

Regional morphometric variation and phenotypic structure of Moorish zebu cows (*Bos indicus*) in Mauritania

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Research Article

Keywords: Animal genetic resources, Body measurements, Dairy cattle, Multivariate analysis, Phenotypic diversity, Mauritania (Sahel)

Posted Date: September 14th, 2026

DOI: <https://doi.org/10.21203/rs.3.rs-10821640/v1>

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Abstract

The Moorish zebu supports pastoral livelihoods in Mauritania, but regional morphometric variation has not been quantified using a common field protocol. To describe phenotypic variation among adult lactating cows from three Mauritanian regions and explore whether the sample contained distinct morphometric groups. A purposive cross-sectional sample included 352 cows from 158 herds in Hodh Chargui, Brakna, and Trarza. Sixteen direct measurements, estimated body weight, 16 zoometric indices, and six qualitative traits were recorded. Regional comparisons used one-way analysis of variance; LDA, PCA, and K-means explored multivariable structure. Associations with recorded milk yield were examined in 349 cows. LDA classification was validated by leave-one-herd-out cross-validation across the 158 sampled herds. Nominal regional differences were most evident for thoracic dimensions, estimated weight, and udder traits. Herd-grouped LDA classified 59.5% of cows to their region of origin, 2.9 points lower than non-grouped cow-level validation (62.4%). Three principal components explained 50.3% of variance. A three-group partition had weak separation (silhouette = 0.281, versus 0.298 for two groups). Teat length showed the largest unadjusted correlation with daily milk yield ($r = 0.381$). The exploratory three-trait model had non-nested cross-validated $R^2 = 0.162$ and RMSE = 1.19 L/d. Sampled cows displayed overlapping regional morphometric variation rather than discrete regional types. This study nonetheless provides the first multi-region, herd-aware morphometric description of Moorish zebu cows in Mauritania, establishing provisional descriptive references while showing why current evidence does not yet support a breed standard, regional genetic subdivision, or phenotypic selection criterion; the proposed clusters and milk model require independent, herd-aware validation.

Introduction

Locally adapted cattle are central to food security and household resilience in arid and semi-arid production systems. They tolerate heat, seasonal feed scarcity, and disease challenges that constrain specialized breeds, while providing milk, meat, traction, and financial reserves (Gaughan et al., 2019; Mapiye et al., 2019). Their continued use nevertheless depends on reliable characterization because poorly documented populations are difficult to manage, conserve, or improve and may be vulnerable to unplanned crossbreeding (Corrales et al., 2010; Martínez-Aguilar, 2020; Parra-Cortés et al., 2021; Rege and Tawah, 1999).

The Moorish zebu is a major cattle resource in the Sahelian and sub-desert zones of Mauritania. It is maintained mainly in extensive pastoral and agropastoral systems and is valued for milk production and adaptation to local environments (ANSADE, 2025; El Hadj et al., 2024). Available breed descriptions remain largely qualitative, and the extent to which body conformation varies among production regions has not been established with a common measurement protocol.

Morphometric measurements and derived indices can describe population structure and provide a first phenotypic reference before genomic investigation (FAO, 2012; Lomillos and Alonso, 2020). Multivariate methods are useful because body traits are correlated and regional differences may reflect continuous gradients rather than sharply separated populations. Similar approaches have revealed substantial within-population variation in indigenous and Creole cattle (Aguirre-Riofrio et al., 2019; Baye et al., 2022; Rojas-Espinoza et al., 2023; Contreras Huamani et al., 2026). PCA summarizes correlated measurements, LDA evaluates supervised regional separation, and clustering can identify candidate phenotypic groups. Cluster-derived groups should, however, be regarded as exploratory unless they show clear separation and are replicated in independent data.

The objectives were therefore to (1) describe body measurements, zoometric indices, and qualitative traits of adult Moorish zebu cows sampled in three Mauritanian regions; (2) quantify regional patterns using univariate and multivariable analyses; (3) explore whether the data supported candidate phenotypic groups; and (4) examine hypothesis-generating associations between morphology and recorded milk yield. Provisional reference values are reported for the sampled cows, explicitly separated from a formal breed standard, regional genetic subdivision, or genetic selection criterion.

Material and methods

Study design, regions, and animals

A cross-sectional survey was conducted between July 2023 and May 2024 in the Hodh Chargui, Brakna, and Trarza regions of Mauritania (Fig. 1).

The dataset included 352 cows from 158 herds: 50 herds (91 cows) in Hodh Chargui, 51 herds (100 cows) in Brakna, and 57 herds (161 cows) in Trarza (Table 1). The herds were identified through the regional technical services of the Ministry of Livestock, collection centers, and livestock breeders' associations, and were selected to cover accessible herds within each region using a non-random sampling method. Sampling was purposive and aimed to include the phenotypic range observed within each region rather than to estimate population prevalence as part of a probabilistic sampling plan. The sampled cows belong to commercial herds located in their area of origin that practice seasonal transhumance, according to statements from the herd owners. Accordingly, all regional summaries and comparisons refer to the sampled cows and should not be interpreted as representative population estimates.

Table 1
Number of herds by region

Region	Number of herd	Cows/herd (mean ± SD)	Min–Max	Mediane
Hodh Chargui	50	1,82 ± 0,68	1–3	2
Brakna	51	1,96 ± 0,71	1–4	2
Trarza	57	2,82 ± 1,54	1–9	3
Overall	158	2,23 ± 1,17	1–9	2

Eligible animals were identified as Moorish zebu from herd-owner genealogical knowledge and locally recognized breed characteristics. Cows were required to be adult, multiparous, lactating, clinically healthy, and free from visible abnormalities or acquired defects that could affect measurement. Cows in advanced pregnancy or severe loss of body condition were excluded. Within herds, animals were selected to capture phenotypic variation while avoiding close relatives when this was known. The same field team applied a common measurement protocol in all regions.

Phenotypic measurements and estimated body weight

Six qualitative traits were recorded: coat pattern (unicolor or multicolor), coat color (eight categories), hump position (thoracic or cervicothoracic), ear carriage, horn presence, and horn shape (five categories). Ear carriage and horn presence were invariant in the sample and were described but excluded from association tests.

Sixteen traits were measured directly: head length, head width, neck length, neck circumference, withers height, heart girth, chest width, chest depth, body length, pelvis length, pelvis width, abdominal girth, teat length, teat diameter, posterior interteat distance, and anterior interteat distance (Fig. 2). Linear body measurements and teat dimensions were expressed in centimetres, as recorded in the field dataset. Linear body measurements were taken using a graduated ruler and a flexible tape measure calibrated in centimeters (accuracy ± 0.5 cm). The length and diameter of the teats, as well as the posterior and anterior inter-teat distances, were measured using a vernier caliper and a graduated ruler, both calibrated in centimeters (accuracy ± 0.1 cm). Teat length was defined as the linear distance between the attachment or junction point of the teat and the tip of the teat opening; teat diameter was measured at the midpoint of the teat shaft. All measurements of the udder and teats were taken with the cow standing in a natural posture and the udder supported manually without tension. Each linear trait was recorded twice in succession by the same operator. The same field team applied the common protocol in all regions. All measurements were taken at a standardized time relative to milking and nursing: the cows were measured immediately before evening milking, with the calf separated from its mother, in order to minimize variations in udder and teat turgor associated with the filling of the milk cisterns.

Body weight was not measured on a scale. It was estimated from heart girth (HG, m) using the equation of Bechir et al. (2010):

$$\text{Estimated body weight (kg)} = 81.71 \times HG^3$$

Because this equation was developed outside the present population and was not externally validated for Moorish zebu cows, the resulting value is termed estimated body weight throughout and is interpreted as a derived morphometric trait rather than a direct weight measurement.

Zoometric indices

Sixteen indices were calculated from the measurements to summarize proportional conformation (Table 2), following commonly used zoometric definitions (SEZ, 2009; Aguirre-Riofrío et al., 2019; Baye et al., 2022). Some indices are exact rescalings or reciprocal transformations of one another and therefore do not provide independent biological evidence. Correlations and regional patterns among derived indices were interpreted descriptively.

Table 2
Definitions of the zoometric indices used in the study

Zoometric index	Formula
Body index	Body length/heart girth×100
Estimated body weight index	Estimated body weight/withers height × 100
Cephalic index	Head width/head length×100
Compactness index	Estimated body weight/withers height
Length index 1	Body length/withers height
Height index	Withers height/body length×100
Thoracic index	Chest width/chest depth×100
Anamorphosis index	(Heart girth) ² /withers height
Pelvic index	Pelvis width/pelvis length ×100
Transverse pelvic index	Pelvis width/withers height ×100
Rump length index	Pelvis length/body length ×100
Over-increase index	Pelvis length/withers height ×100
Depth index	Chest depth/withers height
Balance	(Pelvis width × pelvis length)/(chest depth × chest width)
Body ratio	Withers height/pelvis length
Length index 2	Body length/chest depth

HG, heart girth; EBW, estimated body weight. All ratios were calculated using measurements expressed in consistent units. The body-weight and compactness indices are the same ratio expressed on different scales; other pairs include reciprocal transformations. These indices are therefore descriptive and should not be counted as independent evidence.

Statistical analysis of regional and multivariable structure

Analyses were performed in Python 3.12 using pandas, NumPy, SciPy, scikit-learn, and Matplotlib. Means, standard deviation (SD), and coefficients of variation (CV) were calculated overall and by region. Region was evaluated separately for each measurement and index by one-way analysis of variance, followed, where the omnibus test was significant, by Tukey's honestly significant difference procedure. The statistical model was:

$$\text{varvec}Y_{\text{varvec}i\text{varvec}j} = \text{varvec}\mu + \text{varvec}R_{\text{varvec}i} + \text{varvec}e_{\text{varvec}i\text{varvec}j}$$

where Y_{ij} is the observation for cow j in region i , μ is the overall mean, R_i is the fixed regional effect, and e_{ij} is the residual. The cow was the observational unit. Herd was not included as a random effect; consequently, regional P values are nominal, cow-level comparisons and may be anticonservative when cows within a herd are correlated. No study-wide multiplicity correction was applied. Inference therefore emphasizes coherent patterns and effect magnitude rather than isolated nominal significance.

LDA was applied to 13 standardized core traits (estimated body weight and 12 non-udder body measurements) to explore supervised differentiation among regions. Estimated body weight was derived from heart girth; including both variables introduces mathematical redundancy and may increase the influence of thoracic size. The two discriminant functions, canonical correlations, and Wilks' lambda were calculated, and homogeneity of group covariance matrices was assessed with Box's M test. Classification performance was evaluated by cow-level leave-one-out cross-validation (LOOCV) and compared with the 45.7% accuracy obtained by assigning every cow to the largest regional class. LOOCV did not group cows by herd and therefore estimates internal sample classification rather than performance in independent herds.

PCA was performed on the same 13 standardized core traits. Sampling adequacy was assessed with the Kaiser-Meyer-Olkin statistic and Bartlett's test of sphericity; components with eigenvalues greater than 1 were retained (Kaiser, 1974). K-means clustering was applied to the retained component scores, and candidate values of k from 2 to 10 were compared using the elbow pattern and average silhouette coefficient. Because the partition was generated and described using the same dataset, between-group differences are descriptive and do not constitute independent validation. Association between candidate group and region was examined by chi-square analysis. For sparse qualitative categories, frequencies were emphasized and inferential results were interpreted cautiously. Statistical significance for prespecified tests was set at $P < 0.05$.

Exploratory associations with recorded milk yield and model development

The volume of marketable milk obtained from milking was measured directly for each cow immediately after the morning and evening milkings. The cows were milked twice a day, with the calf allowed to nurse before and after each milking. The daily marketable milk yield (DMM, L/day) corresponded to the sum of the quantities collected during the two milkings. The milk consumed directly by the calf was not quantified and was therefore not included in the DMM.

Thus, this variable represents the amount of milk actually collected during milking and available for human consumption or sale, rather than the cow's total physiological production. This distinction is important in partial-suckling systems, whereas measurement errors in daily production can affect estimates of cumulative lactation yield (Wu et al., 2025).

Total estimated milk production per lactation (TMP, L/lactation) was calculated using the following formula:

$$\text{TMP} = \text{DMM} \times \text{DUL} \times 30$$

where DMM is the average daily quantity of marketable milk obtained per milking (L/day) and DUL is the duration of lactation in months.

The factor 30 corresponds to a convention for converting one month to 30 days, which is also used in approaches based on monthly milk production records (Kokate et al., 2019). The TMP thus constitutes a deterministic approximation of the cumulative quantity of marketable milk, based on the assumption of a constant DMM throughout lactation, and therefore does not reflect the actual variations in the lactation curve. Finally, to avoid mathematical redundancy and collinearity issues, the TMP which is directly derived from the DMM and the DUL was not included alongside these two variables in the predictive or explanatory models.

Daily and cumulative lactation milk-yield values recorded in the survey were available for 349 cows. The analytical dataset did not standardize these records for lactation stage, parity, season, feeding, calf suckling, or milking management. Associations with morphology were therefore prespecified as hypothesis-generating rather than causal, genetic, or suitable for individual selection decisions.

Pearson correlations were calculated between body or udder measurements and daily or cumulative lactation yield. A candidate Moorish zebu Dairy Screening Phenotypic Score (MZ-DSPS) was explored as a research model, not as an estimated breeding value or validated screening tool. Random Forest permutation importance and LASSO regression were applied to 17 candidate traits; variables appearing both among the six highest Random Forest importances and with non-zero LASSO coefficients were retained. An ordinary multiple regression was fitted to the selected variables and evaluated by five-fold cross-validation using R^2 and RMSE. A logistic model for yield above the sample median was assessed by five-fold cross-validated AUC. Variable selection was performed before, rather than within, cross-validation, so reported performance is optimistic. The raw predictor was rescaled to 0-100 using the minimum and maximum predictions in this sample. The resulting score is sample-dependent and requires nested, herd-grouped and external validation before practical use.

Results

Regional variation in body measurements and indices

The 352 cows represented Hodh Chargui (25.9%), Brakna (28.4%), and Trarza (45.7%). CV ranged from 4.8% for withers height to 54.8% for teat diameter. At the nominal 0.05 level, the clearest regional patterns involved estimated body weight, withers height, heart girth, chest width, chest depth, abdominal girth, and udder dimensions (Table 3). Hodh Chargui cows generally had smaller thoracic measurements than cows sampled in Brakna or Trarza, whereas body length and pelvis dimensions showed little regional variation. These cow-level comparisons were not adjusted for herd clustering or study-wide multiplicity.

Table 3
Body and udder traits of sampled Moorish zebu cows by region (mean $\pm$ SD), with unadjusted and herd-aware regional comparisons

Trait	Hodh Chargui (n = 91)	Brakna (n = 100)	Trarza (n = 161)	P (unadjusted)	P (herd-aware, FDR)	ICC (herd)
Estimated body weight (kg)	266.5 $\pm$ 4.9	311.4 $\pm$ 5.1	312.5 $\pm$ 4.3	< 0.001	< 0.001	0.124
Head length (cm)	55.2 $\pm$ 0.4	53.3 $\pm$ 0.3	54.2 $\pm$ 0.2	< 0.001	0.031	0.423
Head width (cm)	19.2 $\pm$ 0.2	18.9 $\pm$ 0.2	18.7 $\pm$ 0.2	0.204	0.330	0.140
Neck length (cm)	44.4 $\pm$ 0.6	43.0 $\pm$ 0.5	44.9 $\pm$ 0.5	0.037	0.103	0.253
Neck circumference (cm)	69.6 $\pm$ 0.6	68.0 $\pm$ 0.8	69.8 $\pm$ 0.5	0.106	0.330	0.159
Withers height (cm)	124.5 $\pm$ 0.6	127.6 $\pm$ 0.5	127.8 $\pm$ 0.5	< 0.001	< 0.001	0.251
Heart girth (cm)	147.9 $\pm$ 0.8	155.8 $\pm$ 0.8	155.9 $\pm$ 0.7	< 0.001	< 0.001	0.153
Chest width (cm)	45.5 $\pm$ 0.7	52.5 $\pm$ 0.7	53.8 $\pm$ 0.7	< 0.001	< 0.001	0.428
Chest depth (cm)	59.3 $\pm$ 0.4	62.6 $\pm$ 0.5	64.3 $\pm$ 0.5	< 0.001	< 0.001	0.326
Body length (cm)	134.2 $\pm$ 0.7	133.9 $\pm$ 0.7	134.4 $\pm$ 0.7	0.880	0.877	0.036
Pelvis length (cm)	43.5 $\pm$ 0.4	44.0 $\pm$ 0.2	43.6 $\pm$ 0.2	0.370	0.346	0.005
Pelvis width (cm)	38.2 $\pm$ 0.4	38.2 $\pm$ 0.2	38.5 $\pm$ 0.2	0.686	0.730	0.096
Abdominal girth (cm)	163.1 $\pm$ 1.1	166.4 $\pm$ 1.1	173.3 $\pm$ 0.9	< 0.001	< 0.001	0.225
Teat length (cm)	6.05 $\pm$ 0.16	4.64 $\pm$ 0.11	5.10 $\pm$ 0.11	< 0.001	< 0.001	0.027
Teat diameter (cm)	3.87 $\pm$ 0.22	2.10 $\pm$ 0.05	2.05 $\pm$ 0.04	< 0.001	< 0.001	0.582
Posterior interteat distance (cm)	5.59 $\pm$ 0.23	3.82 $\pm$ 0.14	4.36 $\pm$ 0.14	< 0.001	< 0.001	0.083
Anterior interteat distance (cm)	9.79 $\pm$ 0.30	8.58 $\pm$ 0.26	9.53 $\pm$ 0.24	0.006	0.011	0.130

Body weight was estimated from heart girth rather than measured on a scale. Teat length and diameter and interteat distances were measured in centimetres. Unadjusted P values are from one-way regional ANOVA; herd-aware P values are from region models with herd-clustered robust standard errors (158 herds nested within region) and Benjamini–Hochberg correction applied jointly across all 33 traits in Tables 3 and 4. After accounting for herd clustering and multiple testing, 21 of 33 traits remained significantly associated with region. Herd-level ICC ranged from 0.005 (pelvis length) to 0.582 (teat diameter), indicating trait-specific clustering that was most pronounced for udder-related measurements.

Table 4
Zoometric indices of sampled Moorish zebu cows by region (mean $\pm$ SD), with unadjusted and herd-aware regional comparisons

Index	Hodh Chargui (n = 91)	Brakna (n = 100)	Trarza (n = 161)	P (unadjusted)	P (herd-aware, FDR)	ICC (herd)
Body index	91.0 $\pm$ 0.6	86.1 $\pm$ 0.6	86.3 $\pm$ 0.5	< 0.001	< 0.001	0.194
Body weight index	213.9 $\pm$ 3.7	243.7 $\pm$ 3.7	244.8 $\pm$ 3.4	< 0.001	< 0.001	0.149
Cephalic index	34.8 $\pm$ 0.4	35.5 $\pm$ 0.3	34.5 $\pm$ 0.3	0.119	0.164	0.052
Compactness index	2.14 $\pm$ 0.04	2.44 $\pm$ 0.04	2.45 $\pm$ 0.03	< 0.001	< 0.001	0.149
Length index 1	1.08 $\pm$ 0.01	1.05 $\pm$ 0.01	1.05 $\pm$ 0.01	0.005	0.007	0.128
Height index	93.0 $\pm$ 0.6	95.5 $\pm$ 0.5	95.4 $\pm$ 0.5	0.004	0.007	0.123
Thoracic index	77.0 $\pm$ 1.2	84.5 $\pm$ 1.5	83.9 $\pm$ 0.9	< 0.001	< 0.001	0.314
Anamorphosis index	176.1 $\pm$ 1.9	190.6 $\pm$ 1.8	191.1 $\pm$ 1.7	< 0.001	< 0.001	0.180
Pelvic index	88.1 $\pm$ 1.0	87.0 $\pm$ 0.6	88.5 $\pm$ 0.5	0.267	0.289	0.104
Transverse pelvic index	30.6 $\pm$ 0.3	30.0 $\pm$ 0.2	30.2 $\pm$ 0.2	0.153	0.237	0.225
Rump length index	32.4 $\pm$ 0.3	32.9 $\pm$ 0.2	32.5 $\pm$ 0.2	0.248	0.314	0.191
Over-increase index	34.9 $\pm$ 0.3	34.5 $\pm$ 0.2	34.2 $\pm$ 0.2	0.041	0.174	0.209
Depth index	0.48 $\pm$ 0.00	0.49 $\pm$ 0.00	0.50 $\pm$ 0.00	< 0.001	< 0.001	0.283
Balance	0.64 $\pm$ 0.02	0.52 $\pm$ 0.01	0.50 $\pm$ 0.01	< 0.001	< 0.001	0.260
Body ratio	2.88 $\pm$ 0.03	2.90 $\pm$ 0.01	2.94 $\pm$ 0.02	0.066	0.237	0.221
Length index 2	2.27 $\pm$ 0.02	2.15 $\pm$ 0.02	2.11 $\pm$ 0.02	< 0.001	< 0.001	0.258

Several zoometric indices showed nominal regional differences that remained significant after herd-aware, FDR-adjusted analysis (Table 4). Hodh Chargui cows had a larger body index and lower thoracic, anamorphosis, compactness, and estimated body-weight indices, consistent with a relatively longer and less compact profile in the sampled cows. Because multiple indices are mathematically dependent, these results describe related expressions of body proportions and do not independently establish dairy or beef aptitude.

Supervised regional differentiation

On the 12 non-redundant traits, the two LDA functions had eigenvalues of 0.464 and 0.160 and canonical correlations of 0.563 and 0.372, respectively. The first function accounted for 74.3% of between-region variation and was associated mainly with chest width, heart girth, and chest depth. Overall regional separation was nominally significant (Wilks' lambda = 0.589; $\chi^2=181.4$; $df = 24$; $P < 0.001$). Leave-one-herd-out cross-validated accuracy across the 158 sampled herds was 59.5% (Table 5), below the cow-level LOOCV accuracy obtained on the same 12 traits (62.4%), confirming that herd-unaware validation overestimated generalization to unseen herds. Both figures exceeded the 45.6% majority-class baseline. Box's M test indicated unequal covariance matrices ($M = 482.48$; approximate $\chi^2=457.90$; $df = 156$; $P < 0.001$), further limiting categorical interpretation.

Table 5
Leave-one-herd-out cross-validated LDA confusion matrix (12 non-redundant traits, 158 herds). Rows are observed regions and columns are predicted regions.

Observed region	Brakna	Hodh Chargui	Trarza
Brakna	40	17	43
Hodh Chargui	7	55	29
Trarza	23	17	121

PCA and exploratory phenotypic partition

The KMO statistic improved to 0.724 and Bartlett's test remained significant ($\chi^2=786.7$; $df = 66$; $P < 0.001$), supporting an exploratory PCA. Three components had eigenvalues greater than 1 and explained 50.3% of total variance. PC1 explained 26.2% and represented overall thoracic development, with the highest contributions from heart girth, withers height, and abdominal girth (estimated body weight was excluded as redundant). PC2 explained 14.4% and was associated more strongly with cephalic dimensions (Fig. 3; full loadings for all three retained components in Table S9); reference intervals for these two component scores are reported in Table S5 for descriptive comparison in future samples. Because estimated weight is derived from heart girth, the loading structure should be confirmed in a reanalysis using direct measurements only. Corresponding zoometric indices followed the same pattern, with the lowest body index and highest thoracic and compactness indices in Morphotype 3 (Table S2). For brevity, the three candidate groups are subsequently labelled Group 1–3 in tables and figures, without implying validated or genetically distinct morphotypes.

On the 12 non-redundant traits, the average silhouette coefficient was highest at $k = 2$ (0.298) and only slightly lower at $k = 3$ (0.281; Fig. 4; individual-level dendrogram in Fig. S1), indicating that the three-group partition is not clearly preferred over a simpler two-group split. For comparability with the rest of the study, the three-group partition is retained below, renumbered by ascending mean heart girth. Its composition changed substantially after removing the redundant weight variable: the resulting exploratory groups contained 154, 80, and 117 cows, with substantial within-group heterogeneity in each (Fig. S2). Group 3 was heaviest and had the widest, deepest chest; Group 2, despite intermediate body size, had the largest head, neck, and teats and the highest MZ-DSPS score; Group 1 was smallest-framed overall (Table 6; full measurements in Table S1). Corresponding zoometric indices followed the same pattern (Table S2). Because the groups were generated from the same variables used to describe them, these contrasts are descriptive and should not be interpreted as independently validated morphotypes.

Table 6
Selected descriptive traits of the three candidate groups

Trait	Group 1 (n = 154)	Group 2 (n = 80)	Group 3 (n = 117)
Live weight (kg)	268.9 ± 2.9 ^a	316.8 ± 7.0 ^b	330.5 ± 4.6 ^b
Withers height (cm)	122.9 ± 0.4 ^a	128.5 ± 0.6 ^b	131.0 ± 0.5 ^c
Heart girth (cm)	148.5 ± 0.5 ^a	156.5 ± 1.0 ^b	159.0 ± 0.7 ^b
Chest width (cm)	47.2 ± 0.5 ^a	49.1 ± 0.7 ^a	58.3 ± 0.7 ^b
Chest depth (cm)	59.6 ± 0.3 ^a	62.5 ± 0.5 ^b	66.4 ± 0.5 ^c
Body length (cm)	130.6 ± 0.5 ^a	138.5 ± 1.0 ^c	136.0 ± 0.6 ^b
Abdominal girth (cm)	161.7 ± 0.9 ^a	173.3 ± 1.2 ^b	174.8 ± 0.8 ^b
Neck circumference (cm)	66.9 ± 0.5 ^a	74.1 ± 0.8 ^c	69.0 ± 0.6 ^b
Teat length (mm)	5.0 ± 0.1 ^a	5.8 ± 0.2 ^b	5.0 ± 0.1 ^a
Predicted MZ-DSPS score	36.7 ± 1.4 ^a	52.7 ± 2.1 ^b	40.0 ± 1.4 ^a

Body measurements of the three candidate groups obtained from the non-redundant (12-trait) PCA/K-means partition. Different superscript letters within a row indicate significant differences (Tukey's HSD, $P < 0.05$). Live weight, not used to form the groups, is shown descriptively. Group 2 is distinctive for the largest head, neck, and teats despite intermediate body size; Group 3 is heaviest and has the widest, deepest chest; Group 1 is smallest-framed overall (Table 6).

Geographic and qualitative distribution of exploratory phenotypic groups

The distribution of the exploratory groups differed among the sampled regions ($\chi^2=58.7$; $df = 4$; $P < 0.001$; Table 7). Group 3 comprised 51.7% of sampled Trarza cows but only 17.7% of sampled Hodh Chargui cows, whereas Group 1 was proportionally more frequent in Hodh Chargui. This association describes the present sample; it neither estimates representative regional frequencies nor distinguishes genetic differentiation from environment, management, age structure, herd effects, or purposive sampling.

Table 7
Distribution of the three candidate groups within the sampled regions.

Region	Group 1, n (%)	Group 2, n (%)	Group 3, n (%)
Hodh Chargui	59 (34.9)	6 (7.5)	26 (17.7)
Brakna	45 (26.6)	20 (25.0)	35 (23.8)
Trarza	50 (29.6)	34 (42.5)	76 (51.7)

Ear carriage was horizontal and horns were present in all cows. Hump position was associated with candidate group ($\chi^2=35.1$; $df = 2$; $P < 0.001$): a thoracic hump occurred in 84.4%, 81.3%, and 53.8% of Groups 1, 2, and 3, respectively. Coat pattern, coat color, and horn shape showed no clear association, although several categories had small cell counts (Table S3).

Exploratory relationships with milk yield

Among the 349 cows with recorded milk-yield data, mean cumulative lactation yield was 685.4 ± 273.9 L. Teat length had the largest unadjusted correlation with daily yield ($r = 0.381$; $P < 0.001$), followed by teat diameter ($r = 0.249$; $P < 0.001$). Estimated body weight and heart girth were not detectably related to daily yield. Teat length also had the largest correlation with cumulative lactation yield ($r = 0.327$; $P < 0.001$), followed by body length, teat diameter, interteat distances, and abdominal girth. These unadjusted associations were not corrected for multiple testing and do not account for lactation stage, parity, season, nutrition, calf suckling, or herd management.

Random Forest and LASSO converged on teat length, teat diameter, and body length as predictors in the exploratory MZ-DSPS model (full ranking of all 17 candidate predictors in Table 8 and Table S6).

Using teat length, teat diameter, and body length as predictors, in the full-sample regression, standardized coefficients were 0.393, 0.174, and 0.227, respectively. The raw prediction equation was:

$$\text{varvec}D \backslash \text{varvec}M \backslash \text{varvec}Y = -2.518 + 0.0298 \backslash \text{varvec} * \backslash \text{varvec}B \backslash \text{varvec}L + 0.1255 \backslash \text{varvec} * \backslash \text{varvec}T \backslash \text{varvec}D + 0.2664 \backslash \text{varvec} * \backslash \text{varvec}L$$

DMY: Predicted daily milk yield (Liter/day)

where BL is body length (cm), TD is teat diameter (cm), and TL is teat length (cm).

Table 8
Exploratory performance of the candidate three-trait milk-yield model.

Indicator	Estimate	Evaluation status
Full-sample R^2	0.187	Apparent fit
Five-fold cross-validated R^2	0.162	Variable selection not nested
Five-fold cross-validated RMSE	1.19 L/d	Variable selection not nested
Correlation of rescaled score with daily yield	$r = 0.432$	Apparent, full-sample
AUC, logistic model	0.614	Five-fold cross-validated
AUC, continuous rescaled score	0.635	Apparent, full-sample
Sensitivity at Youden threshold	34.0%	Cross-validated logistic model
Specificity at Youden threshold	88.6%	Cross-validated logistic model

The cross-validated logistic ROC curve is shown in Fig. 5. Performance was modest and sensitivity was low. The model is therefore insufficient for individual screening, selection, or breeding decisions and is retained only as a hypothesis-generating analysis pending nested herd-grouped cross-validation and independent validation. AUC improved at more extreme yield thresholds but remained modest overall (Table S7).

The distribution of MZ-DSPS tertile classes differed among candidate morphotypes (Table S8; Fig. S3), but the association was weak and the score and clustering share overlapping morphometric inputs, so this comparison is descriptive rather than an independent cross-validation of either method.

Discussion

This study provides a quantitative description of adult, multiparous, lactating Moorish zebu cows sampled in three Mauritanian production regions. The principal finding is not a set of sharply delimited regional types but overlapping morphometric variation. Regional patterns were most evident for thoracic size, estimated body weight, and udder traits. Cow-level LDA classification exceeded the majority-class baseline but showed extensive overlap, reflecting unequal covariance matrices and, initially, herd-unaware validation.

The mean withers height (126.9 cm) and estimated body weight (300.3 kg) overlapped values reported for other West African zebu populations (Moussa et al., 2017; Ouédraogo et al., 2021). Direct comparison should nevertheless be cautious because estimated weight was calculated from an equation developed outside the study population. The lower observed variation in skeletal dimensions than in teat traits is broadly consistent with morphometric studies of indigenous and Creole cattle (Baye et al., 2022; Rojas-Espinoza et al., 2023; Contreras Huamaní et al., 2026). Part of the teat variation may reflect lactation stage, parity, measurement timing, and milking conditions, none of which were available for adjustment. Consequently, the percentile intervals in Table S4 are provisional descriptions of the sampled class of cows rather than diagnostic limits for the breed.

The three-group partition summarized major axes of phenotypic variation, including overall size, thoracic development, and body proportions. Because estimated body weight was mathematically redundant with heart girth, it was excluded in a non-redundant 12-trait reanalysis (Sections 2.4, 3.3): the average silhouette coefficient of 0.281 at $k = 3$, however, indicates considerable overlap. Group composition were 154/80/117 cows, with a previously undetected group (Group 2) emerging as distinctly larger-headed and higher-scoring for the MZ-DSPS index despite intermediate body size. The observed geographic imbalance among the identified groups provides useful descriptive information on the regional distribution of the morphometric profiles, but it should not be interpreted as independent evidence of their biological distinctiveness. Because the same morphometric traits were used to define the clusters, the observed association between cluster membership and geographic origin may partly reflect the structure of the variables used for classification rather than a genuine population differentiation. Moreover, environmental conditions, herd management, production systems, and sampling structure may contribute to phenotypic differences between regions and generate similar clustering patterns without necessarily indicating distinct biological or genetic groups. This interpretation is consistent with previous work showing that geographic proximity and morphological classification do not necessarily correspond to underlying genetic structure in cattle populations (Li & Kantanen, 2010). From a methodological perspective, cluster solutions should therefore be considered exploratory until their reproducibility has been demonstrated using stability analyses and independent validation datasets, ideally collected separately from the data used for cluster construction (Ullmann et al., 2021). Accordingly, the groups identified in the present study are best regarded at this stage as phenotypically defined morphometric profiles rather than definitive morphotypes or management units. Confirmation through independent sampling, assessment of cluster stability, and, if the objective is to infer biological or genetic differentiation, genomic characterization would provide stronger evidence for their reproducibility and biological relevance.

The stronger unadjusted correlations of teat traits than overall body size with recorded milk yield are biologically plausible but remain highly confounded. The candidate model explained only 16.2% of yield variation under non-nested cross-validation and had an AUC of 0.614 with low sensitivity. Predictor selection occurred before cross-validation, and yield was not standardized for major environmental and physiological determinants. These results do not support use of the model as a screening or selection tool; they identify hypotheses for subsequent standardized milk-recording studies.

The findings have two cautious practical implications. First, repeatable direct measurements such as withers height, body length, heart girth, and pelvis dimensions may contribute to a standardized field description of adult cows. A formal breed standard would require representative sampling of males, younger animals, additional production areas, and repeated seasons. Second, future conservation and genomic surveys should cover all three regions while avoiding the assumption that administrative boundaries correspond to genetic subpopulations.

The study has several limitations. Sampling was purposive rather than probability based and included only adult lactating females. Age, parity, body condition, season, and transhumance history were unavailable. Body weight was estimated with an equation not validated in the study population; the resulting redundancy with heart girth was addressed by excluding estimated weight from the PCA, LDA, and clustering analyses reported above. Several zoometric indices were mathematically dependent. LDA covariance matrices remained heterogeneous, and although cross-validation was regrouped by the 158 sampled herds (reducing apparent accuracy from 62.4% to 59.5%), generalization to fully independent herds and regions remain unconfirmed; cluster separation was weak (silhouette below 0.30 for both $k = 2$ and $k = 3$), and the same data were used to choose and describe the clusters. Multiple traits were tested without study-wide multiplicity adjustment. Milk-yield analyses lacked standardized recording variables, while model development used neither nested cross-validation nor an independent test set. These limitations restrict inference to the sampled cows and make herd-aware phenotypic and genomic validation essential.

Conclusions

Moorish zebu cows sampled in Hodh Chargui, Brakna, and Trarza displayed measurable but overlapping morphometric variation. PCA and K-means provided a weak exploratory three-group summary of this variation, not evidence of discrete or genetically differentiated morphotypes. The measurements supply provisional descriptive references for sampled adult lactating females, while the associations with recorded milk yield remain hypothesis-generating. The current three-trait model is insufficient for screening or breeding decisions.

Representative sampling, repeated and standardized measurements, herd-aware models, direct weighing, nested validation, and genomic analysis are required before formal breed standards, regional genetic subdivisions, or selection criteria are proposed.

Declarations

Conflict of 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.

Individual contributions by the co-authors

Youssef El Hadj: Conceptualization, Methodology, Investigation, Data curation, Formal analysis, Writing - original draft. Mohamed Ould Ahmed: Conceptualization, Methodology, Investigation, Data curation, Formal analysis, Supervision, Validation, Writing - original draft, Writing - review and editing. Abir Hamrouni: Formal analysis, Writing - review and editing. Sidi Hamady: Data curation, Writing - review and editing. M'Naouer Djemali: Supervision, Validation, Writing - review and editing. Ali Ould Mohamed Salem Boukhary: Supervision, Validation, Writing - review and editing.

Statement of Animal Rights

Measurements were non-invasive and no experimental treatment was imposed. The protocol was approved by the Research Ethics Committee of the University of Nouakchott (reference 2022/2023). Adult herd owners or managers provided verbal consent; the interviewer documented consent by signing the survey form.

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

During the preparation of this work, the authors used Claude (Anthropic) and ChatGPT (OpenAI) to assist with translation, language editing, organization, and formatting. After using these tools and services, the authors reviewed and edited the content as needed and take full responsibility for the content of the publication.

Funding

This work was supported by the National Office for Livestock and Pastoralism Research and Development (ONARDEP) and the National Agency for Scientific Research and Innovation (ANRSI), Mauritania.

Acknowledgements

The authors thank the farmers and field technicians who participated in the survey and Jeyid Yacoub Daye for preparing the study-area map.

Data availability

The de-identified analytical dataset, data dictionary, and analysis code are available from the corresponding author upon reasonable request, subject to confidentiality restrictions protecting participating farms.

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Figures

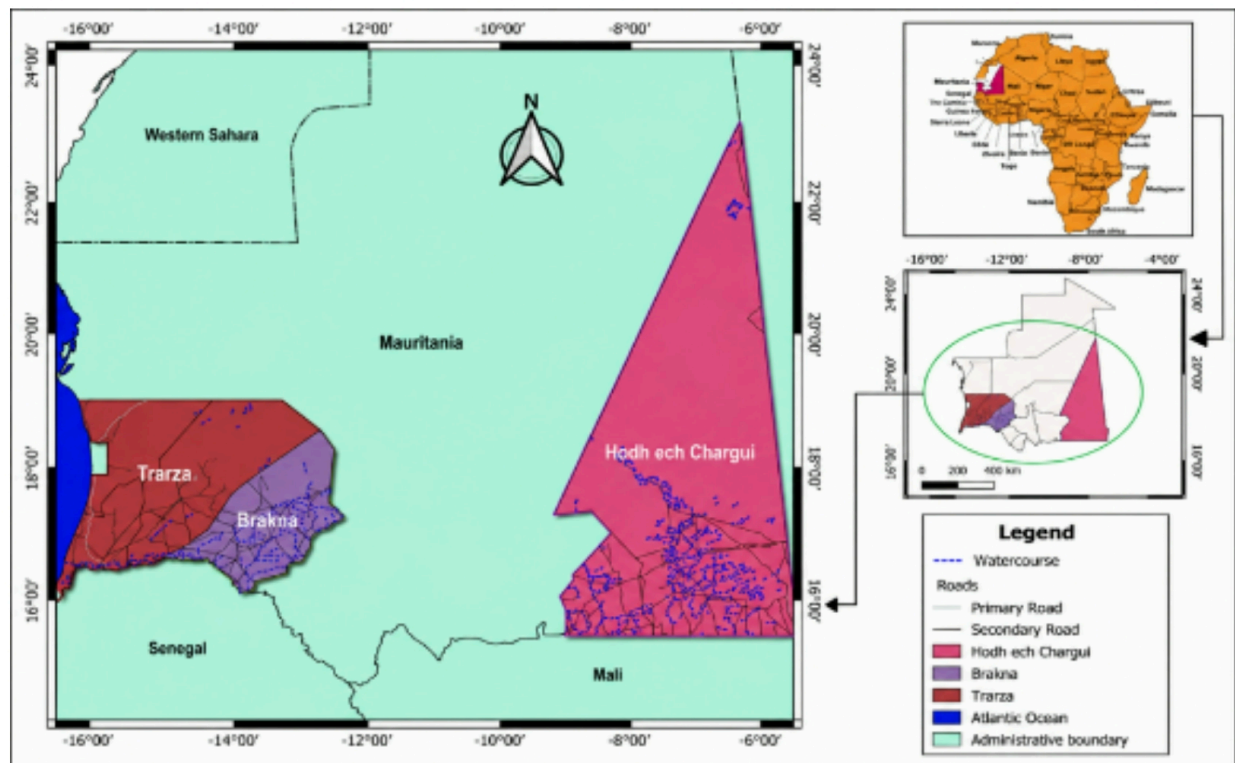


Figure 1

Locations of the three study regions in Mauritania

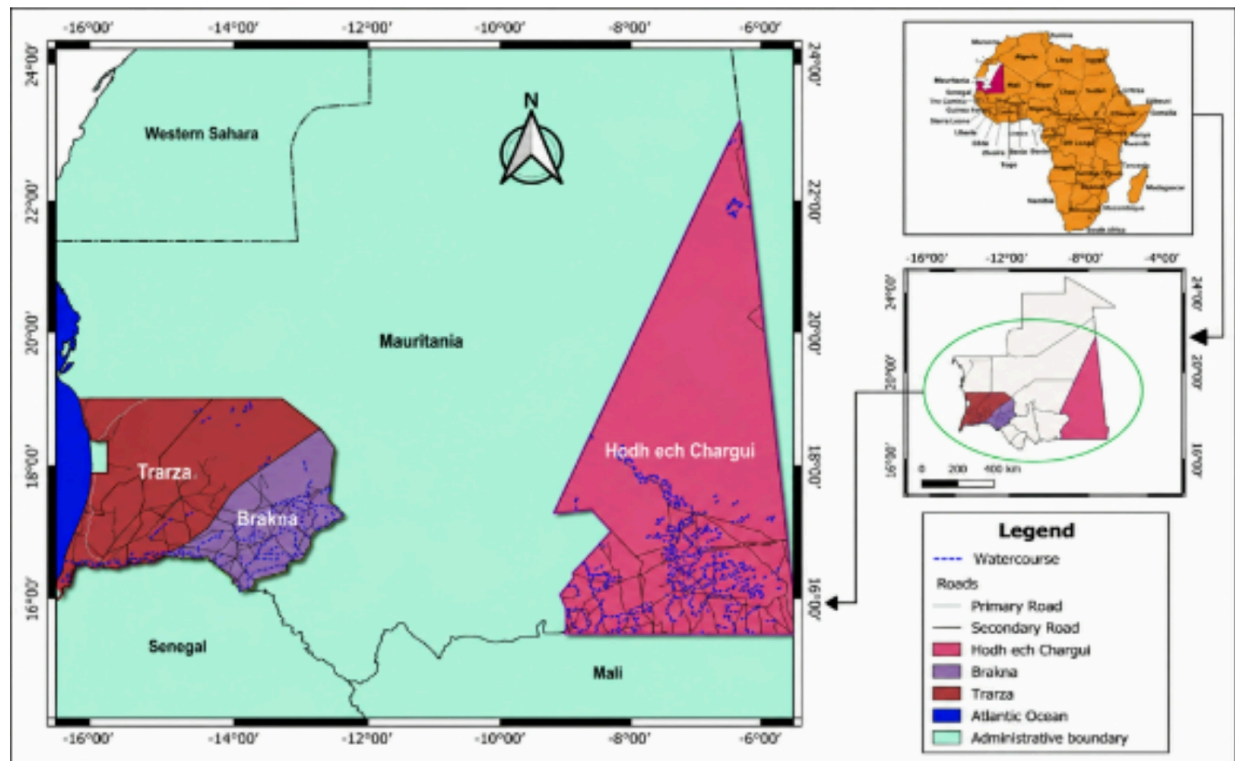


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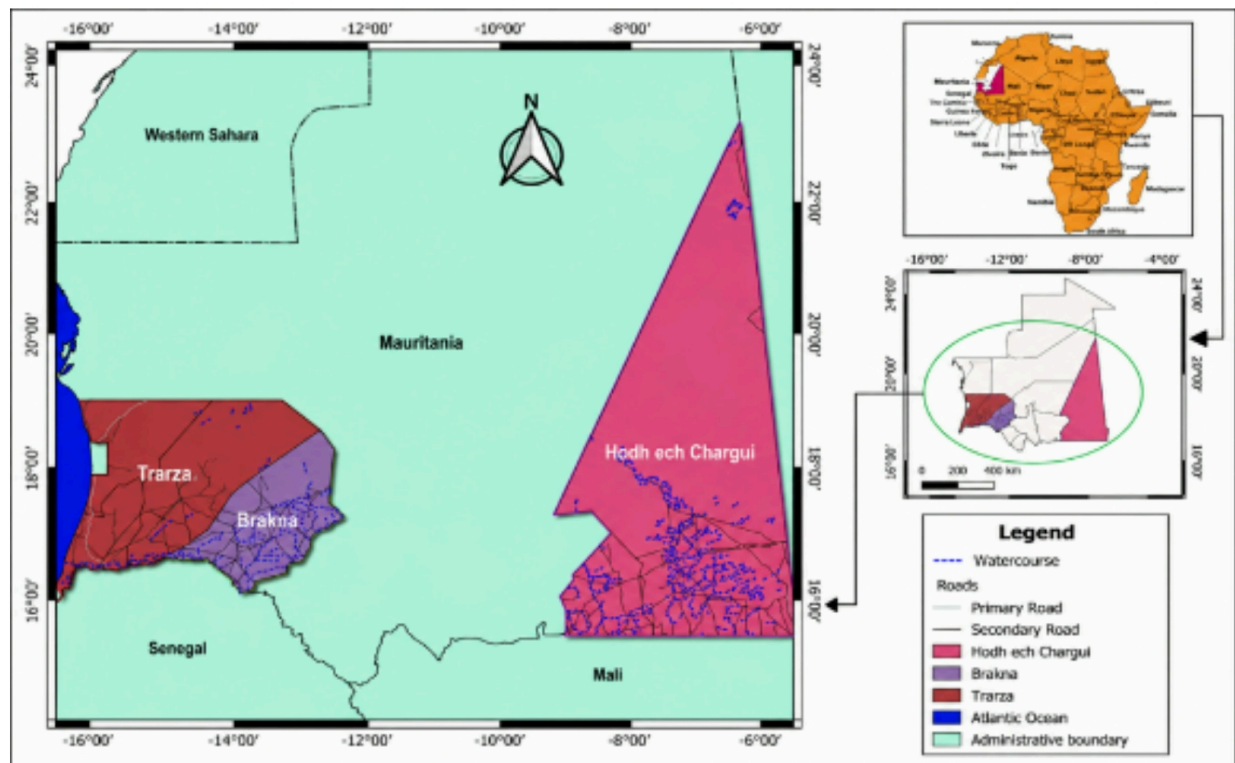


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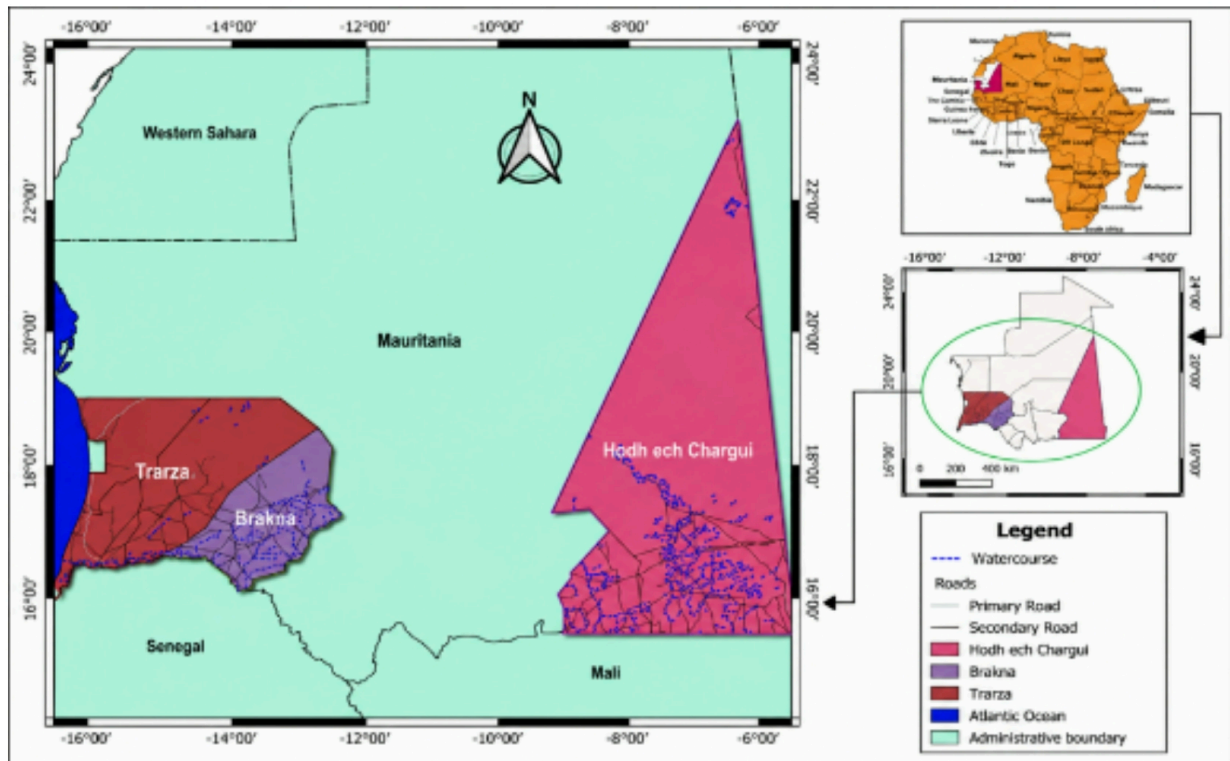


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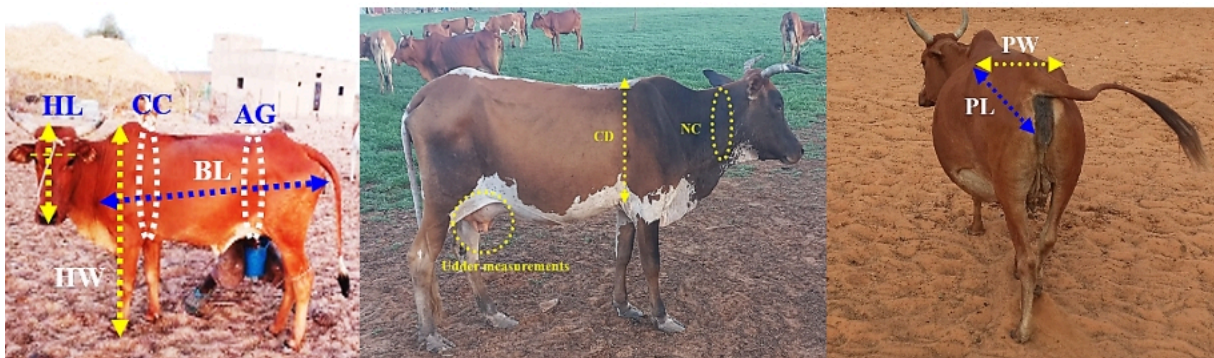


Figure 2

Body and udder measurements recorded in Moorish zebu cows. (a) Head length (HL), chest circumference/heart girth (CC), withers height (HW), abdominal girth (AG), and body length (BL); (b) chest depth (CD), neck circumference (NC), and the udder region within which teat length, teat diameter, and posterior and anterior inter-teat distances were measured; (c) pelvis width (PW) and pelvis length (PL), viewed from the rear.

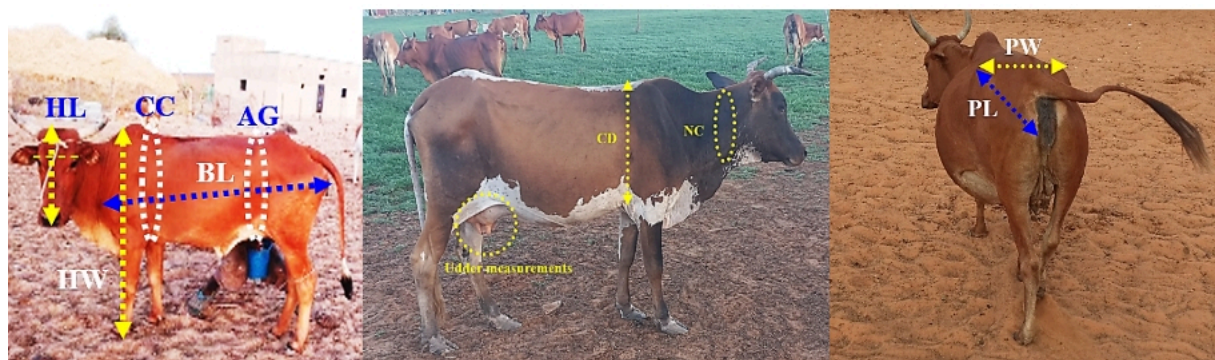


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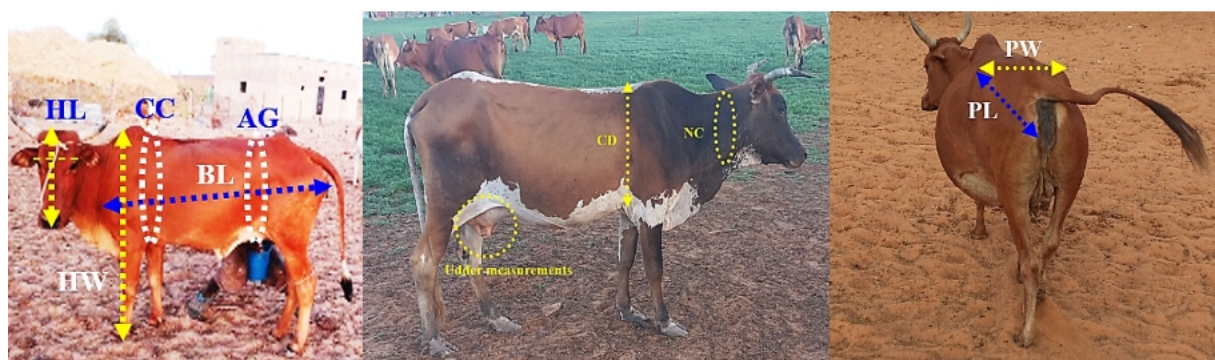


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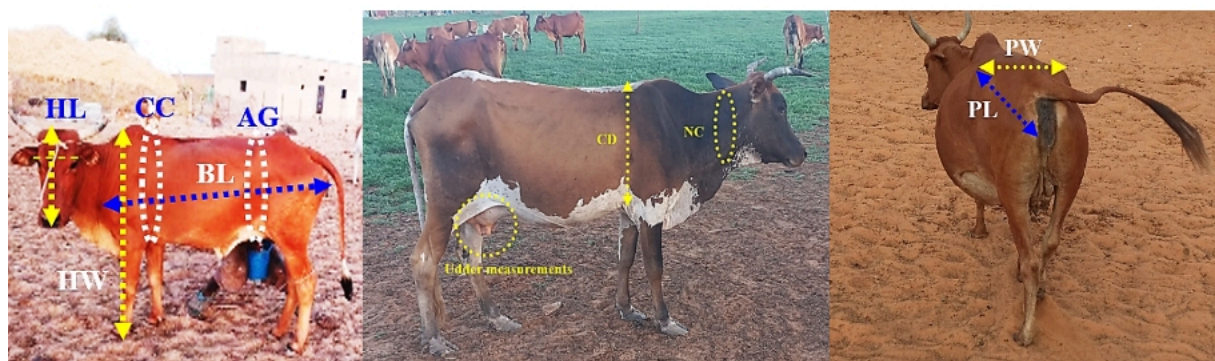


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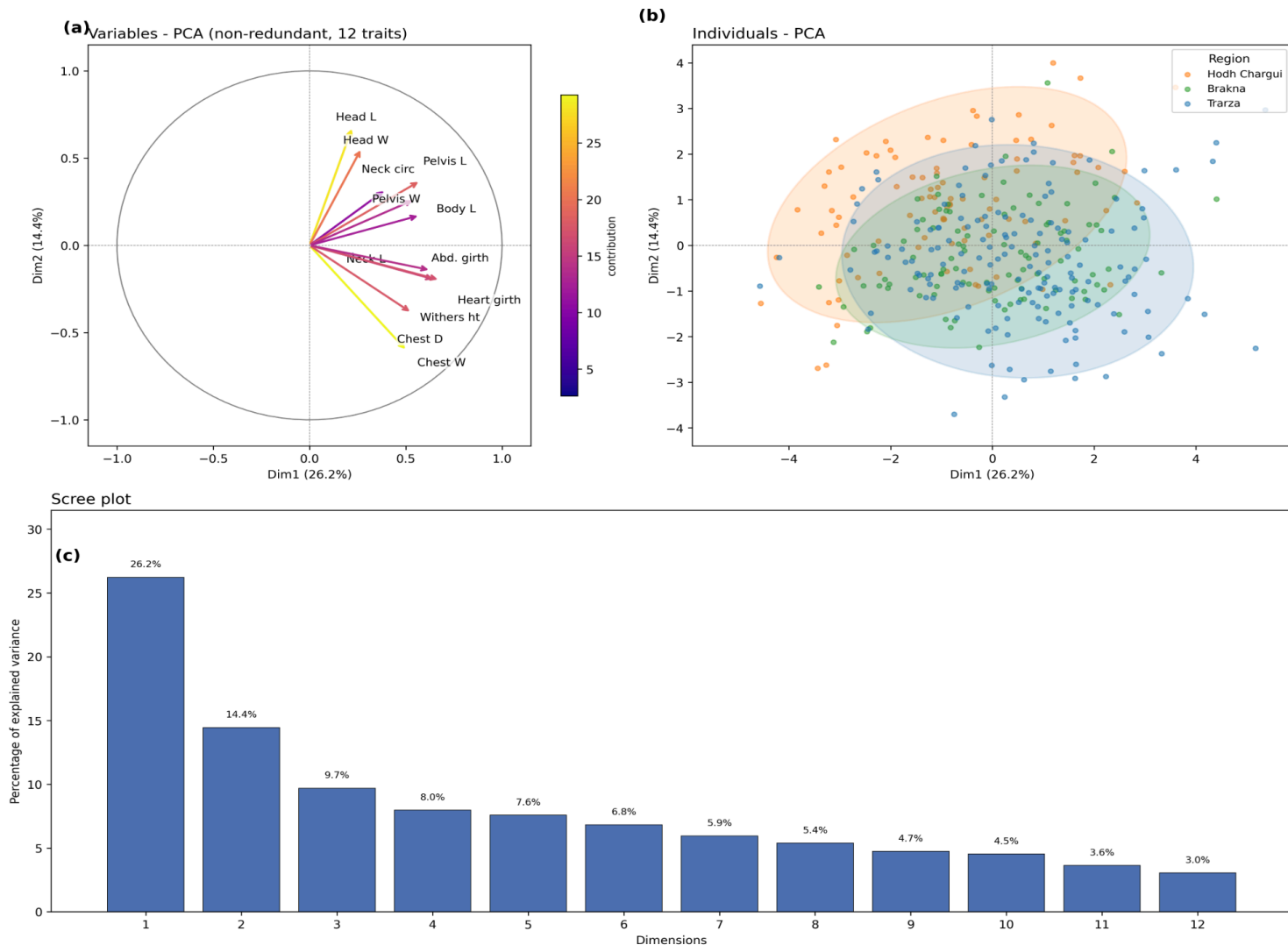


Figure 3

Exploratory principal component analysis of the 12 non-redundant standardized core morphometric traits (estimated body weight excluded as a deterministic function of heart girth): variable contributions, cow projections by region, and explained variance.

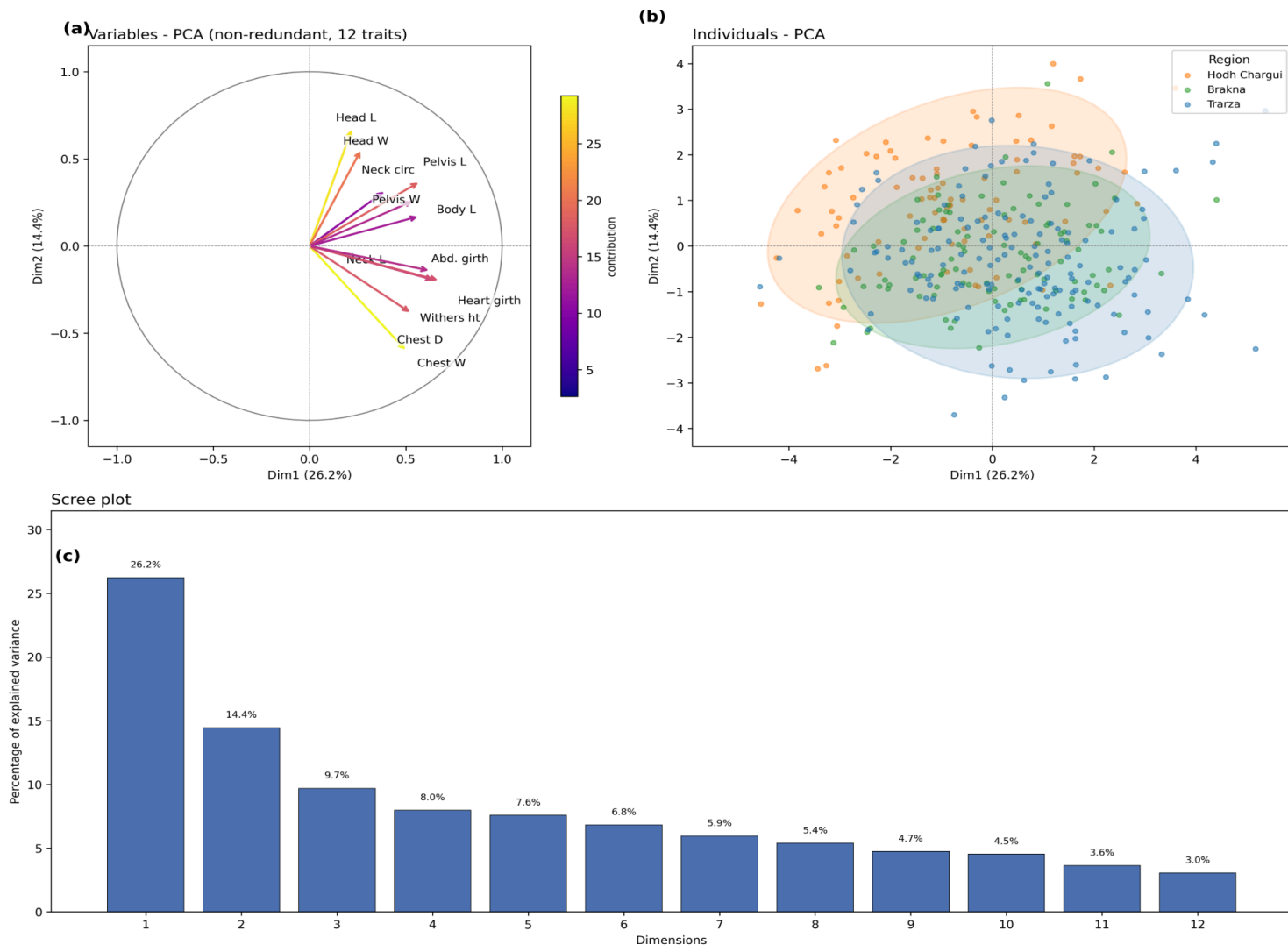


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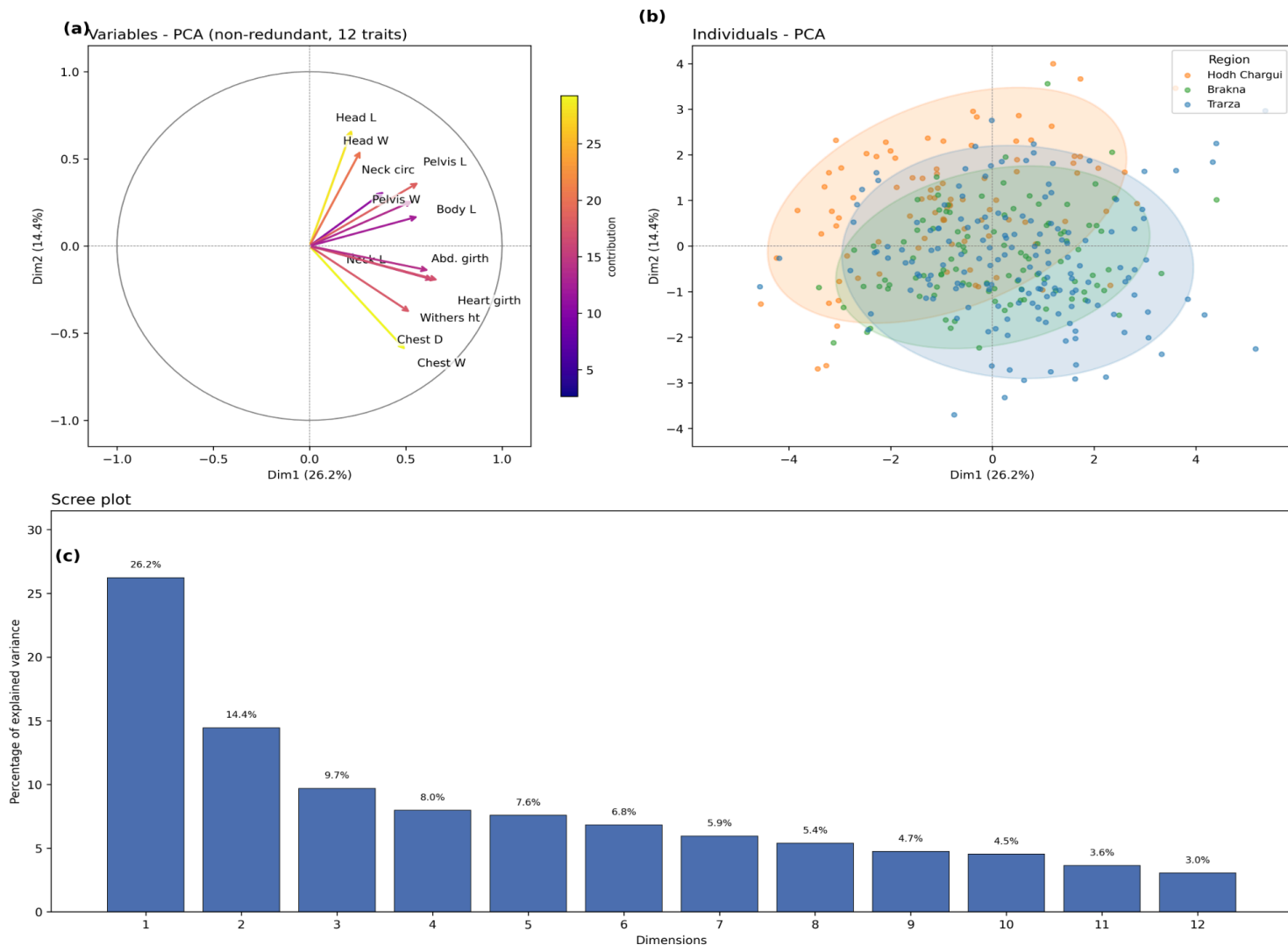


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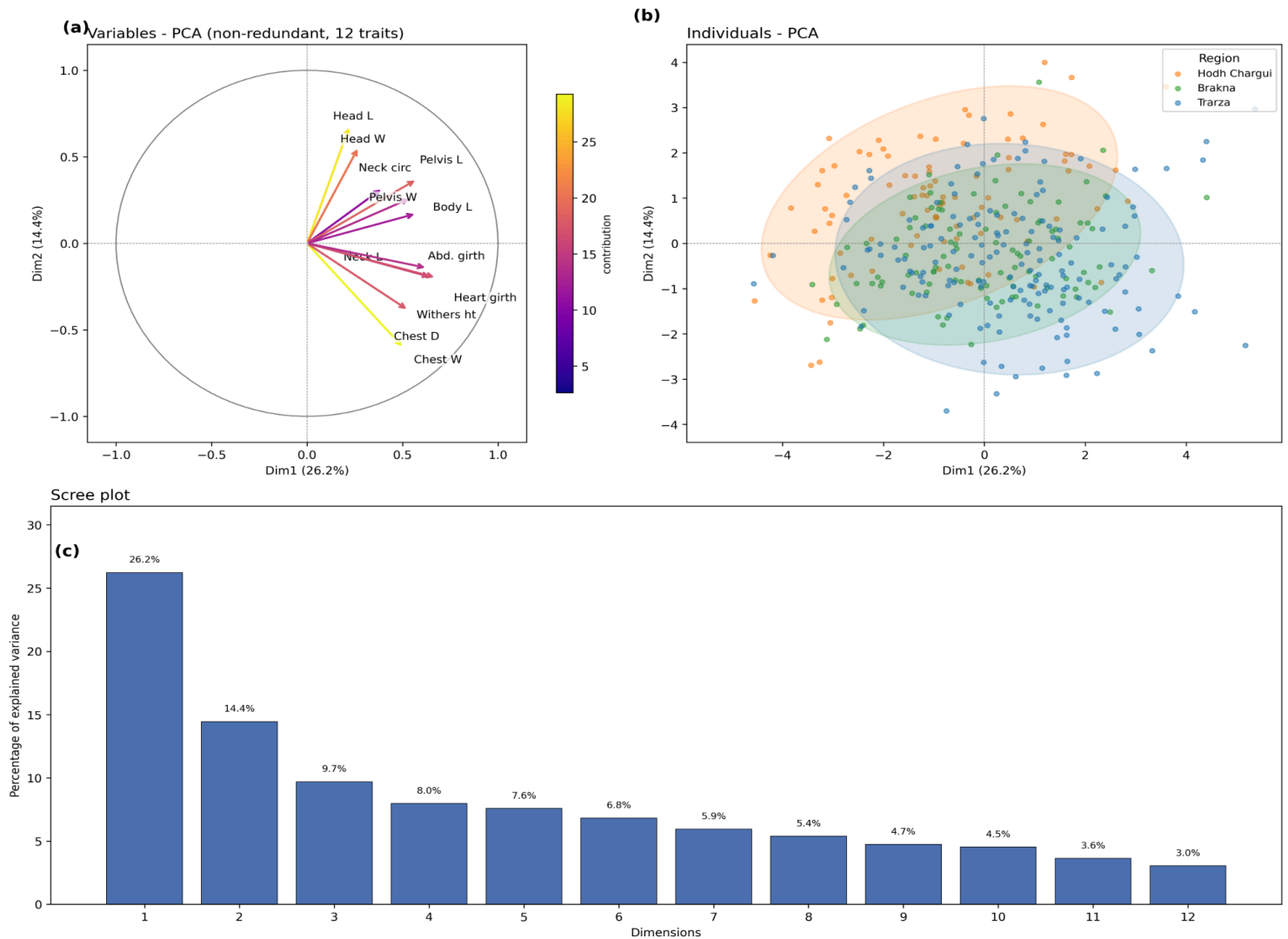


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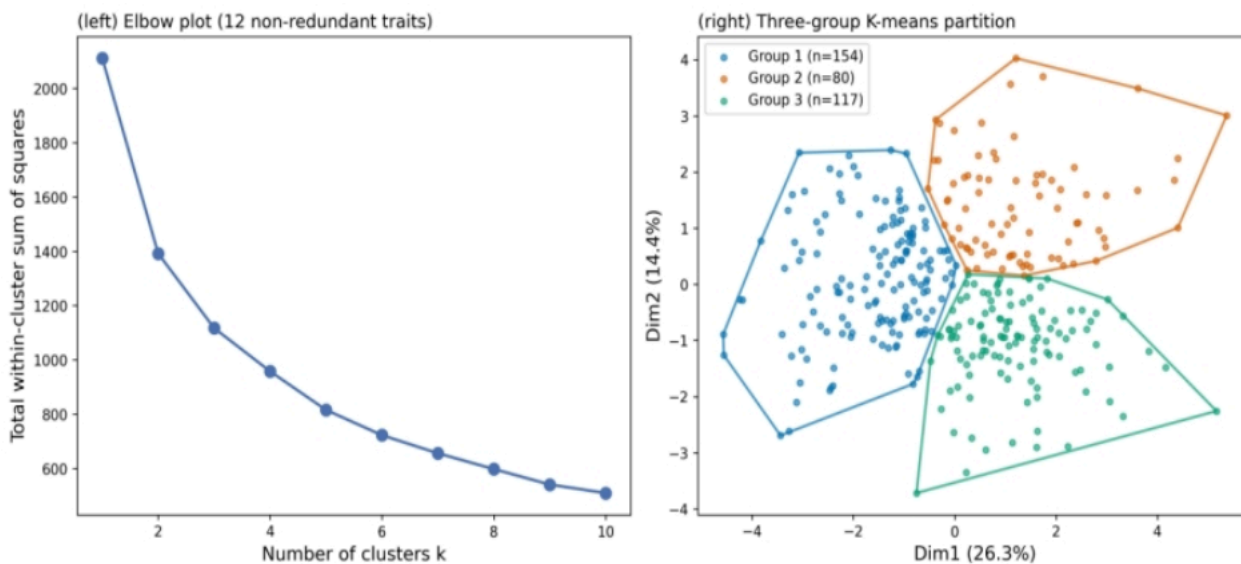


Figure 4

Selection and visualization of the exploratory three-group partition: elbow plot (left) and projection on the first two principal components (right).

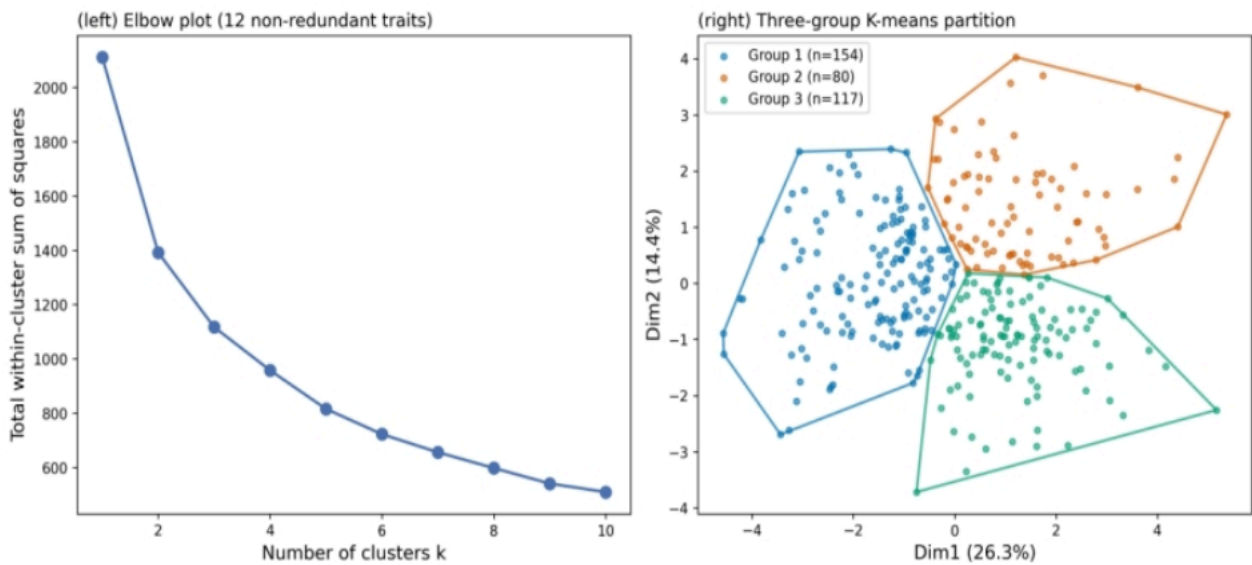


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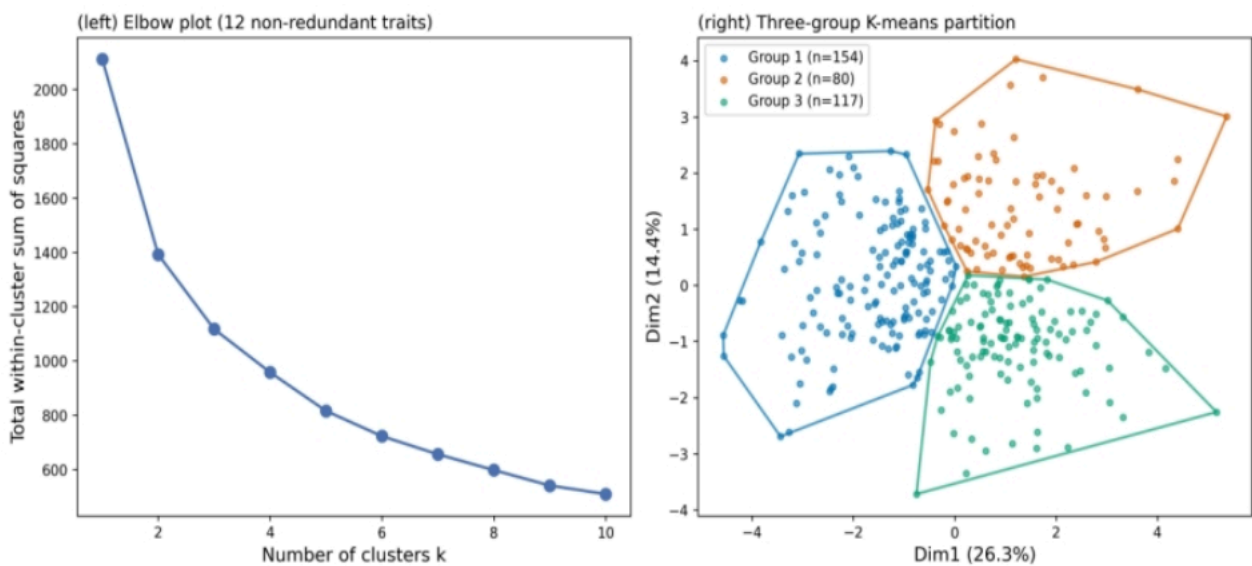


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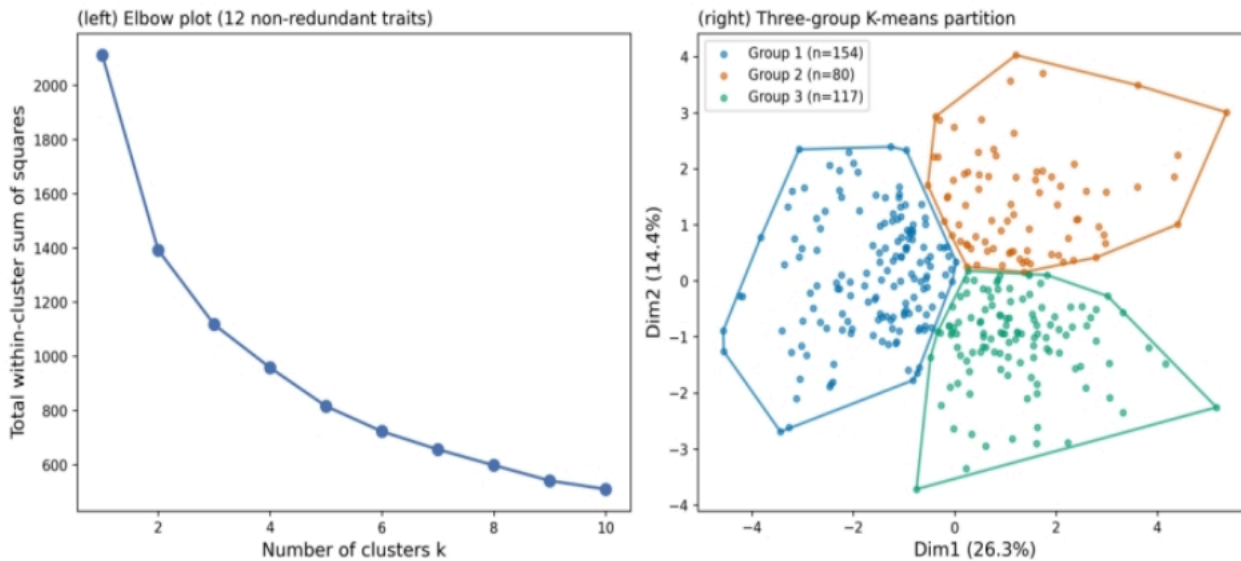


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Selection and visualization of the exploratory three-group partition: elbow plot (left) and projection on the first two principal components (right).

ROC curve: MZ-DSPS classification of high- vs low-yielding Moorish zebu cows (median daily milk yield split)

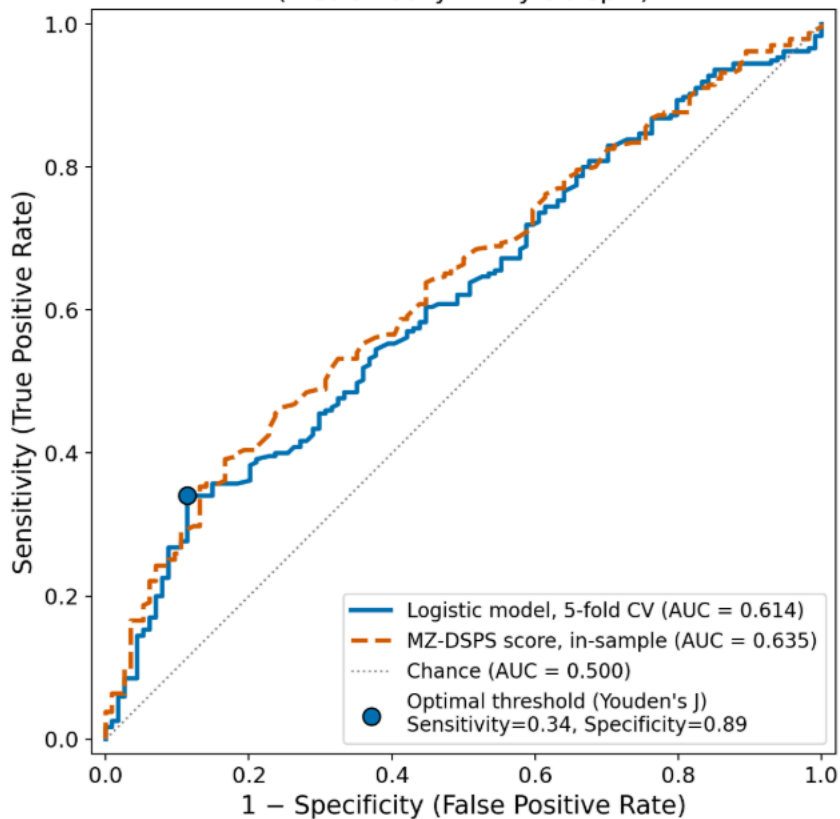


Figure 5

Receiver operating characteristic curves for above-median recorded daily milk yield. The solid curve is the five-fold cross-validated logistic model; the dashed curve is the apparent performance of the continuous full-sample rescaled score.

ROC curve: MZ-DSPS classification of high- vs low-yielding Moorish zebu cows (median daily milk yield split)

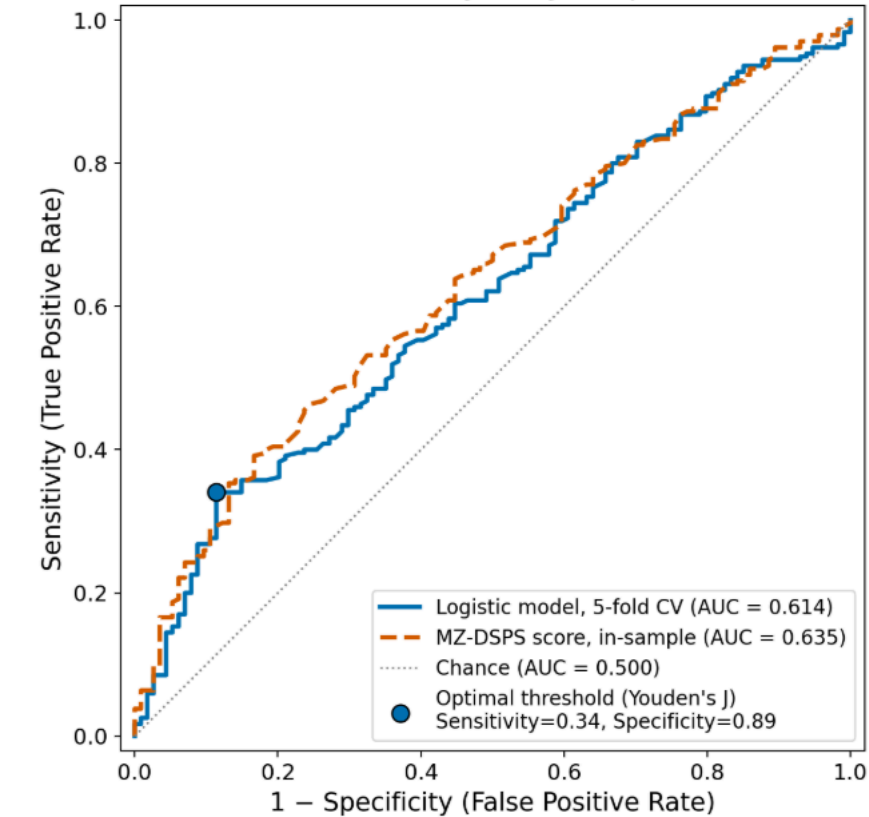


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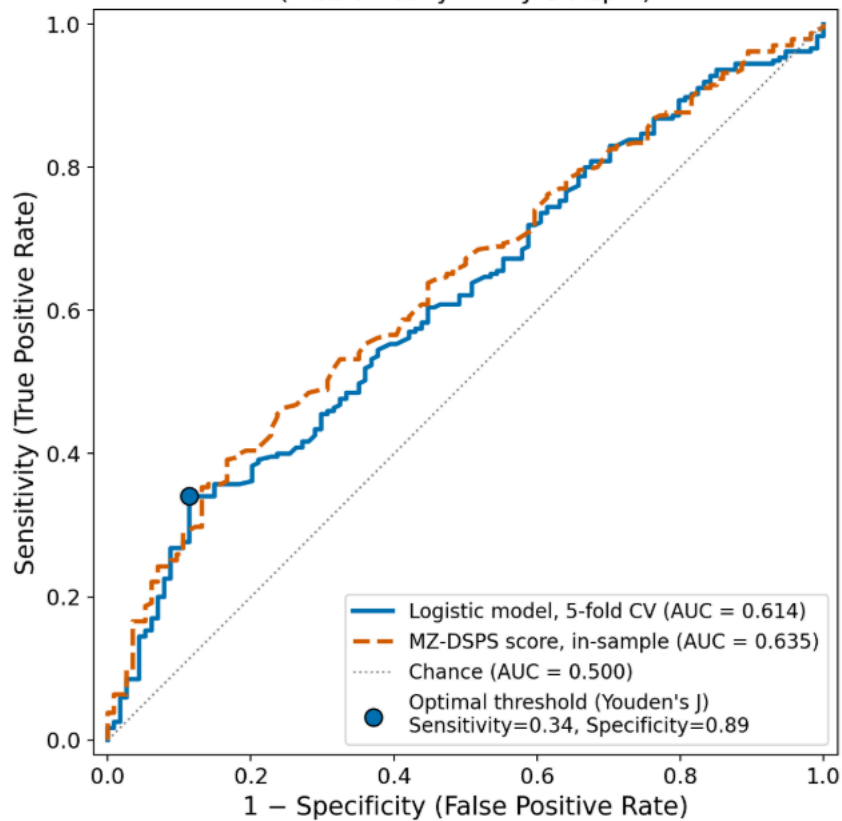


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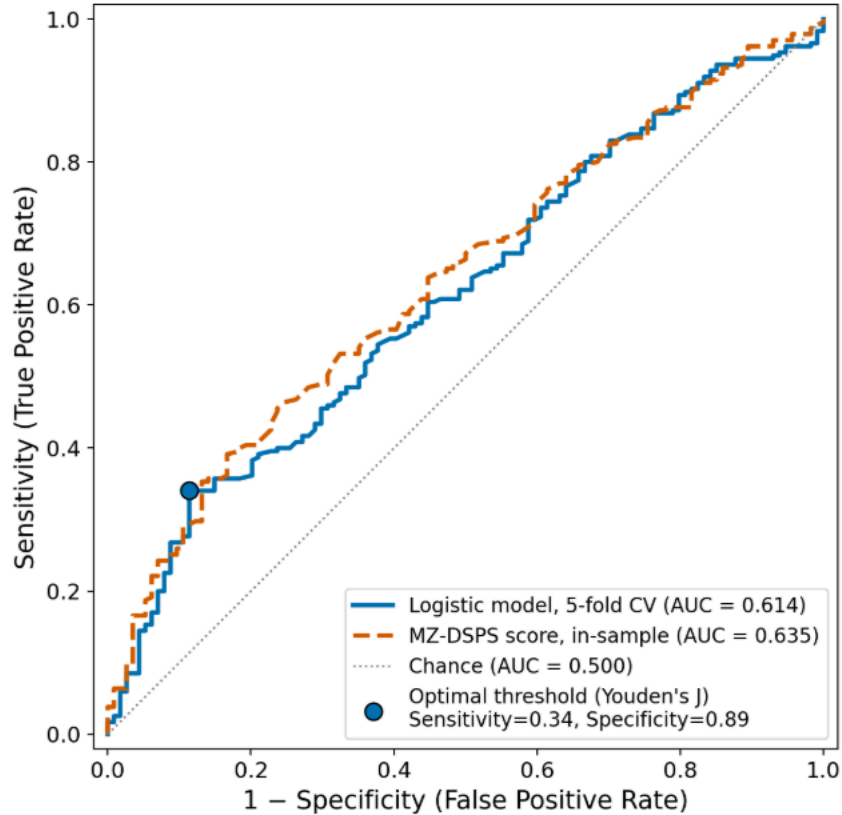


Figure 5 Receiver operating characteristic curves for above-median recorded daily milk yield. The solid curve is the five-fold cross-validated logistic model; the dashed curve is the apparent performance of the continuous full-sample rescaled score.

Supplementary Files

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