WIL as well as in FER, has been recently reported as involved in growth trait in domestic goat [128].

Signatures of selection for reproductive traits

The highest number of loci under selection related to reproductive biology was observed in POI and ANG, with five and four genes, respectively, showing SOS. This was followed by CRE, SAA, and FER, each of which had only one locus associated with reproduction among the total genes detected under selection. In contrast, none of the genes showing signs of under selection in WIL, cashmere goat breeds, BOE, and ALP were related to reproductive traits (Table 3). The selection signals detected in POI on the five genes involved in reproductive biology suggest a selection pressure for precocity and efficient reproduction, as these traits are directly related to proficient milk production. In this regard, POI showed SOS on *CEP250*, *LMTK2*, and *TMC1*, which are associated with fertility [129–131], *THAP11*, a gene involved in embryogenesis [132], and *CAMK1D*, reported as associated with age at first calving [133]. Analysis of the ANG population revealed selection for efficient reproduction. For this breed, SOS was observed in four genes involved in reproductive biology, including *KDM1A* and *TEX46*, both of which are involved in spermatogenesis [134, 135], and *SMC1B* and *ADAMTSL1*, which are important for normal reproductive function in various species [136, 137]. *STIM1* and *ADAM18*, two loci associated with fecundity and spermatogenesis in goats [36, 138], were under selection in SAA and CRE, respectively. Meanwhile, FER

Table 3 Genes related to reproductive traits, skin and hair follicle biology, milk productive traits, feed intake and efficiency, general metabolism, and temperament showing signatures of selection

Reproductive traits		Skin and hair follicle biology		Milk productive traits		Feed intake and efficiency, general metabolism and temperament	
Gene	**Group/breed[a]**	**Gene**	**Group/breed[a]**	**Gene**	**Group/breed[a]**	**Gene**	**Group/breed[a]**
CNNM1	FER	*SORCS3*	FER	*TMEM165*	FER	*CRCP*	ANG
KDM1A	ANG	*ASTN2*	AER	*NOA1*		*NFX1*	
SMC1B		*PKHD1*		*DLC1*	ERL	*ACAD11*	CRE
ADAMTSL1		*FER*	ALA	*CADPS2*	AER	*BBX*	
TEX46		*GPR158*		*FHOD3*		*CNTN6*	BOE
ADAM18	CRE	*FGF12*	ERL	*SYT1*	ALA	*VWA8*	POI
CEP250	POI	*SV2B*	LIA	*KCND3*	BOE		
CAMK1D		*MYO5C*	POI	*TFDP2*	POI		
LMTK2		*MITF*	ALP	*SLC18A2*			
THAP11				*COX15*	ALP		
TMC1							
STIM1	SAA						

WIL Wild goats, *FER* Feral goats, *AER* Aerbasi cashmere goats, *ALA* Alashan cashmere goats, *ERL* Erlangshan cashmere goats, *LIA* Liaoning cashmere goats, *ANG* Angora goats, *CRE* Creole goats, *BOE* Boer

[a]Group/breed showing significative selection signals

showed SOS on *CNNM1*, which is related to the cell cycle and differentiation of spermatogenic cells in mice [139].

Signatures of selection for pigmentation, hair follicle biology, and fibre traits

Unsurprisingly, the highest number of genes involved in hair follicle biology were under selection in cashmere goat breeds (Table 3). However, it is noteworthy that none of the genes under selection in ANG in our sample were related to fiber traits. Although the role of some of the following genes in goat fibre development is unknown, we may assume some relation to cashmere traits (i.e., quantity, fibre length, or color) due to their role in the hair follicle biology. In this regard, AER showed selection signals on *PKHD1*, a locus involved in human skin and hair pigmentation [140], and *ASTN2*, a gene involved in hair follicle development and orientation [141], potentially influencing hair length, as proposed for Yak [142]. ALA showed SOS in FER, which was reported as a hub gene in the catagen phase of the hair follicle cycle in Yak [143], and *GPR158*, a gene located in the sparse and wavy hair (swh) locus in mouse which controls hair follicle size and density as well as fiber curvature [144]. Finally, *FGF12*, a gene already described as associated with Alashan cashmere production [145], has been found under selection in ERL, while *SV2B*, reported as potentially involved in Pashmina production, was under selection in LIA [146]. Two genes involved in pigmentation, *MYO5C* and *MITF*, have been identified as undergoing selection in POI and ALP, respectively. *MYO5C* is a gene related to the transport of melanin into melanocytes and associated with coat pigmentation [147]. At the same time, *MITF* is a well-known locus involved in the white spotting coat pattern in various species and was recently described under selection in goats [148]. Similarly, selection signals were observed in FER for *SORCS3*, a gene associated with coat color in goats [149].

Signatures of selection for milk productive traits

Signatures of selection for milk productive traits were detected in FER, cashmere goats, milk-producing goats, and BOE (Table 3). *TFDP2* and *SLC18A2*, genes known to be related to lactation, milking speed, and milking temperament, were under selection in POI [150, 151], while ALP showed selection for *COX15*, a gene linked to milk fat content and composition [152]. The SOS observed for AER in milk-related genes, such as *CADPS2* and *FHOD3*, associated with milk production traits in buffalo [153] and cattle [154], respectively, may indicate selection pressure for milk production. Similarly, the selection signals found in ERL and ALA for the loci *DLC1* and *SYT1*, associated with milk yield in dromedaries [155] and milk fat metabolism in cattle [156], further suggest selection for milk production in these two dual-purpose cashmere breeds. As suggested by ADMIXTURE analysis, FER genome clearly showed selective pressure for milk production, as confirmed by the detection of SOS in *NOA1* and *TMEM165,* two genes associated with milk production and mammary calcium transport function [157, 158]. Finally, *KCND3*, a candidate gene affecting milk fat and protein percentage in cattle [159], was found under selection in BOE.

Signatures of selection for feed intake and efficiency, general metabolism, and temperament

Three loci, *CRCP, ACAD11,* and *CNTN6*, associated with feed efficiency and residual feed intake [160–162], were under selection in FER, CRE, and BOE, respectively. *VWA8*, a candidate gene for temperament in sheep [163], showed SOS in POI, while CRE showed selection signals in *BBX*, previously associated with supernumerary nipple [164] (Table 3). ANG showed selection signals for *NFX1*, a gene that plays various roles, including gene regulation, embryonic development, cellular growth and differentiation, and an organism's immune response in multiple species, as reviewed [165].

Cross-population signatures of selection

Cross-population analyses revealed signals of divergent selection, reflecting differences in environments, pathogens, farming systems, and productive traits that influence each goat population.

The highest number of signals of divergent selection was observed when comparing the two most divergent groups: wild (WIL) and domestic goats. Several significantly enriched pathways relevant to goat biology were identified, including the adherens junction pathway, choline metabolism pathway, and phospholipase D signaling pathway. Indeed, adherens junctions are fundamental for the development of animal tissues and organs and have played a central role in animal evolution, particularly in pathogen infection [166]. Moreover, the alveolar epithelial barrier, composed of tight junctions and adherens junctions, plays a crucial role in safeguarding against invading pathogens, including *Mycobacterium tuberculosis* [167]. The choline metabolism pathway is another relevant pathway essential for efficient milk production [168]. Similarly, the phospholipase D signaling pathway is involved in membrane traffic within the secretory pathway of specific mammalian cell lines, such as those responsible for milk protein secretion in mammary epithelial cells [169]. However, the genes involved in these pathways, as well as those with the highest number of SNPs (16 to 4) under divergent selection, reflect differences in environment, pathogen exposure, farming systems, and selection for productive traits between wild and domestic goats. Indeed, as reported in Supplementary Table 17A, *PARD3B*, *PTPRJ*, *CTNNA3, IFNGR2,* and *NIPAL2* have been associated with resistance to common infectious diseases in ruminants [170–174], while *CPQ* is linked to adaptation to deficit-water conditions [175]. Similarly, signals of divergent selection have been detected in *PLPP3, AKT3, PLD1, DGKB, DGKG*, and *MAP2K1,* which are associated with milk traits [176–180], and in *HHAT,* which is involved in body weight at weaning and lactation persistency [181]. Other loci showing divergent selection signals between wild and domestic groups are known to be involved in reproductive biology, such as *PDE4D* [182], *PDE10A* [183], *PDE1A* [182], *ADCY9* [184], *ITGB3* [185], *STIM1* [186], *FGB* [187], *PDE4C* [188], *ADAM18* [138], *DOP1B* [189], and *CACNA1E* [190]. Moreover, divergent selection signals have also been observed for *CNGB3,* which is associated with light sensitivity in goats, and is essential for the seasonal pattern in reproductive activity related to annual variations in photoperiod [191]. Finally, signals of divergent selection have been observed in genes associated with domestication, such as *RRM1* [192], as well as in genes linked to behavior, cognition, and neurogenesis, including *ERC2* [11, 193] and *ULK4* [194].

The main divergent selection signals detected in the cross-population analysis between FER and WIL encompass genes linked to environmental adaptability, immune response, and reproduction (Supplementary Table 17B). Four genes were involved in high-altitude adaptation and thermo-sensitivity, including *ARAP2* [63], *DSG2* [195], *IYD* [77], and *DEPDC1B* [60]. In comparison, six genes were involved in the immune response to ruminants' bacterial and parasitic infections, such as *TRIM59* [196], *DNAJC15* [197], *WDR64* [198], *ANKRD29* [73], *COMMD1* [199], and *INPP4B* [200]. Moreover, signals of divergent selection have been observed in *FARP1* [122], *ZNF175* [201], *CACNA1E* [190], *SMOC2* [199], and *GRAMD1B* [202], which are loci involved in reproductive biology; in *HECW1*, a gene associated with yearling greasy fleece weight in sheep [203], and in *CADM2* and *STK10*, which are related to growth and carcass quality traits [204, 205]. Finally, divergent selection has been detected in *OR5M3*. This olfactory receptor may play a crucial role in selection and evolution by alerting animals to potential threats, such as predators or foods containing parasites, bacteria, or harmful chemicals. *OR5M3* also assists animals in locating food and potential mates [206].

Analysis of FER and domestic goats suggests divergent selection between the two groups in reproductive biology, disease resistance, and feeding behavior (Supplementary Table 17C). The highest number of SNPs (ranging from 17 to 13) showing signals of divergent selection were located in genes related to reproduction, such as *KIAA1549L* [207], *STIM1* [186], and *PBX4* [208], and in genes associated with resistance to paratuberculosis, such as *SLC17A1* [209] and *MRC1* [210]. Divergent selection was also observed in *OR6A2*, an olfactory receptor associated with feeding intake and behavior, as reviewed in [211].

Analysis of divergent selection between fiber-producing goats (cashmere and ANG) and meat-producing goats revealed signals of divergent selection that reflect differences in farming system, environment, and selection for fiber-productive traits (Supplementary Table 17D).

Divergent selection has been detected for *GBP5*, a gene involved in the immune response to pathogens such as *Mycobacteria* [212] and viruses [213]. Similarly, *ABHD6* and *CLPB*, which are involved in the modulation of adaptive thermogenesis and thermotolerance [214, 215], along with *STIM1* [186], a gene associated with fecundity in goats, were found to be under divergent selection between the two goat groups. Finally, three genes involved in hair follicle biology, *ADCY2, EPHA4,* and *KIAA1217*, showed divergent selection signals between goats selected for fibre- and meat-production, suggesting a potential role in goat's fibre features such as density, curvature, and diameter. *ADCY2* and *EPHA4* have been implicated in the regulation of hair growth and development. In particular, *EPHA4* is expressed in dermal papilla cells, hair follicle bulge, secondary hair germs, and hair matrix, functioning as an anagen-inducing signal, and playing a key role in the generation process of new hair follicles [216, 217]. The influence of *EPHA4* in fibre production has been described in fine-wool sheep, where the gene has been proposed as important for inducing fine-hair follicle regeneration [216]. Similarly, *KIAA1217* is a gene that controls hair follicle size and density, as well as fibre curvature, in the mouse [144]. None of the genes potentially involved in carcass traits showed detectable signals of divergent selection. This may be due to the presence of ANG samples in the fibre-producing goat group, which, as already mentioned, showed a consistent level of admixture with the meat-producing goat population.

The primary signals of divergent selection between fiber-producing goats (cashmere and ANG) and milk-producing goats have been found in genes associated with milk traits, such as *CP* [218], *CEP120* [219], *RGMB* [153], and *AHCYL1* [220] (Supplementary Table 17E) Additionally, divergent selection signals have been observed in genes related to other productive traits, including *ARHGAP10*, a gene involved in fiber elongation [221], as well as *STON2* and *MED12L*, which are associated with body weight [222] and reproduction [223], respectively. Signals of divergent selection have also been detected in genes related to environmental adaptation, such as *BCL2L13*, which is linked to heat stress tolerance [11, 224], and *NAMPT* and *PCDH12*, both involved in hypoxic adaptation to high altitudes [225, 226]. Lastly, divergent selection has been observed in loci associated with the general immune response, including *RFX3* [227], *ATP13A4* [228], and *SCNN1B*, which are related to the immune response to mastitis [229].

The final cross-population analysis includes both milk- and meat-producing goats, revealing signals of divergent selection for genes related to milk productive traits, such as *MYRIP, TXNL1, ROR1,* and *SH2D4A* [187, 230–232], as well as loci involved in meat production, including *UBL3* [233], *ATP2B2* [39], *STON2* [222], *CLASP1* [234], *COL12A1* [235] and *DTNA* [236]. Divergent selection between the two groups has also been observed for *MARCHF11* and *PLCZ1*, two genes involved in reproductive traits [237, 238], as well as for *TAAR2*, a chemosensory receptor in the olfactory epithelium [239], and *PER3*, a circadian rhythm regulator in goats [240]. It is noteworthy that signals of divergent selection between milk- and meat-producing goats were found exclusively on genes mainly involved in productive traits. Conversely, no loci potentially related to environmental adaptability or immune response exhibited detectable signals, suggesting a possible case of convergent selection for environmental adaptation between the two goat populations.

Limitations

This work presents preliminary results on selection signals in different goat populations, and several limitations must be highlighted.

First, the small sample size did not allow for a wider identification of SOS. Further studies with a larger sample size are required to confirm these preliminary findings.

Additionally, individuals from livestock population often exhibit a high degree of genetic relatedness which could result in population structure, altering the assessment of selection signatures. To reduce this bias, we filtered out individuals with an identity-by-descent (IBD) PI-HAT score of 0.5 or higher from our sample.

Furthermore, the study requires functional validation of the detected selection signals by integrating gene expression analysis or Genome-Wide Association Studies (GWAS) to assess the true phenotypic impact of the variants.

Conclusions

It is well established that, despite millennia of domestication, environmental and natural selection have played a greater role than artificial selection in shaping the goat genome. This is especially evident in breeds like cashmere goats, which are raised in harsh environments and show the highest number of loci under selection for environmental adaptation and disease resistance. In contrast, fewer genes were selected for traits related to productivity, such as carcass characteristics, milk composition, fiber quality, fertility, and feed efficiency. Cross-population analyses revealed the most divergent selection between wild and domestic goats, involving genes related to domestication, behavior, immune response, and productivity. Wild and feral goats also showed divergence in genes associated with olfactory receptors, high-altitude and thermal adaptation, fleece weight, and reproduction.

Divergent selection was observed between feral and domestic goats in genes linked to disease resistance, reproduction, and feeding behavior. Comparisons among

domestic goats revealed selection differences based on production purpose: fiber-producing breeds showed divergence from both meat and dairy breeds in genes related to thermotolerance, immune response, fecundity, hair follicle development, and fiber traits. Similarly, meat vs. milk producers showed divergence in genes tied to productivity, reproduction, and circadian rhythm. However, little divergence in environmental adaptation was seen between meat and dairy goats, likely due to their intensive management and reduced exposure to environmental pressures.

In conclusion, this study identifies novel genes under selection for both productivity and environmental adaptation in goats. To the best of our knowledge, this is the first description of selective signals in this species for most of these loci. While the functional effects of many of these variants remain to be determined, these findings offer a valuable foundation for breeding resilient goats suited to future challenges such as climate change and emerging diseases.

Abbreviations

AER	Aerbasi cashmere goats
ALA	Alashan cashmere goats
ALP	Alpine goats
ANG	Angora goats
BOE	Boer goats
CRE	Creole goats
ERL	Erlangshan cashmere goats
FER	Feral goats
LIA	Liaoning cashmere goats
POI	Poitevine goats
SAA	Saanen goats
SNP	Single Nucleotide Polymorphism
SOS	Signatures Of Selection
WIL	Wild goats

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s12864-025-12133-4.

Supplementary Material 1

Supplementary Material 2

Supplementary Material 3

Supplementary Material 4

Supplementary Material 5

Supplementary Material 6

Supplementary Material 7

Supplementary Material 8

Supplementary Material 9

Supplementary Material 10

Supplementary Material 11

Supplementary Material 12

Supplementary Material 13

Supplementary Material 14

Supplementary Material 15

Supplementary Material 16

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Authors' contributions

S.P.: study conception, analysis, drafting of the manuscript; A.F.R.G.: analysis; G.D.: analysis; M.A.: critical review of the manuscript; Z.J.: critical review of the manuscript; S.H.: critical review of the manuscript; C.R.: study conception, critical review of the manuscript; financial support; V.N.: study conception, drafting of the manuscript, critical review of the manuscript.

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Data availability

The samples generated by previous projects and used in this study are available in the NCBI Sequence Read Archive (SRA) [PRJEB37122, PRJEB4371, PRJNA310684, PRJNA338022, PRJNA378894, PRJNA387635, PRJNA399234].

Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare no competing interests.

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