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Morphological divergence of Creole goats across Peruvian ecosystems

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ABSTRACT

Peruvian Creole goats constitute a genetically distinct population shaped by long-term crossbreeding and adaptation. Peru spans ecological gradients that likely drive regional phenotypic differentiation, yet the morphometric basis remains poorly resolved. We assessed the concordance between morphometric structuring of goats, ecosystem distribution, and regional origin. Body weight (BW) and seven linear body measurements (LBM) were recorded in 515 adult female goats sampled across five ecosystems and seven regions. Low-dimensional structure for BW and LBM was explored using uniform manifold approximation and projection with k-means clustering, and cluster separability was assessed using a linear support vector machine. Six body conformation indices supported body-type interpretation. Four morphometric clusters were identified, structured by Andean shrublands (AS), plains seasonally dry forest (PSDF), and inter-Andean seasonally dry forest (IASDF). Clusters C1 and C3 were dominated by AS goats (77% and 79%, respectively), revealing two morphotypes: a convexilinear form with elevated pelvic indices (C1) and a lighter, shorter, longilinear form (C3). Clusters C2 and C4 were mainly formed by PSDF (54%) and IASDF goats (66%), respectively, with C2 characterized by greater stature and thoracic robustness, and C4 by a narrower pelvic conformation. In contrast, goats from the other ecosystems exhibited greater heterogeneity. Each cluster was dominated by >60% of goats from a single region, with C1, C2, C3, and C4 associated with Ica, Piura, Ayacucho, and Amazonas, respectively. These findings establish the first ecosystem-based national morphometric framework for Peruvian Creole goats, linking body conformation to ecological and geographic context and informing conservation and potential geographical indications.

1. Introduction

Peruvian Creole goats are central to subsistence livestock systems, thriving in environments where other domestic species fail to prosper (Silanikove, 2000). Their origin traces back to crossbreeding among Granadina, Murciana, Malagueña, Anglonubian, and other breeds, followed by long-term adaptation across Peruvian physiography (Corredor et al., 2024; Gómez-Urviola et al., 2016). At present, they are predominantly raised in extensive, low-input systems that rely almost exclusively on heterogeneous rangeland ecosystems for forage (Palomino Guerrera et al., 2024; Paredes Chocce et al., 2024; E. A. Sessarego et al., 2025; V. Temoche et al., 2025).

Peru's ecological diversity encompasses 36 recognized ecosystems, classified according to natural region, bioclimate, vegetation cover, physiography, and altitude (Ministerio del Ambiente, 2019). Goat husbandry, however, is largely confined to several of them, with the seasonally dry forests (SDF) ecosystems as the most representative. Each ecosystem poses unique constraints, including variation in forage

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biomass, elevation, slope, and precipitation patterns (Bailey et al., 2015; Velado-Alonso, 2022; Zandler et al., 2023). Together, these constraints shape the adaptive responses required for livestock survival.

Such adaptations are frequently manifested in morphological traits. Ecological and geographical attributes influence livestock phenotypes, promoting the differentiation of distinct biotypes or even breeds, occasionally without marked genetic divergence (Getaneh et al., 2022a; Hailemariam et al., 2018; López Aguirre et al., 2023; Ntonga et al., 2025; Whannou et al., 2021). These phenotypic outcomes are also affected by management practices, particularly breeding strategies (Akounda et al., 2023; Nantongo et al., 2024). In addition, production objectives represent a major selective force, as meat-oriented animals are preferentially selected along the northern coast of Peru, whereas dairy-oriented animals are favored in the central coast and southern highlands (E. A. Sessarego et al., 2025; V. Temoche et al., 2025). Although genetic differentiation exists among regional Creole goat populations (Corredor et al., 2025), the corresponding phenotypic dimension of this divergence remains largely unexplored. Moreover, existing studies focus primarily on regional morphometric characterizations of Creole goats (Acosta-Granados et al., 2025; Haro-Reyes et al., 2025; Palomino-Guerrera et al., 2024; E. Sessarego et al., 2025; V. A. Temoche et al., 2024), lacking a comparative, nationwide perspective and an explicit ecological framework.

Here, we address this knowledge gap by clustering Peruvian Creole goats at a national scale based on morphometric similarity, evaluating the concordance between these groupings and the ecosystems of origin. We hypothesize that morphological clustering will parallel ecosystem zonation. Establishing links between environmental conditions and caprine morphotypes provides a basis not only for targeted management and conservation strategies but also for the design of community-based selection programs and the future development of geographical indications. Such designations emphasize the connection between regional resources and agricultural products, thereby enhancing their cultural and economic value while promoting rural development (Aprile et al., 2012; De La Barra et al., 2018).

2. Methods

2.1. Study area

Creole goats were sampled nationwide from smallholder farms distributed across five ecosystems representative of Peru's caprine production systems: plains seasonally dry forest (PSDF), hills and mountains seasonally dry forest (HMSDF), inter-Andean seasonally dry forest (IASDF), coastal desert (CD), and Andean shrubland (AS) (Table 1, Figs. 1 and 2). The ecosystem classification followed the National Ecosystem Map of Peru (Ministerio del Ambiente, 2019). Sampling encompassed seven of the twenty-four regions of the country: Amazonas (Utcubamba), Ayacucho (Cangallo, Huamanga, Santillana, Lucanas, Vilcashuaman), Ica (Chincha), La Libertad (Otuzco y Santiago de Chuco), Lima (Canta, Huaral, Huaura), Piura (Morropon, Piura, Sullana), and Tumbes (Contralmirante Villar, Tumbes), covering a total of seventeen provinces. Together, these regions contained more than half of the national goat population (SIEA-MINAGRI, 2025).

The importance of ecosystems lies in their distinct environmental conditions and vegetation types (Linares-Palomino et al., 2022), with directly influence goat performance. The CD is an arid to hyper-arid ecosystem, characterized by tillandsias, scrubs and cactaceae species (Ministerio del Ambiente, 2019). Goats raised in these areas rarely rely solely on native vegetation. Crop residues and *lomas* vegetation (seasonally fog-fed hills) are essential feed resources, supporting an effective transhumance system (Paredes Chocce et al., 2024).

In contrast, AS occurs at higher elevations (1500–4500 masl) and is dominated by woody plants and shrubs. Among the seasonally dry forests, HMSDF is characterized by denser and more diverse woody vegetation and receives higher annual precipitation (~500 mm) than PSDF. PSDF, by comparison, is semi-arid and resembles an open arboreal savanna. IASDF vegetation is dominated by legumes and cacti. In the Amazonas region, annual precipitation averages about 550 mm and mean temperatures range from 24 to 25 °C (Linares-Palomino et al., 2022; Ministerio del Ambiente, 2019).

2.2. Sampling procedures

A total of 515 adult female Creole goats (≥3 years old, estimated by dental eruption patterns) were sampled across ecosystems and regions, from 33 to 120 samples per region, (Supplementary Table 1) between September and November 2023. Goats belonged to herds managed under extensive systems, grazing mainly on natural vegetation and, where available, crop residues near the farms. Sampling was conducted early in the morning, before animals were released to pasture, to minimize variation associated with feed intake and physical activity.

Table 1
Characteristics of Peruvian ecosystems following MINAM's classification. Information was taken from MINAM (Environment Ministry of Peru) supporting documentation of the National Map of Ecosystems (MINAM, 2018; Ministerio del Ambiente, 2019).

Attribute	Ecosystem				
	Plains Seasonally Dry Forest	Hills and Mountains Seasonally Dry Forest	Inter-Andean Seasonally Dry Forest	Coastal Desert	Andean Shrubland
Natural region	Coast	Coast	Andean	Coast	Andean
Bioclimate	Highly arid, arid	Arid, semi-arid	Semi-arid	Hyper-arid, arid	Sub-humid
Vegetation formation	Forest	Forest	Forest	Herbs and deciduous succulents	Shrubland
Physiography	Alluvial plain, Colluvio-alluvial, Marine terrace	Hills and mountains	Mountain (high plateus) and hills	Plains, hills, mountain	Mountain
Altitude (m.a.s.l.)	0 – 500	400 – 2000	500 – 2500	0 – 2500	2000 – 3500
Common vegetable species	*Prosopis pallida, P. limensis, Vachellia macracantha, Colicodendron scabridum, Caesalpinea paipai.*	*Eriotheca ruizii, Bursera graveolens, Loxopterigium huasango, Ceiba trichistandra, Terminalia valverdae, Geoffroea striata, Cochlospermum vitifolium, Erythrina smithsiana, Tillandsia usneoides, Pithecellobium multiflorum, Handroanthus chrysanthus, Caesalpinia paipai.*	*Eriotheca discolor, E. peruviana y E. vargasii, Vachellia macracantha, Bougainvillea peruviana, Pithecellobium excelsum, Parkinsonia praecox, Leucaena trichodes, Sapindus saponaria, Colicodendron scabridum, Melocactus bellavistensis, Armatocereus rauhii, Brownigia altissima, Espostoa lanata.*	*Tillandsia* spp., *Prosopis* spp., *Vachellia macracantha, Colicodendron scabridum, Trichocereus* spp., *Browningia candelaris.*	*Kageneckia lanceolata, Mutisia acuminata, Barnadesia dombeyana, Tecoma stans, Caesalpinia spinosa, Schinus molle, Austrocilindropuntia subulata, Pitcairnia* spp., *Puya spp*

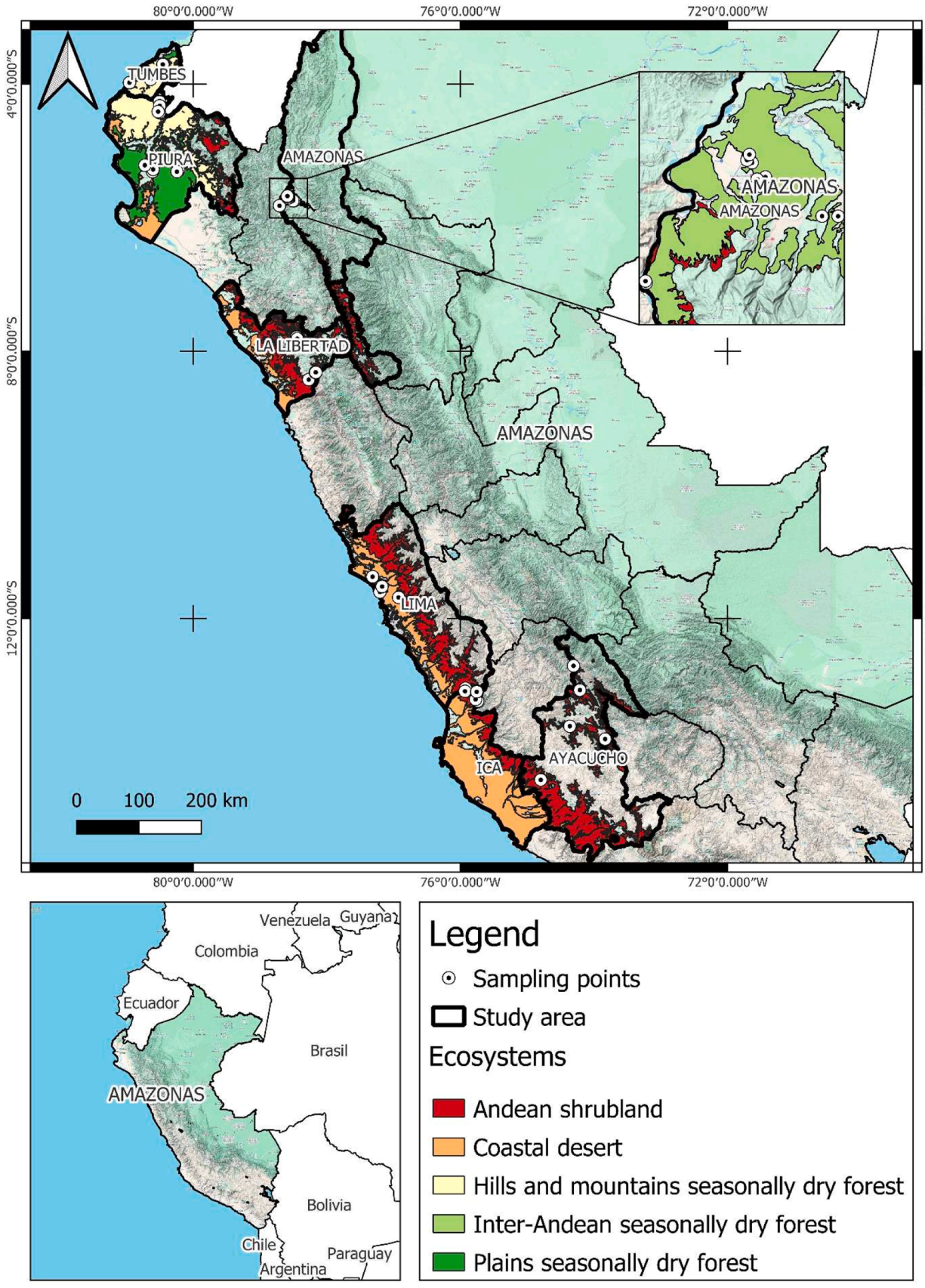

Fig. 1. Sampling site map across Peruvian ecosystems and regions.

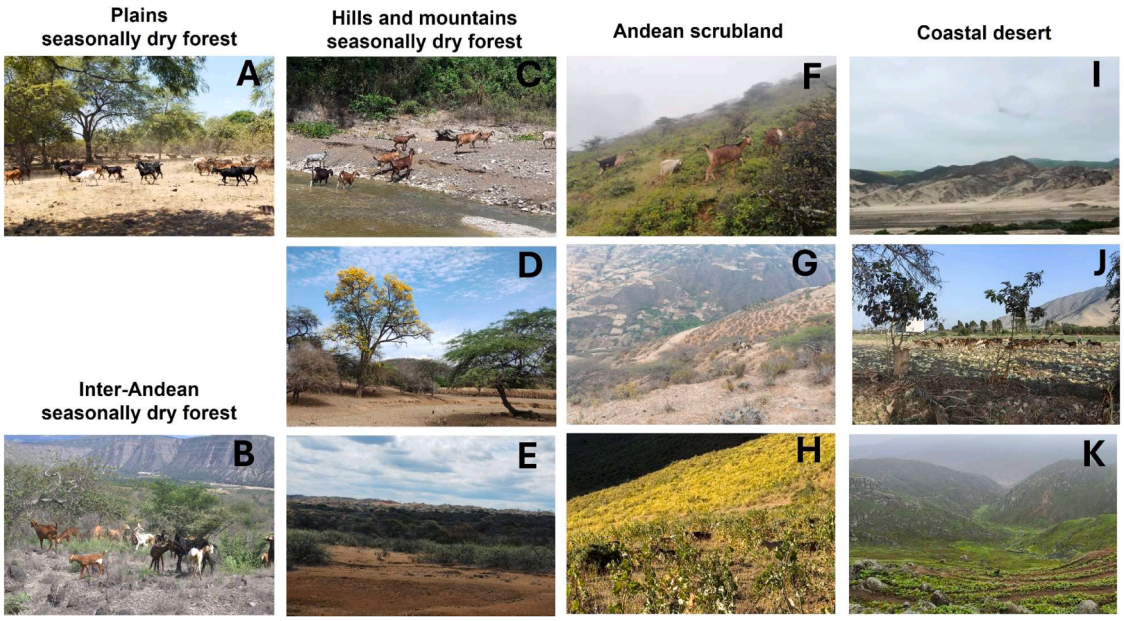

Fig. 2. Representative ecosystems for caprine production in Peru. A: plains seasonally dry forest (PSDF) in Chulucanas, Piura; B: inter-Andean seasonally dry forest (IASDF) in Amazonas; C: riparian area of hills and mountains seasonally dry forest (HMSDF) in Casitas, Tumbes; D: typical 'guayacan' tree (*Handroanthus chrysanthus*), HMSDF in Lancones, Piura; E: HMSDF in Lancones, Piura; F: Andean shrubland (AS) in Otuzco, La Libertad (high vegetation coverage); G: Andean shrubland (AS) in Otuzco, La Libertad (short vegetation coverage); H: AS in San Juan de Yanac, Ica; I: coastal desert (CD) in Huaral, Lima; J: crop residues in agriculture zone in Huaral, Lima, K: lomas (seasonally fog-fed hills) within CD in Sayan, Lima.

Body weight (BW) and seven linear body measurements (LBMs) are described in Supplementary Table 2. They were taken according to previous publication on Creole goats in the SDF (Haro-Reyes et al., 2025). The measured traits included chest width (CW), thoracic perimeter (TP), withers height (WH), rump height (RH), rump width (RW), rump length (RL), and body length (BL). Body weight was measured using a hook-type scale, while LBMs were obtained using a flexible measuring tape and a measuring stick. These measurements were used to derive six body conformation indices: corporal index (COI), pelvic index (PEI), proportionality index (PROI), transversal pelvic index (TPI), longitudinal index (LPI), and compactness index (CPI). The indices were computed to characterize body types and to support interpretation of potential productive attributes. Detailed criteria for body type classification based on these indices are provided in a previous publication (Haro-Reyes et al., 2025).

2.3. Statistical analysis

Descriptive statistics were first computed to characterize the morphometric variation within the sampled population. To explore the underlying multivariate structure, standardized data (body weight and LBMs) were analyzed using Uniform Manifold Approximation and Projection (UMAP). UMAP is a non-linear algorithm for high-dimensional reduction and low-dimensional visualization (Härdle et al., 2024; McInnes et al., 2020). The analysis employed a correlation-based distance metric with 30 nearest neighbors and a minimum distance of 0.1. These parameters provide an optimal balance between local continuity (morphological similarity among individuals) and global integrity of the morphometric space. The resulting two-dimensional embedding (UMAP1 and UMAP2) facilitated visualization of population structuring and potential clustering patterns across ecosystems and regions.

The robustness of the selected UMAP configuration was evaluated through a sensitivity analysis. The embedding and subsequent clustering were repeated using alternative combinations of neighborhood size (15–50 neighbors), minimum-distance values (0.0–0.3), and random seeds, while keeping the number of clusters constant. Cluster stability was assessed using the Adjusted Rand Index (ARI). The mean ARI across repeated runs was 0.82, indicating a high level of consistency in cluster membership under reasonable parameter variation.

K-means clustering was applied to the UMAP projection to identify groups of morphologically similar individuals. The optimal number of clusters was selected using the average silhouette width (ASW), which quantifies within-cluster cohesion and between-cluster separation. Clustering solutions with $k = 3$–5 exhibited comparable ASW values ($|\Delta \text{ASW}| \leq 0.012$). A four-cluster solution ($k = 4$) was selected because it captured the highest level of structural complexity while remaining within the stability plateau of the clustering solution. The proportions of individuals from each ecosystem and region within each cluster were then calculated to evaluate geographical patterns in morphometric clustering.

To further evaluate the separation among the identified clusters, a linear Support Vector Machine (SVM) classifier was implemented. All seven LBMs and body weight were included simultaneously as predictors, and cluster membership was used as the response variable. Model performance was assessed using repeated k-fold cross-validation (10 folds, 10 repeats), ensuring robust estimation of predictive performance without reliance on a single training–testing split. The SVM was fitted with a linear kernel and a regularization parameter $C = 1$.

Model performance was evaluated using overall accuracy, Cohen's Kappa coefficient, precision, recall, and F1-score, allowing balanced assessment across clusters. In addition, model complexity was characterized by the number of support vectors contributing to the definition of the separating hyperplanes. The linear SVM operated under a multiclass one-vs-one framework, resulting in six pairwise binary classifiers. From these classifiers, coefficient vectors ($\boldsymbol{w_{ij}}$) and intercepts ($\boldsymbol{b_{ij}}$) were extracted to reconstruct the decision functions,

$$f_{ij}(x) = \boldsymbol{w}_{ij}^{T}\boldsymbol{x} + \boldsymbol{b}_{ij}$$

which were combined through a majority voting scheme to assign individuals to clusters.

Finally, statistical differences among clusters for the body weight, LBMs and body conformation indices were assessed using one-way ANOVA followed by Tukey's post hoc tests. This analysis quantified

the extent to which explanatory variables differentiated the identified groups. All analyses were conducted in R software version 4.5.0 (R Core Team, 2025).

3. Results

3.1. K-means clustering after UMAP reveals morphometric patterns across ecosystems

Mean ± standard deviation morphometric values (body weight and LBMs) by ecosystem and region suggested potential differences among populations (Supplementary Table 3). However, multivariate analysis was required to reveal clearer structure. The UMAP projection showed distinct clustering patterns across ecosystems (Fig. 3). Cluster 1 (C1) and Cluster 3 (C3) were dominated by individuals from the Andean shrubland (AS), representing 77% and 79% of each cluster, respectively (Table 2). Conversely, 47% and 32% of all AS animals were assigned to C1 and C3 (Table 3), indicating that these two clusters together encompassed nearly 80% of goats from the AS ecosystem.

Cluster 2 (C2) was dominated by PSDF goats (54%), whereas Cluster 4 (C4) was dominated by IASDF goats (66%). The representation of PSDF and IASDF in C2 and C4 was particularly strong, with 93% of all PSDF animals found in C2 and 95% of IASDF animals in C4 (Tables 1 and 2). Therefore, integration of UMAP and k-means effectively captured the ecosystem-level differentiation of morphometric traits among populations.

Regional composition provided additional insights into cluster distribution (Fig. 3). The AS ecosystem, occurring mainly in Ayacucho, La Libertad, and Ica, showed internal subdivision: C1 was almost entirely composed of goats from Ica and La Libertad, whereas C3 represented mainly those from Ayacucho. Interestingly, most animals from the Cangallo province (Ayacucho) appeared in C2, indicating partial morphological convergence with PSDF-type goats. In contrast, nearly all individuals from Piura clustered together, regardless of whether they originated from PSDF or HMSDF zones. This was particularly evident from a province within region approach (Supplementary Figure 1). Goats from Sullana province (HMSDF, Fig. 4) grouped with the rest of Piura provinces (mostly PSDF in Morropon and Piura) rather than with Tumbes, despite the latter's closer ecosystemic and geographic proximity. Regions such as Lima, entirely representing the Coastal Desert (CD), showed broader dispersion across clusters, though animals from Canta tended to group within C2 (Supplementary Figure 1), while those from Huaura and Huaral were more heterogeneously distributed.

Table 2
Proportion of goats within UMAP clusters by ecosystems and by regions. AS: Andean shrubland; CD: coastal desert; HMSDF: hills and mountains seasonally dry forest; IASDF: inter-Andean seasonally dry forest; PSDF: plains seasonally dry forest.

	Clusters			
	1	2	3	4
Ecosystem				
AS	0.77	0.22	0.79	0.15
CD	0.13	0.15	0.11	0.03
HMSDF	0.09	0.09	0.02	0.17
IASDF	0.01	0.00	0.02	0.66
PSDF	0.00	0.54	0.06	0.00
Total	1.00	1.00	1.00	1.00
Region				
Amazonas	0.01	0.00	0.02	0.66
Ayacucho	0.00	0.14	0.69	0.01
Ica	0.61	0.08	0.09	0.06
La Libertad	0.16	0.00	0.01	0.07
Lima	0.13	0.15	0.11	0.03
Piura	0.00	0.62	0.06	0.00
Tumbes	0.09	0.01	0.02	0.17
Total	1.00	1.00	1.00	1.00

Table 3
Proportion of goats within ecosystems and regions by UAMP clusters. AS: Andean shrubland; CD: coastal desert; HMSDF: hills and mountains seasonally dry forest; IASDF: inter-Andean seasonally dry forest; PSDF: plains seasonally dry forest.

	Clusters				
	1	2	3	4	*Total*
Ecosystem					
AS	0.47	0.14	0.32	0.07	1.00
CD	0.35	0.40	0.20	0.05	1.00
HMSDF	0.28	0.30	0.04	0.38	1.00
IASDF	0.03	0.00	0.03	0.94	1.00
PSDF	0.00	0.93	0.07	0.00	1.00
Region					
Amazonas	0.03	0.00	0.03	0.94	1.00
Ayacucho	0.00	0.24	0.75	0.01	1.00
Ica	0.77	0.10	0.07	0.06	1.00
La Libertad	0.73	0.00	0.03	0.24	1.00
Lima	0.35	0.40	0.20	0.05	1.00
Piura	0.00	0.94	0.06	0.00	1.00
Tumbes	0.38	0.03	0.06	0.53	1.00

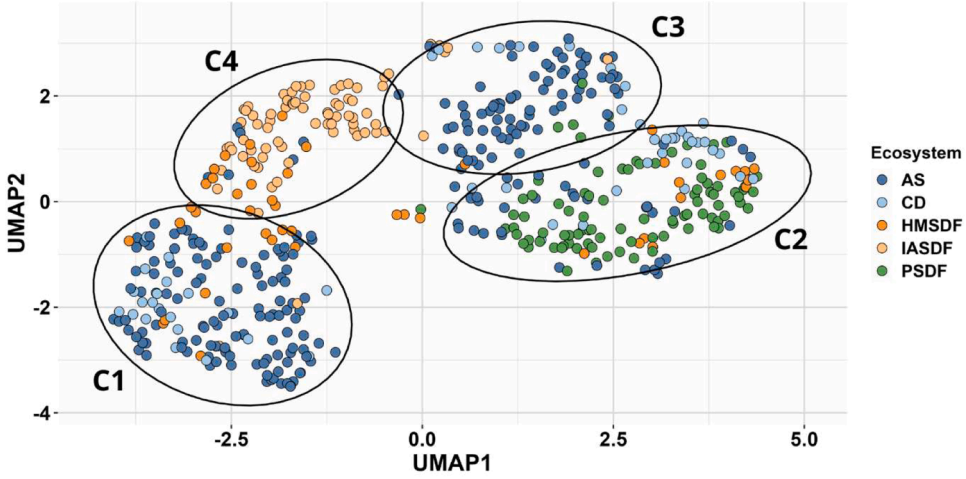

Fig. 3. UMAP plot showing creole goat clusters (k = 4; C1-C4) across ecosystems.

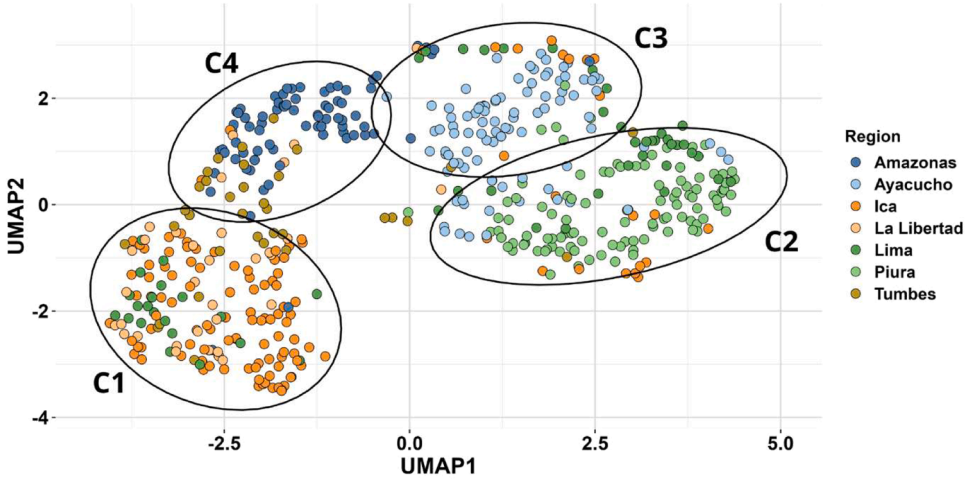

Fig. 4. UMAP plot showing creole goat clusters (k = 4; C1-C4) across regions.

3.2. Performance of the linear SVM model and morphometric discrimination of Creole goats

Linear SVM was trained on body weight and seven LBMs predictors and evaluated using repeated k-fold cross-validation. The model achieved consistently high classification performance across the four morphometric clusters. All performance metrics, including accuracy, Cohen's Kappa, precision, recall, and F1-score, exceeded 0.90 (Table 4), indicated strong agreement between observed and predicted classifications beyond chance and a balanced level of discrimination among clusters. The low standard errors associated with all metrics further indicated stable model performance across resampling iterations, supporting the robustness of the validation strategy employed.

The final model (C = 1, linear kernel) was defined by 153 support vectors, approximately 30% of the total observations (n = 515). This proportion reflects the level of complexity required to define separating hyperplanes in a multivariate space. Moreover, the low training error observed (3.7%) indicates an adequate model fit, with no evidence of overfitting.

Within the multiclass linear SVM framework using a one-vs-one strategy, discrimination among clusters was achieved through six binary hyperplanes. The corresponding coefficients ($\boldsymbol{w}_{ij}$) and intercepts ($\boldsymbol{b}_{ij}$) are reported in Table 5 and represent the contribution of each morphometric variable to the definition of the separating hyperplanes. The sign of each coefficient reflects the direction of its effect on classification. Collectively, these parameters defined the decision functions $f_{ij}(x) = \boldsymbol{w}_{ij}^{T}x + \boldsymbol{b}_{ij}$, which were used for individual assignment under a majority-voting scheme.

3.3. UMAP clusters revealed distinct morphometric traits among groups

Cluster-based comparisons of BW and LBMs revealed differentiated morphotypes (Table 6). Goats in cluster 1 (C1) were heavier (BW), with larger TP greater stature (WH, RH) compared with those in cluster 3 (C3), which in were shorter but longer-bodied (RL, BL). Notably, both clusters corresponded to AS populations, though C1 was primarily associated with Ica and La Libertad, and C3 with Ayacucho. Cluster 2 (C2) included the shortest animals (BL) but with longer rump length (RL), whereas C4 comprised the narrowest goats (CW, RW).

Body conformation indices, calculated as shown in Supplementary Table 4, allowed to better explain morphometric differences. C1 showed a distinctly high Pelvic Index (PEI), indicating a higher rump width compared to rump length. C2 displayed the lowest COI and highest PROI, describing animals with taller and more compact proportions. C3 exhibited the highest COI, consistent with a longilinear type, and a low PROI, reflecting elongated but lower-bodied individuals. C4 goats presented the lowest PEI, indicative of narrower pelvic conformation. Across clusters, the Compactness and Pelvic Proportions Indices (CPI, TPI, LPI) suggested that most morphotypes retain features typical of dairy-type goats, characterized by lighter body mass relative to height.

Table 4
UMAP model performance metrics (mean ± standard error).

C	Accuracy	Kappa	Precision	Recall	F1-score
1	0.933 ± 0.004	0.909 ± 0.05	0.936 ± 0.004	0.927 ± 0.004	0.928 ± 0.003

4. Discussion

Ecomorphology, largely explored in wild species, investigates how animal morphology adapts to environmental conditions that constrain survival and performance (Schwab et al., 2023). These adaptations encompass mechanisms to withstand increasing temperatures driven by climate change, as well as body adjustments that enhance access to food resources across heterogeneous landscapes (Barlow et al., 2023; Ryding et al., 2021). Genomic studies have further supported the existence of local adaptation within populations of the same breed (Manunza et al., 2023). In domestic species, however, morphological variation reflects not only environmental adaptation but also the influence of human management and production goals. Archaeozoological evidence indicates substantial biometric changes in domestic animals over the past centuries, driven by human selection (Mureau et al., 2025). Selective breeding for body types suited to specific production purposes, such as in dairy and meat livestock, has become a recurrent practice within and across breeds (Hansen, 2000; Tefera & Tefera, 2025). For instance, selection signature analyses in indigenous sheep revealed that community-based breeding programs can induce detectable morphometric and potential genomic shifts within a decade (Rekik et al., 2022).

In our study, the National Ecosystem Map provided an ecological framework for classifying regions characterized by common biotic and abiotic conditions (Bryce et al., 1999; Loveland & Merchant, 2004). Using a UMAP approach, we identified distinct morphological clusters that partially followed those ecosystem boundaries. Moreover, regional variation within ecosystems contributed to the observed differentiation.

Three ecosystems (AS, PSDF and IASDF) showed the strongest correspondence with UMAP clusters. Interestingly, goats from the AS were split between clusters C1 and C3, aligning with their geographic origin from Ica and Ayacucho, respectively. Despite sharing the same ecosystem and close spatial proximity, these populations exhibited

Tabla 5
Coeficients (w_{ij}) and intercepts (b_{ij}) of the binary one-vs-one classifiers from the linear SVM model, together with the mean and standard deviation (SD) of the variables in their original scale. BW: body weight, CW: chest width, TP: thoracic perimeter, WH: withers height, RH: rump height, RW: rump width, RL: rump length, BL: body length.

	w_{ij}								b_{ij}
	BW	CW	TP	WH	RH	RW	RL	BL	
1 vs 2	0.126	0.302	0.429	0.657	0.169	0.435	−3.256	1.241	0.253
1 vs 3	1.447	−0.510	1.492	−0.169	1.119	0.791	−2.014	−2.052	−0.218
1 vs 4	0.544	0.902	0.712	−0.167	0.293	1.177	−2.807	−0.568	0.064
2 vs 3	1.030	−0.583	0.758	−0.071	0.074	0.313	1.370	−2.284	−0.691
2 vs 4	1.130	1.043	0.663	−0.597	−0.690	1.881	0.180	−3.591	0.029
3 vs 4	−0.416	2.223	−0.260	−1.002	0.460	−0.123	−2.644	1.774	0.350
For data scale									
Media	46.521	19.216	84.175	69.850	72.195	17.187	20.506	69.878	
SD	11.134	2.704	7.221	6.251	6.178	2.491	3.008	8.790	

Table 6
Morphometric traits (mean ± SD) of the four clusters found by UMAP analysis. SD: standard deviation; BW: body weight, CW: chest width, TP: thoracic perimeter; WH: withers height; RH: rump height, RL: rump length; BL: body length; COI: corporal index; PEI: pelvic index; PROI: proportionality index; TPI: transversal pelvic index; LPI: longitudinal pelvic index; CPI: compactness index. $^{a-d}$ Letters represent significant differences ($p < 0.05$) after Tukey test between clusters for each trait.

	Cluster			
	1	2	3	4
BW	$51.6^{d} \pm 0.82$	$47.4^{c} \pm 0.82$	$39.6^{a} \pm 1.08$	$43.8^{b} \pm 0.98$
Linear body measurements				
CW	$20.0^{c} \pm 0.20$	$18.8^{b} \pm 0.20$	$20.2^{c} \pm 0.27$	$17.8^{a} \pm 0.24$
TP	$87.9^{b} \pm 0.54$	$83.4^{a} \pm 0.54$	$81.2^{a} \pm 0.71$	$82.4^{a} \pm 0.65$
WH	$71.7^{b} \pm 0.50$	$68.9^{a} \pm 0.64$	$68.1^{a} \pm 0.64$	$70.0^{ab} \pm 0.59$
RH	$74.4^{b} \pm 0.50$	$71.2^{a} \pm 0.48$	$70.5^{a} \pm 0.63$	$71.9^{a} \pm 0.56$
RW	$18.3^{c} \pm 0.19$	$17.3^{b} \pm 0.19$	$16.6^{ab} \pm 0.24$	$16.0^{a} \pm 0.22$
RL	$17.9^{a} \pm 0.18$	$22.4^{c} \pm 0.18$	$19.6^{b} \pm 0.23$	$22.3^{c} \pm 0.21$
BL	$72.0^{b} \pm 0.60$	$63.4^{a} \pm 0.60$	$75.9^{c} \pm 0.79$	$71.0^{b} \pm 0.72$
Body conformation **indices**				
COI	$81.9^{b} \pm 0.44$	$76.1^{a} \pm 0.44$	$93.3^{d} \pm 0.58$	$86.1^{c} \pm 0.53$
PEI	$102.9^{d} \pm 0.70$	$76.9^{b} \pm 0.70$	$84.9^{c} \pm 0.91$	$71.7^{a} \pm 0.84$
PROI	$100.0^{b} \pm 0.64$	$109.3^{c} \pm 0.64$	$90.4^{a} \pm 0.84$	$98.9^{b} \pm 0.77$
TPI	$25.6^{c} \pm 0.18$	$25.0^{bc} \pm 0.18$	$24.3^{b} \pm 0.24$	$22.8^{a} \pm 0.22$
LPI	$24.1^{a} \pm 0.18$	$27.7^{b} \pm 0.23$	$31.0^{c} \pm 0.21$	$31.5^{c} \pm 0.18$
CPI	$71.6^{c} \pm 0.92$	$68.5^{c} \pm 0.92$	$57.8^{a} \pm 1.21$	$62.0^{b} \pm 1.11$

marked morphological divergence. Similar patterns have been reported in other species, such as indigenous Benin sheep, where morphotypes from contiguous areas within the same vegetation zone differed substantially in body conformation (Whannou et al., 2021). The divergence observed among AS goat populations suggests that local environmental conditions, management strategies, or production practices among other factors may override broader ecosystem-level similarities. Although these factors were not directly assessed in this study, previous work provides relevant context. Goat production systems in Ica and Ayacucho differ in sanitary management intensity. A greater proportion of herds are dewormed more than twice annually in Ica than in Ayacucho (48% versus 30%) (E. A. Sessarego et al., 2025). In addition, regional variation in vegetation composition may contribute to divergence. *Acacia macracantha* (locally known as "Huarango") has been reported as a frequent forage species in Ayacucho's AS grazing systems (Palomino Guerrera et al., 2024). However, it is not commonly listed as a characteristic species of the AS (Ministerio del Ambiente, 2019). This discrepancy suggests localized ecological differentiation.

Differences between C1 (predominantly from Ica) and C3 (predominantly from Ayacucho) were significant for body weight and all LBMs, but chest width. C1 animals exhibited larger overall dimensions, except for rump and body length. Body conformation indices, particularly CPI, COI, PROI, and PEI, more effectively captured these contrasts. These indices indicated that C3 goats were more compact (greater body mass relative to height), brevilinear (greater thoracic volume relative to body length), medium-bodied in height-to-length proportions, and convexilinear, with rump width exceeding rump length. In contrast, C1 goats were less compact, longilinear, shorter-bodied, and lacked a convexilinear conformation. Convexilinearity, reflected in PEI or greater RW, has been associated with enhanced reproductive fitness (Silva-Jarquin et al., 2019). However, evidence from other ruminants links greater RW to improved meat yield (Jourshari et al., 2023). This finding suggests that C1 goats may also possess meat production potential, albeit mediated through different morphological traits.

Over 90% of goats from the PSDF and IASDF ecosystems were assigned to clusters C2 and C4, respectively, although approximately one-third of individuals within each cluster originated from other ecosystems. This pattern suggests partial ecosystem-driven morphological differentiation. Goats in C2 exhibited the greatest rump length (together with C4) but the shortest body length. Index-based analyses further revealed pronounced thoracic development and tall body conformation, reflected by low COI and high PROI values, consistent with a dairy-type morphology (Chacón et al., 2011; Getaneh et al., 2022b). This phenotype may also reflect adaptation to management systems with reduced mobility or partial confinement. C4 goats exhibited the lowest PEI, driven by narrower rump width combined with greater rump length. Previous studies associate lower PEI with reduced kidding capacity and lower meat potential (Granero et al., 2023; Silva-Jarquin et al., 2019). Therefore, evaluation of the functional implications of this trait requires integration of direct reproductive and productive performance metrics.

Goats from CD and HMSDF exhibited the greatest morphological heterogeneity, spanning multiple clusters. Such variability likely arises from husbandry and cultural practices promoting genetic exchange. In Peru, outbreeding is facilitated by farmer connectivity and the active trading of animals, resembling dynamics observed in other goat production systems where animal exchange enhances gene flow across regions (Berthouly et al., 2009; Lysholm et al., 2020). In CD, some herds still practice transhumance, migrating for a few months each year to the coastal *Lomas* or highland pastures (Fig. 1, J–L), particularly when crop residues are scarce (Paredes Chocce et al., 2024). Transhumance, characterized by seasonal herd mobility in search of fresh forage (Velamazán et al., 2024), has been associated with increased heterozygosity (Colli et al., 2018), due to frequent outbreeding during herd interactions. Consistent with this, goats from the Huaral district within CD were more frequently assigned to AS-associated clusters than animals from other districts (Supplementary Figure 2). This pattern suggests interactions with highland morphotypes. However, data on mating patterns and grazing routes are needed to confirm this interpretation. Overall, this morphological heterogeneity is consistent with genomic reports of low inbreeding in regional goat populations based on SNP analyses (Corredor et al., 2024).

Goats from HMSDF were mainly distributed between clusters C2 and C4. In C2, HMSDF goats from Piura clustered together with those from the PSDF (mostly from Piura). This grouping appeared to follow regional

rather than ecosystemic patterns. Similarly, in South African Nguni goats, LBMs were unaffected by agroecological zone (Mathapo et al., 2024). Unexpectedly, Tumbes goats (HMSDF) clustered closely with IASDF goats from Amazonas, despite the large geographic and ecological separation. Comparable cross-ecoregional clustering has been described in Benin's indigenous sheep, where animals from distinct agroecological zones exhibited similar morphotypes (Whannou et al., 2021). These findings suggest that morphological convergence cannot be explained solely by ecological conditions and may instead reflect the influence of other factors, such as husbandry traditions, management practices, proximity trade-offs and selection objectives.

Overall, our results reveal a heterogeneous relationship between ecosystem classification and morphology, with strong ecosystem–morphotype correspondence in some ecosystems but extensive overlap in others. Although these ecosystems are representative of the broader distribution of Creole goats, the inclusion of additional regions may reveal further heterogeneity not captured in the present analysis. Whether these morphometric patterns correspond to underlying genetic differentiation remains to be determined.

Although this study highlights the potential influence of ecosystemic conditions on the morphology of Peruvian Creole goats, its scope was limited by the lack of detailed pedigree and production records, which restricted the ability to trace gene flow among herds. Likewise, other phenotypic indicators, such as production and phaneroptic traits, were not assessed. These traits likely interact with environmental and management factors and can contribute to differentiation of local ecotypes, as in Ethiopian local goat breeds (Gatew et al., 2019). Nonetheless, this is the first nationwide analysis of goat morphology in Peru using an ecosystem-based framework, providing a foundation for future studies integrating genetic, phenotypic, and management data to better understand the drivers of morphological diversity.

5. Conclusions

Using a UMAP-based approach, this study identified distinct morphometric groupings of Peruvian Creole goats at the national scale. The clearest group differentiation was observed in the AS, PSDF, and IASDF ecosystems, with clusters partially reflecting their regions of origin. In contrast, for other ecosystems, local factors beyond ecosystem classification appear to play a stronger role in shaping morphotypes. Together, these findings provide a foundation for defining ecosystem- or regional-specific morphotypes that, when integrated with animal performance data and ecological or geographic context, could support future geographic indications and enhance the value of local goat production systems.

Ethical statement

The study did not involve experimental or invasive procedures, and therefore ethical committee approval was not required. Body measurements were collected during routine management activities without causing additional distress. Animal husbandry practices complied with the Peruvian National Law No. 30,407 on Animal Protection and Welfare.

Consent to participate

Oral informed consent was obtained from all herd owners prior to data collection.

Declaration of generative AI and AI-assisted technologies in the manuscript preparation process

Statement: During the preparation of this work the authors used ChatGPT in order to revise grammar and style of the manuscript. After using this tool/service, the authors reviewed and edited the content as needed and take full responsibility for the content of the published article.

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CRediT authorship contribution statement

José Antonio Haro-Reyes: Writing – review & editing, Writing – original draft, Visualization, Validation, Methodology, Formal analysis, Data curation, Conceptualization. **Emmanuel Alexander Sessarego:** Writing – review & editing, Supervision, Project administration, Investigation, Conceptualization. **Miguel Enrique Paredes Chocce:** Writing – review & editing, Investigation, Formal analysis. **Víctor Alexander Temoche:** Writing – review & editing, Investigation. **José Antonio Ruiz Chamorro:** Writing – review & editing, Resources, Project administration, Conceptualization. **Juancarlos Alejandro Cruz-Luis:** Writing – review & editing, Resources, Project administration, Funding acquisition, Conceptualization. **Danny Julio Cruz:** Writing – review & editing, Writing – original draft, Visualization, Validation, Methodology, Formal analysis, Data curation, Conceptualization.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.vas.2026.100776.

Data availability

The data supporting the findings of this study are available upon request.

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