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Diet Composition and Forage Selectivity of Creole Goats Across Five Herd-Grazing Territories in a Peruvian Semi-Arid Andean Shrubland

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Simple Summary

Creole goat farming in the semi-arid Andean shrublands of Peru plays an essential role in ensuring food security in rural areas. However, under grazing systems, goats often face seasonal forage scarcity. This study aimed to identify the dietary taxa selected by these animals and determine how grazing territories influence their diet composition. We found that grazing territory location influenced diet quality more than individual animal traits, showing that a herd's nutrition depends primarily on where the goats graze. Thirty-two dietary taxa were identified, but the rate of occurrence in the feces was concentrated primarily on five dietary taxa, most notably *Vachellia macracantha* (contributing 47% to the diet) and *Croton collinus* (17%). *Vachellia macracantha* was the dominant browse source for goats in this area. Understanding this natural grazing pattern could help goat farmers control access to specific slopes or ravines and conduct herd grazing routing toward higher-quality vegetation. Furthermore, identifying nutritional deficits during dry periods could help the farmer devise affordable supplementation strategies. We suggest that future work assess the socio-economic feasibility and adoption of targeted feeding strategies such as local multinutrient blocks among local farmers to enhance livestock productivity and rural livelihoods.

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Abstract

This study assessed the relative effect of animal-intrinsic factors (AIF, age category, body condition, and height at withers) and herd-grazing territory (HGT)on botanical composition of the diet (BCD) and forage selectivity of Creole goats in a semi-arid Andean shrubland of Peru. The BCD employed a microhistological technique using fecal samples from 40 non-gestating goats (five herds). Distance-based redundancy analysis and Permutational multivariate analysis of variance (PERMANOVA) were utilized. The Jacobs selectivity index was calculated using a mixed linear model. The AIF and HGT explained 31.8% of the variation in BCD, with predominant variation in HGT ($p < 0.01$). PERMANOVA confirmed that BCD differed significantly among HGTs ($p < 0.01$), but not among the AIF ($p > 0.05$). *Vachellia macracantha* obtained the highest frequency of occurrence (100%) and relative contribution (46.96%) to the diet, followed by *Croton collinus*

(97.5%; 16.96%), *Senna incarnata* (97.5%; 6.79%), *Bouteloua disticha* (82.5%; 5.70%), and *Chloris radiata* (80.0%; 5.41%). *Vachellia macracantha* obtained positive selectivity indices (0.31–0.86), while *Croton collinus* (−0.60 to −0.22) and *Senna incarnata* (−0.67 to −0.26) remained negative. In conclusion, diet composition differed among HG, but we detected no significant associations with the measured animal-intrinsic factors.

Keywords: browsing; creole goats; diet selectivity; grazing behavior; microhistological analysis; *Vachellia macracantha*

1. Introduction

Goat farming is essential for small-scale farmers, particularly in arid and semi-arid regions around the world [1,2]. In communities with limited resources, this activity supports agricultural livelihoods, economic returns, and social well-being [3]. Goats provide products such as milk and meat [1,4]. They have also adapted well to harsh climates and can efficiently utilize low-quality fibrous materials. Additionally, they require minimal resources to raise [5,6].

The Creole goat production system in Peru is highly diverse, reflecting its adaptation to different ecological conditions and production environments. This diversity is reflected in the morphological differences among goat populations associated with distinct ecosystems, management practices, feeding resources, and levels of intensification [7,8]. According to estimates from 2022, Peru had a population of 1,767,612 goats, of which 85,926 were located in the La Libertad region [9]. These figures highlight the importance of goat production in the region and the need to better understand the feeding ecology of Creole goats in these particular environmental conditions.

Goats can feed on a diverse range of vegetation, including shrubs, forbs, and tree foliage, because they are mixed browsers and grazers. These characteristics enable Creole goats to thrive in semi-arid environments where other livestock may struggle [10]. Their feeding strategy is preferential and driven by the nutritional attributes of plants, including nitrogen content and secondary plant compounds such as tannins, which influence their forage selection among locally accessible dietary taxa [11]. Additionally, their foraging behavior and their geographical heterogeneity play significant roles in ecosystem management because selective grazing influences plant community dynamics, biodiversity, and soil nutrient cycling [12,13].

In small ruminants, selectivity is the ability of these dietary taxa to select and consume certain dietary taxa or components based on their nutritional characteristics, secondary metabolite content, palatability, forage availability, season, the animal's own ingestive behavior, and previous grazing experience [14,15]. Stocking density, group size, and competition are also key factors influencing foraging behavior in social animals such as goats [16,17]. Similarly, characteristics of the goats themselves, such as height at the withers, age, and body condition, can influence foraging behavior and diet selectivity [18,19].

While some factors influencing the diet composition and forage selectivity of goats are known, few studies have examined Creole goats in Peruvian ecosystems. Some studies have examined the production practices and management of Creole goats in various Peruvian ecosystems [7,8,20]. However, this is one of the first studies to attempt to fill this knowledge gap in the semi-arid premontane shrublands of northern Peru, where Creole goats are primarily fed in extensive systems. The objective of this study was to evaluate the effects of animal-intrinsic factors (age category, body condition, and height at withers)

and herd-grazing territory on the diet composition and forage selectivity of Creole goats grazing in a semi-arid Andean shrubland in Peru.

2. Materials and Methods

2.1. Study Site

The study was conducted in the northern Peruvian Andes, in the Mashual Cruz de Pecop Peasant Community, Otuzco, La Libertad (7°46′58.22″ S, 78°26′54.99″ W). This area is situated between 1600 and 2400 m above sea level. The communal rangeland extended over 560 ha. Mean annual rainfall was 429 mm, derived from historical data (1971–2013), with December and March having the highest rainfall. The mean maximum temperature ranged from 26.1 °C (March) to 28.1 °C (September), and the minimum temperatures ranged from 15.1 °C (July) to 16.9 °C (March). Meteorological data were obtained from the Callanca Meteorological Station operated by the Servicio Nacional de Meteorología e Hidrología del Perú (SENAMHI) monitoring network located in Otuzco [21].

Figure 1 displays the selected areas, which correspond to a semi-arid shrubland formation characterized by three predominant vegetation subtypes defined by plant associations of *Senna incarnata*, *Vachellia macracantha*, and *Croton collinus*, occurring in different combinations.

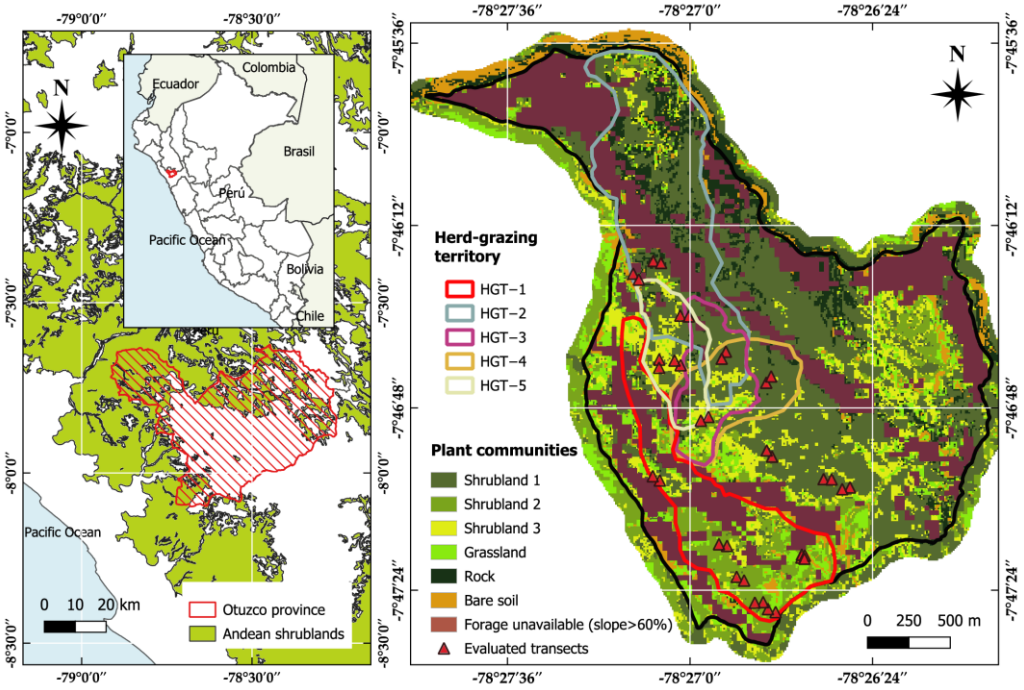


Figure 1. Vegetation types in grazing areas for Creole goats in a semi-arid Andean shrubland of Peru. Shrubland 1: *Vachellia macracantha* – *Croton colinus*; Shrubland 2: *Croton colinus*; Shrubland 3: *Senna Incarnata - Vachellia macracantha*.

2.2. Animal Selection, Measurements and Management

This study followed a descriptive, observational, cross-sectional design. Creole goats were observed under their usual grazing conditions, without the application of experimental treatments or manipulation of their management practices.

From a total of 580 animals (belonging to ten herds), 40 non-gestating Creole goats were selected from five herds, averaging 7 to 9 goats per herd (See Supplementary materials Table S1). Goats were classified into two age categories based on dentition

(permanent incisors): sub-adults (1–2 pairs) and adults (3–4 pairs). Body condition was measured as poor (≤1.5) and regular (1.5–2.5). Withers height was measured employing a zoometric cane. These three animal-intrinsic factors (AIF) were determined following the standard FAO guidelines [22].

Goats grazed daily from 07:00 to 17:00 h within the communal grazing system. Women herded the animals daily and confined them in the evenings. Although animals shared a large communal pasture, each herd showed territorial grazing patterns. Therefore, "herd–grazing territory" (HGT) represented the combined influence of the specific features of each grazing area, including the availability and composition of the vegetation, as well as the grazing management applied by each herder and the herd's social response (collective foraging experiences and preferences for specific dietary taxa). To account for these differences, the affiliation of each of the 40 goats to one of the 5 evaluated herds was individually identified. The HGT were mapped using a Global Positioning System (GPS) during multiple visits with local goat herders (Figure 1).

2.3. Vegetation Sampling

Forage availability was assessed during the dry season using a stratified random sampling design within the grazing areas. A total of 16 randomly located 50 m line-point intercept transects, each with 10 quadrats, were established to quantify vegetation cover and structural composition of the main dietary taxa [23].

To ensure representative sampling, the vegetation transects were distributed proportionally across the grazing areas. Along each 50 m transect, we evaluated 50 equidistant interception points at one-meter intervals using the Line-Point Intercept (LPI) method [24]. At each sampling point, a graduated rod was lowered perpendicular to the ground to record all dietary taxa in contact with the vertical projection and to measure vegetation height, accounting for multiple structural layers. The specific cover percentage for each dietary taxon was calculated by dividing the number of points at which the dietary taxon was present by the total number of points evaluated per transect (N = 50) and expressing the result as a percentage.

In addition, ten 2 × 1 m quadrats were systematically placed along each transect to assess the number of dietary taxa and to collect representative samples for taxonomic identification and microhistological reference preparation [23]. All dietary taxa within quadrats were identified to the lowest possible taxonomic level, and later assigned to the local botanical reference collection. Plant community occurrence was represented as percent cover by dietary taxa and ecological group, including trees, shrubs, grasses, and forbs (herbaceous broadleaf dietary taxa).

Additionally, samples of individual predominant tree, shrub, and herbaceous dietary taxa were collected [25]. Then, samples were analyzed at the Laboratorio de Evaluación Nutricional de Alimentos at the Universidad Nacional Agraria La Molina (UNALM) using the Association of Official Analytical Chemists methods [26]. The chemical composition analysis included moisture (method 950.46), crude protein (method 984.13), crude fiber (method 962.09), crude fat (method 920.39), crude ash (method 942.05), and in vitro dry matter digestibility (ANKOM Daisy incubator, USA).

2.4. Diet Microhistological Analysis

Fecal samples were obtained directly from the rectums of 40 selected goats via routine palpation. Veterinary lubricant and palpation gloves were used to minimize stress and prevent injury. The animals were restrained manually, one by one, within the community's handling facilities. This approach avoided prolonged isolation and ensured a calm environment for the animals. The entire process was non-invasive, rapid, and carried out by trained personnel in accordance with the best veterinary practices for animal

welfare. Furthermore, the community authorities and the owners granted permission to access the grazing areas and to handle and sample the animals.

The samples were preserved in a 5% formaldehyde solution, placed in labeled individual vials, and subsequently stored in a cooler. The botanical composition of the diet was based on the procedure described by Sparks and Malechek [27], following the modified protocol of the Microhistology Laboratory at the Instituto Nacional de Tecnología Agropecuaria (INTA), Estación Experimental Agraria Bariloche, Argentina [28]. Analyses were conducted at the Laboratorio de Ecología y Utilización de Pastizales (LEUP) at the Universidad Nacional Agraria La Molina (UNALM).

Fecal samples were oven-dried at 60 °C for 48–72 h to express results on a dry matter (DM) basis and ground to 1 mm. The ground sample was then rehydrated in 70% ethanol and subjected to thermal digestion in a water bath. It was subsequently washed and cleared with sodium hypochlorite and stained with alcoholic safranin for 24 h. The digested material was mounted in gelatin-glycerin using a standardized metal template to prepare five slides per sample. Twenty microscopic fields were examined per slide, resulting in a total of 100 fields per sample. Dietary taxa were identified by recognizing the diagnostic characteristics of epidermal and non-epidermal tissues. During microscopic observation, the presence of each dietary taxon in each field was recorded, regardless of the number of fragments observed. Finally, the relative frequencies of occurrence of the identified dietary taxa were calculated to determine the botanical composition of the diet.

Microscopic identification was based on a reference catalog from the LEUP-UNALM, which included 47 local species (trees, shrubs, forbs, and grasses) and followed the protocol developed by INTA Bariloche, as well as standard anatomical literature [29–34]. The descriptive characterization covered leaves, young stems, sheaths, seeds, flowers, and fruits, in accordance with standardized botanical criteria. Detailed descriptions were provided for cellular architecture (size, shape, sinuosity, and cell wall thickness), short cells, stomatal types and their associated subsidiary/accessory cells, trichomes, inclusions, fibers, and non-epidermal structures (parenchymal sheaths and sclerenchyma).

Furthermore, the selection of the dominant taxa in the diet was based on a quantitative criterion—relative contribution (≥5%)—prioritizing this over frequency of occurrence [35].

2.5. Forage Availability

Forage availability was estimated within each herd-grazing territory (HGT) in two stages. First, the coverage of each of the four predominant vegetation groups—scrubland 1, scrubland 2, scrubland 3, and grassland—was estimated using supervised classification of 2024 Sentinel-2 images corresponding to the study period (Kappa = 0.89). Biomass was estimated using the Adelaide method [36] after calibrating the evaluator to achieve R^2 values greater than 0.84. Second, the availability of each dietary taxon was calculated from dietary taxon-specific biomass and the proportional coverage of the vegetation group, respectively. As a result, a weighted biomass estimate for each dietary taxon within each HGT was obtained.

2.6. Selectivity Index

The frequency of occurrence (F_i) represents the percentage of samples in which a specific dietary taxon was identified as follows:

$$F_i = \frac{\sum_{i=1}^{n} I(p_{ij} > 0)}{n} \times 100$$

where F_i is the frequency of occurrence of the dietary taxon I; p_{ij} is the value recorded for the dietary taxon i in sample j; I (p_{ij}> 0) is an indicator function that takes the value of

1 when the dietary taxon was present and 0 when it was absent; and n represents the total number of samples evaluated.

Likewise, the relative contribution of each dietary taxon (C_i) was calculated as follows:

$$C_i = \frac{\sum_{j=1}^{n}(p_{ij})}{\sum_{i=1}^{s}\sum_{j=1}^{n} p_{ij}} \times 100$$

where C_i is the relative contribution of the dietary taxon i; p_{ij} is the value recorded for dietary taxon i in sample j; s is the total number of dietary taxa identified; and n represents the total number of samples evaluated.

Both indicators were used to identify the dietary taxa of greatest dietary importance and to select the five most representative for the selectivity index analysis.

The selectivity index was calculated using the modified Ivlev–Jacobs index [37]:

$$D_{ijk} = \frac{r_{ij} - p_{ik}}{r_{ij} + p_{ik} - 2r_{ij}p_{ik}}$$

where D_{ijk} is Jacobs' selectivity index for dietary taxon i in animal j belonging to herd-grazing territory k; r_{ij} is the proportion of dietary taxa in the diet of animal j; and p_{ik} is the proportional availability of dietary taxa within herd-grazing territory k. They range from 0.5 to 1 for strong selection, from 0.1 to 0.49 for weak selection, from −0.09 to 0.09 for indifference, from −0.1 to −0.49 for weak avoidance, and from −0.5 to −1.0 for strong avoidance [38].

2.7. Statistical Analysis

Diet composition was organized into a matrix of percentage consumption of plant taxa by individual animal, excluding taxa not consumed by any animal. Dissimilarities in diet composition were calculated using Bray–Curtis distances with Lingoes correction. The effects of HGT and AIF on diet composition were assessed using distance-based redundancy analysis (dbRDA) and Permutational multivariate analysis of variance (PERMANOVA). Global model significance and the marginal effects of individual predictors, adjusted for the remaining terms, were assessed using 10,000 permutations. Body condition and withers height were included as covariates. When the herd was significant, paired comparisons were performed using PERMANOVA with Holm adjustment. We conducted permutation tests for HGT using unrestricted permutations, and we additionally assessed associations with animal-intrinsic factors using permutations restricted within HGTs. Each animal contributed one observation to the diet composition analysis.

For the selectivity analysis, the five dietary taxa with the highest occurrence frequency (Fi, % of animals that consumed it) and the highest relative contribution to the diet (Ci, % of total occurrence) were selected. Jacobs' selectivity index was analyzed using a generalized linear mixed-effects model (GLMM) with a beta distribution and a logit link function. Since the index ranges from −1 to 1, its values were transformed as Y = (D + 1)/2 to obtain a response bounded between 0 and 1. Five species-specific selectivity indices were calculated for each animal, and individual identity was included as a random intercept to account for dependence among observations from the same animal. Dietary taxa, herd, age category, and the dietary taxa × HGT and dietary taxa × age category interactions were included as fixed effects, whereas body condition score and withers height were included as continuous covariates. The general formulation of the model was as follows:

$$Logit\left[Y_{ijkl}/\mu_j\right] = \mu + S_i + HG_k + A_l + (S \times HG)_{ik} + (S \times A)_{il} + \beta_1 BC_J + \beta_2 H_J + \mu_j + \varepsilon_{ijkl}$$

where $Y_{ijkl} = (D_{ijkl} + 1)/2$ is the transformed Jacobs' selectivity index, D_{ijkl} is the observed Jacobs selectivity index for dietary taxon i evaluated in animal j, belonging to herd-grazing territory k and age category l; μ, is the intercept; S_i, is the fixed effect of dietary

taxon; HG_k is the fixed effect of herd-grazing territory; A_l is the fixed effects of age category (sub-adult or adult); $(S \times HG)_{ik}$ is the interaction between dietary taxon and herd-grazing territory; $(S \times A)_{il}$ is the effect of the interaction between vegetal specie and age category; BC_J, is the body condition; H_J, is the heigh to the withers; β_1 and β_2 are the regression coefficients associated with body condition and withers height, respectively; u_j is the random effect of the animal j, assumed as $\mu_j \sim N(0, \sigma 2)$, which models the correlation between repeated observations obtained from the same individual.

The GLMM was fitted by maximum likelihood using the glmmTMB package (version 1.1.14). Model convergence, the positive definiteness of the Hessian matrix, and random-effect variance were examined, and model adequacy was assessed using simulated residuals (DHARMa package version 0.5.0, 1000 simulations). Fixed effects were evaluated using type III Wald chi-square tests. To interpret the species × HGT interaction, pairwise comparisons between dietary taxa within each HGT and comparisons of each species across HGTs were performed using estimated marginal means (emmeans package version 2.0.4). We back-transformed estimated marginal means and their pointwise 95% confidence intervals to the original Jacobs' selectivity index scale. Analyses were performed using R software (version 4.6.1).

3. Results

3.1. Botanical Composition of the Diet

Thirty-two dietary taxa were recorded in the diet of Creole goats (Table 1). The frequency of occurrence (Fi) and the relative contribution to the diet (Ci) varied widely among dietary taxa. *Vachellia macracantha* had the highest frequency of occurrence (100%) and the highest relative contribution to the diet (46.96%), followed by *Croton collinus* (97.5%; 16.96%), *Senna incarnata* (97.5%; 6.79%), *Bouteloua disticha* (82.5%; 5.70%), and *Chloris radiata* (80.0%; 5.41%).

Table 1. Frequency of occurrence and relative contribution to the diet of the dietary taxa consumed by Creole goats.

Dietary Taxon	Plant Functional Group	n	F_i (%)	C_i (%)
Vachellia macracantha	Tree	40	100.0	46.96
Croton collinus	Shrub	39	97.5	16.96
Senna incarnata	Shrub	39	97.5	6.79
Bouteloua disticha	Grass	33	82.5	5.70
Chloris radiata	Grass	32	80.0	5.41
N.N.3	------	38	95	4.72
Baccharis gnidiifolia	Shrub	27	67.5	4.28
N.N.2	------	11	27.5	2.02
Eragrostis tenuifolia	Grass	21	52.5	1.28
Dalea carthagenensis	Shrub	19	47.5	1.25
Melinis minutiflora	Grass	16	40	0.67
Amaranthus hybridus	Forb	24	60	0.64
Paspalum humboldtianum	Grass	12	30	0.45
Nassella mucronata	Grass	10	25	0.38
Dichondra microcalyx	Forb	6	15	0.36
Mesosphaerum sidifolium	Forb	11	27.5	0.34
Poa sp.	Grass	4	10	0.32
Spermacoce remota	Forb	7	17.5	0.27
N.N.1	------	5	12.5	0.21
Arcytophyllum thymifolium	Shrub	7	17.5	0.15

Sida spinosa	Forb	7	17.5	0.15
Wedelia latifolia	Forb	5	12.5	0.11

Note: n is the number of animals in which the occurrence of each dietary taxon was recorded; fi is the frequency of occurrence (%); Ci is the relative contribution to the diet (%). N.N.1, N.N.2, and N.N.3: They are unidentified dietary taxa (dicotyledons).

However, it is important to highlight that two of the four unidentified dietary taxa in the BCD showed a similar Cm in the diet of Creole goats.

3.2. Effects of Herd-Grazing Territory and Animal-Intrinsic Factors on Diet Composition

Distance-based redundancy analysis (dbRDA) using Lingoes-corrected Bray–Curtis distances showed that the set of explanatory variables (herd-grazing territory, age category, body condition, and withers height) explained 31.8% of the variation in diet composition ($R^2 = 0.318$, adjusted $R^2 = 0.169$) (See Supplementary materials Table S2). The overall model was significant ($F = 2.13$, $p < 0.001$). The first two canonical axes were significant ($p < 0.01$) and together accounted for 63.9% of the constrained variation explained by the model (Figure 2). Among the variables evaluated, only herd type had a significant effect on diet composition ($F = 2.27$, $p < 0.01$), whereas AIF did not ($p > 0.05$). Variance inflation factors (VIFs) ranged from 1.13 to 3.10, indicating no substantial collinearity among the predictors included in the dbRDA model.

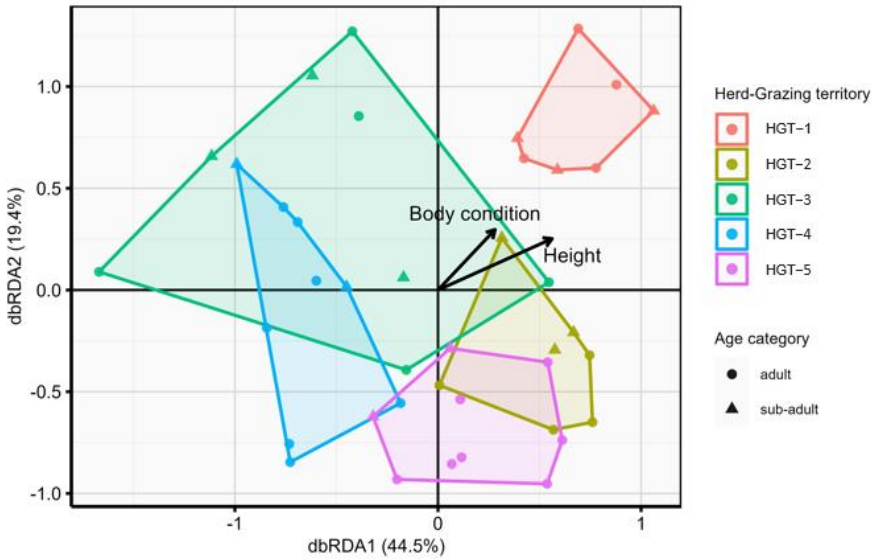


Figure 2. Distance-based redundancy analysis (dbRDA) of the botanical composition of Creole goat diets across herd-grazing territories (HGT). Points represent individual goats, with symbols indicating age categories. Polygons represent convex hulls enclosing the observations within each HGT. Arrows represent the body condition score and withers height vectors. The percentages shown on the axes indicate the proportion of constrained variation represented by each dbRDA axis.

Figure 2 showed differences in diet composition among the HGTs. In particular, the individuals in HGT−1 were clearly distinct from the other HGTs, whereas HGT−2, HGT−3, and HGT−5 showed greater overlap. The animals in HGT−4 occupied an intermediate position, with partial separation from the other groups.

The PERMANOVA analysis confirmed that diet composition differed significantly among HGT ($p < 0.01$), while age category ($p > 0.05$), body condition ($p > 0.05$), and withers height ($p > 0.05$) did not show significant effects. Paired comparisons showed significant differences in most herds (Table 2). In contrast, no differences were detected between

HGT−3 and HGT−4 ($p > 0.05$) or between HGT−2 and HGT−5 ($p > 0.05$). Multivariate dispersion differed among HGTs ($F = 3.57$, $p = 0.014$), although no pairwise differences remained significant after Holm adjustment ($p > 0.05$).

Table 2. Holm-adjusted *p*-values for pairwise PERMANOVA comparisons of diet composition among herd-grazing territories (HGT).

	HGT−2	HGT−3	HGT−4	HGT−5
HGT−1	0.077	**0.007**	**0.003**	**0.003**
HGT−2		**0.016**	**0.001**	0.196
HGT−3			0.196	**0.002**
HGT−4				**0.004**

Holm correction was applied across all 10 pairwise comparisons among the five HGTs. Bold values indicate statistically significant differences (adjusted $p < 0.05$).

3.3. Nutritional Composition of Dominant Dietary Taxa

The proximate chemical composition of the main dietary taxa identified in the feces is presented in Table 3. Regarding crude protein (CP), the dietary taxa (*Vachellia macracantha* and *Senna incarnata*) recorded concentrations of 16.0% and 13.1%, respectively—higher values than those observed for the grasses (*Bouteloua disticha* and *Chloris radiata*), which both showed similar contents of 8.0%. Regarding crude fiber (CF), *Vachellia macracantha* had a concentration of 9.1%, while *Chloris radiata* reached 25.0%.

Table 3. Nutritional composition of dominant dietary taxa consumed by Creole goats in a semi-arid scrubland of Peru.

Dietary Taxa	Moisture (%)	Crude Protein (%)	Ether Extract (%)	Crude Fiber (%)	Crude Ash (%)	Nitrogen-Free Extract (%)	Organic Matter (%)	IVDMD (%)
Trees								
Vachellia macracantha	10.2	16.0	3.8	9.1	4.4	56.5	95.6	45.2
Shrubs								
Croton collinus	6.8	10.5	3.2	18.7	9.7	51.1	90.3	53.2
Senna incarnata	9.0	13.1	2.5	9.2	5.9	60.3	94.1	56.4
Grasses								
Bouteloua disticha	7.3	8.0	1.9	24.9	12.2	45.7	87.8	43.7
Chloris radiata	7.4	8.0	2.1	25.0	10.6	46.9	89.4	50.4

Note: *IVDMD: in vitro dry matter digestibility.*

Regarding the in vitro dry matter digestibility (IVDMD), variability was observed among the analyzed dietary taxa. For instance, *Vachellia macracantha* recorded a value of 45.2%, whereas *Chloris radiata* reached 50.4%. These results demonstrate that nutritional attributes vary specifically for each evaluated taxon, without following a uniform pattern based on growth category.

Figure S1 (See Supplementary Materials) illustrates the key epidermal features used for the microhistological identification of the five dominant dietary taxa.

3.4. Forage Selectivity

Jacobs' selectivity index clearly depended on the HGTs, as evidenced by the significant interaction between dietary taxa and HGT ($\chi^2 = 99.05$, df = 16, $p < 0.001$). Among the five dietary taxa evaluated in the different HGTs (Figure 3), *Vachellia macracantha* was the only one that presented positive selectivity indices in all of them (0.24–0.76), while *Croton colinus* (−0.67 to −0.20) and *Senna incarnata* (−0.59 to −0.25) showed negative estimated indices in all HGTs.

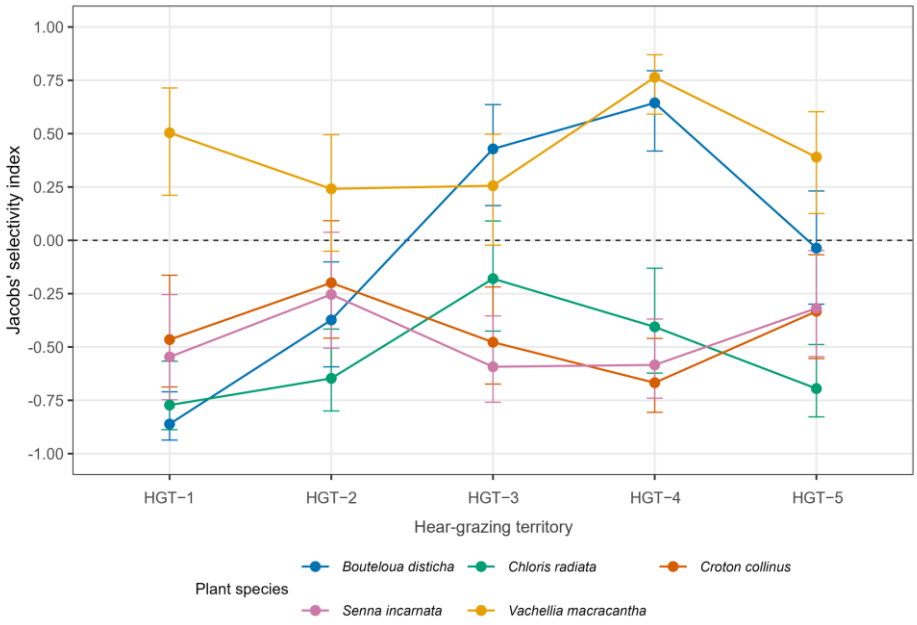


Figure 3. Estimated marginal means (± 95% confidence interval, CI) of the Jacobs selectivity index for the five dietary taxa evaluated in each herd-grazing (HGT) territory. Different letters indicate significant differences between dietary taxa within each HGT, back-transformed to the original index scale.

The greatest variation between herds was observed in *Bouteloua disticha*, whose selectivity index went from −0.86 in HGT−1 to 0.64 in HGT−4 (Δ = 1.51), passing through −0.37 (HGT−2), 0.43 (HGT−3), and −0.04 (HGT−5). In comparison, *Chloris radiata* showed less variation (−0.77 to −0.18) and maintained negative indices in four of the five HGTs (Figure 3).

Tests against zero with Holm adjustment showed evidence of positive selectivity for Bouteloua disticha in HGT−3 and HGT−4 and for *Vachellia macracantha* in HGT−1 and HGT−4. Negative selectivity indices differed significantly from zero for *Chloris radiata* in HGT−1, HGT−2, and HGT−5; *Croton collinus* and *Senna incarnata* in HGT−1, HGT−3, and HGT−4; and *Bouteloua disticha* in HGT−1 (See Supplementary materials Tables S3–S5).

In addition to the dietary taxa × HGT interaction, significant main effects of dietary taxa ($\chi^2 = 155.06$; df = 4; $p < 0.001$) and HGT ($\chi^2 = 20.28$; df = 4; $p < 0.001$) were detected. Age category did not show a significant main effect on selectivity ($\chi^2 = 1.05$; df = 1; $p = 0.306$). The interaction between dietary taxa and age category was not significant ($\chi^2 = 3.21$; df = 4; $p = 0.523$), indicating no evidence that juveniles and adults modify their preferences differently among the dietary taxa evaluated. Likewise, body condition ($\chi^2 = 0.06$; df = 1; $p > 0.938$) and wither height ($\chi^2 = 1.55$; df = 1; $p = 0.213$) did not show significant effects on the selectivity index (Figure 3).

4. Discussion

4.1. Dietary Botanical Composition

The majority of the Creole goat diet in this study consisted of tree and shrub dietary taxa such as *Vachellia macracantha*, *Croton collinus*, and *Senna incarnata* (70.7%; see Table 1). Other research studies also support the dominance of woody dietary taxa in goat diets [39–42]. Goats are flexible mixed-feeding herbivores in grassland ecosystems that exhibit a pronounced preference for browsing on shrubs, particularly when forbs and grasses are limited [13].

Conversely, studies in different ecosystems demonstrate that the botanical composition of a goat's diet varies, but is always dominated by a few dietary taxa, ranging from seven to 15 [15,43]. Similarly, although the diet of the Creole goats in this study consisted of a greater number of dietary taxa (see Table 1), only five dietary taxa were dominant.

4.2. Influence of AIF and Herd-Grazing Territory on Diet Composition

The set of considered variables (AIF and herd-grazing territory) explained 31.8% of the variation in diet composition; however, this variation was primarily associated with herd-grazing territory (Figure 2). Additionally, under the conditions of this study, no evidence was found of the effects of age category, body condition, or withers height on the diet composition of Creole goats (Figure 3). These findings underscore the significance of herd-grazing territory in the dietary composition of Creole goats in a semi-arid Andean region of Peru. Similarly, other investigations have found that the diets of grazing ruminants are influenced by genetics at the individual level, as well as by the social herd environment, including the animal's previous browsing experience, weather conditions, and the nutritional characteristics and availability of dietary taxa depending on the season [15,40,44–46].

However, because each herd was associated with its own grazing territory, HGT represented a combined sampling unit. Thus, we cannot attribute the observed differences separately to herd characteristics or local forage conditions. Furthermore, shared conditions within HGTs may affect the independence assumptions of individual-level permutation tests, which limits the interpretation and generalization of these findings beyond the five sampled herd-grazing territories. Additionally, the limited number of subadult goats (n = 13), restricted variation in body condition, and differences in withers height among HGTs may have reduced our ability to detect associations with animal-intrinsic factors. Therefore, the absence of significant associations should not be interpreted as evidence that these traits have no biologically relevant effect on diet composition.

4.3. Nutritional Quality of Dominant Forage Taxa

In this study, the tree and shrub taxa evaluated exhibited higher crude protein concentrations and lower crude fiber contents than the analyzed grasses (Table 3). This trend aligns with observations by various authors who have noted that the crude protein values of shrub taxa in the diets of arid-zone animals range from 11.3% to 20.4%, whereas grasses exhibit lower values ranging from 3.5% to 4.3% [47–49]. However, the results in Table 3 show distinct in vitro dry matter digestibility patterns among individual taxa, such as between *Vachellia macracantha* and *Chloris radiata*. This demonstrates that nutritional quality varies among taxa rather than following a uniform standard for the entire woody vegetation layer. Despite this, the general literature often reports high digestibility for certain forage shrubs in semi-arid zones [48,50,51].

As the goat is a browser and a significant portion of its diet consists of shrubs and trees, it indirectly consumes dietary taxa with high nutritional value and better digestibility [52]. However, this depends on various factors such as dietary taxa, nutritional content

(including secondary compounds), biomass availability, animal characteristics, climate conditions, and previous browsing experience, which promote more uniform resource use across the herd [40,44,45].

The literature supports that goats consume dietary taxa with moderate tannin content because they exhibit constitutive expression of salivary tannin-binding proteins (TBSPs) in their saliva as a survival mechanism in this environment [53]. Nevertheless, it is important to highlight that a favorable combination of nutritional attributes, such as relatively high protein content, lower structural component content, and greater digestibility, may contribute to the selection of woody dietary taxa by goats [46,54].

4.4. Mechanisms and Implications of Forage Selectivity

Goats are characterized as excellent browsers with very selective diets [10]. In this study, goats exhibited a significant preference for *Vachellia macracantha* (Table 1 and Figure 3). This tree taxon is one of the most representative of the seasonally dry tropical forests of northern Peru [55]. As in our study (Figure 3), different Vachellia dietary taxa are preferred by goats in African countries. Their preference could be linked to the moderate fiber content (neutral and acidic detergent fiber), which is directly related to a higher protein and energy content [56,57]. However, *Vachellia macracantha* contains condensed tannins. Goats have demonstrated tolerance to tannins in their diet due to the presence of TBSP in their saliva [53,58].

Conversely, goats avoided *Croton collinus* and *Senna incarnata* (Figure 3). Avoiding certain dietary items in their diet may be related, in part, to the potential presence of phenolic compounds, varying concentrations of secondary metabolites, and other factors [11,41,42]. However, this study did not determine the presence or concentrations of secondary metabolites in all dietary taxa evaluated. Consequently, their potential contribution to the observed avoidance is a hypothesis, not a proven mechanism. Further exploration of these components in native shrubs is required.

Finally, this study showed that selectivity is not a fixed property of the dietary taxa or a uniform characteristic of the goat dietary taxa. It can depend on the herd behavior and grazing context. For instance, variation in the *Bouteloua disticha* dietary taxon's preference or avoidance could be related to differences in plant characteristics (e.g., nutritional composition), the goats' feeding experience, and the herd's collective behavioral patterns [46], as well as other previously mentioned factors.

One of the main strengths of this study is that it provides new baseline information on the diet composition and forage selectivity of Creole goats in an understudied, semiarid Andean shrubland ecosystem. Additionally, by examining differences among grazing territories of herds under communal conditions, this study improves our understanding of how herd-grazing territory influences feeding patterns of goats in extensive production systems. These findings will be useful for future research and the development of context-specific grazing management strategies.

However, some limitations must be acknowledged. The absence of fences in communal grazing areas allowed occasional uncontrolled mixing among herds and interactions with other dietary taxa of livestock. Additionally, daily variations in herders' management decisions were a potential source of confounding factors that could not be fully controlled. These unmeasured factors may have influenced herd movements and foraging patterns. Finally, since the findings reflect the specific herds, management conditions, and botanical composition of the study area in one season of the year (dry season), further research across a wider range of shrubland ecosystems and grazing conditions is needed before extrapolating these results to broader geographical or ecological scales.

5. Conclusions

This research demonstrates the critical role of herd-grazing territory in shaping the dietary composition and selectivity of Creole goats in Peruvian shrublands. Additionally, *Vachellia macracantha* was documented as a dominant dietary tree taxon browsed by Creole goats. Overall, these findings inform the design of grazing strategies focused on vegetation diversity and herd management, especially during the dry season. Understanding this natural grazing pattern will enable goat farmers to control access to specific slopes or ravines and direct their herds to graze on higher-quality vegetation. Furthermore, identifying nutritional deficits during dry periods could help farmers devise affordable supplementation strategies. We recommend future studies assess the socio-economic feasibility and adoption of targeted feeding strategies, such as providing local multinutrient blocks, among local farmers to improve livestock productivity and rural livelihoods.

Supplementary Materials: The following supporting information can be downloaded at https://www.mdpi.com/article/10.3390/ani16233748/s1. Table S1. Characteristics of Creole goats sampled across five herd-grazing territories in a semi-arid Peruvian shrubland. Table S2. Global and marginal results of distance-based redundancy analysis (dbRDA) and PERMANOVA for diet composition in Creole goats. Table S3. Model-estimated Jacobs' selectivity indices and 95% confidence intervals for five dietary taxa across herd-grazing territories. Table S4. Pairwise comparisons of dietary taxa within each herd-grazing territory based on the beta generalized linear mixed model. Table S5. Pairwise comparisons of herd-grazing territories within each dietary taxon based on the beta generalized linear mixed model. Figure S1. 1. Photomicrograph of the leaf epidermis of Vachellia macracantha. 2. (A) Stellate trichome (10X. (B) Trichome base (40X). (C) Stellate trichome of Croton collinus. 3. Photomicrograph of the leaf epidermis of Senna incarnata. 4. Detailed photomicrograph of the leaf epidermis of Bouteloua disticha (40X). 5. Detailed photomicrograph of an epidermal fragment of Chloris radiata (40X). CE: epidermal cells, ES: stomata, ZI: intercostal zone, CC: short cells, AG: presence of prickles, ZC: coastal zone, TR: trichomes, CL: long cells.

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Informed Consent Statement: Informed consent was obtained from all animal owners involved in the study. Prior to sample collection, the aims and non-invasive procedures of the research were explained orally to the local livestock producers, who gave their verbal consent. Additionally, formal written authorization to conduct sampling and research activities within the territory was granted by the President of the Community.

Data Availability Statement: The data with the main characteristics of the selected herds in a semi-arid Peruvian scrubland is provided in Supplementary Materials.

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Abbreviations

The following abbreviations are used in this manuscript:

AIF	Animal-intrinsic factor
HGT	Herd-grazing territory
BCD	Botanical composition of the diet
PERMANOVA	Permutational multivariate analysis of variance
dbRDA	Distance-based redundancy analysis
GPS	Global Positioning System
UNALM	Universidad Nacional Agraria La Molina
INTA	Instituto Nacional de Tecnología Agropecuaria
Fi	Frequency of occurrence
C_i	Contribution of each dietary taxon
S	Dietary taxon
A	Age category
N.N.	Unidentified dietary taxon (dicotyledons).
IVDMD	In vitro dry matter digestibility
CI	Confidence interval
SD	Standard deviation

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